Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
1433B	AVTEQGHELSNEER	Yes	533.59	304.2	7.00	69.8	33.8	36751	ND	ND	No
1433B	AVTEQGHELSNEER	Yes	533.59	634.3	7.00	69.8	24.8	10858	ND	ND	No
1433B	AVTEQGHELSNEER	Yes	533.59	747.4	7.00	69.8	33.8	26988	ND	ND	No
1433B	AVTEQGHELSNEER	Yes	533.59	876.4	7.00	69.8	33.8	21485	ND	ND	No
1433B	DNLTLWTSENQGDEGDAGEGEN	No									
1433B	SELVQK	Yes	352.2	275.2	6.20	46.4	27	207881	ND	ND	No
1433B	SELVQK	Yes	352.2	374.2	6.20	46.4	18	213663	ND	ND	No
1433B	SELVQK	Yes	352.2	487.3	6.20	46.4	18	623035	ND	ND	No
1433B	SELVQK	Yes	352.2	616.4	6.20	46.4	18	56523	ND	ND	No
1433B	TAFDEAIAELDTLNEESYK	Yes	1080.01	635.3	23.79	140.3	50	4007	ND	ND	No
1433B	TAFDEAIAELDTLNEESYK	Yes	1080.01	748.4	23.79	140.3	47	3371	ND	ND	No
1433B	TAFDEAIAELDTLNEESYK	Yes	1080.01	769.3	23.79	140.3	53	2542	ND	ND	No
1433B	TAFDEAIAELDTLNEESYK	Yes	1080.01	983.5	23.79	140.3	50	2438	ND	ND	No
1433B	YLIPNATQPESK	Yes	680.86	277.2	11.89	88.8	32.5	1333499	ND	ND	No
1433B	YLIPNATQPESK	Yes	680.86	460.2	11.89	88.8	41.5	374275	ND	ND	No
1433B	YLIPNATQPESK	Yes	680.86	760.4	11.89	88.8	41.5	55070	ND	ND	No
1433B	YLIPNATQPESK	Yes	680.86	971.5	11.89	88.8	32.5	349158	ND	ND	No
1433E	AAFDDAIAELDTLSEESYK	Yes	1044.49	591.2	23.94	135.7	48.5	8029	ND	ND	No
1433E	AAFDDAIAELDTLSEESYK	Yes	1044.49	704.3	23.94	135.7	45.5	6261	ND	ND	No
1433E	AAFDDAIAELDTLSEESYK	Yes	1044.49	742.3	23.94	135.7	51.5	5181	ND	ND	No
1433E	AAFDDAIAELDTLSEESYK	Yes	1044.49	956.5	23.94	135.7	57.5	2357	ND	ND	No
1433E	EDLVYQAK	Yes	483.25	346.2	9.39	63.3	20.8	240157	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
1433E	EDLVYQAK	Yes	483.25	509.3	9.39	63.3	20.8	1127184	ND	ND	No
1433E	EDLVYQAK	Yes	483.25	608.3	9.39	63.3	23.8	296662	ND	ND	No
1433E	EDLVYQAK	Yes	483.25	721.4	9.39	63.3	23.8	96975	ND	ND	No
1433E	HLIPAANTGESK	Yes	619.33	251.2	7.96	80.9	32.8	482492	ND	ND	No
1433E	HLIPAANTGESK	Yes	619.33	364.2	7.96	80.9	29.8	277086	ND	ND	No
1433E	HLIPAANTGESK	Yes	619.33	874.4	7.96	80.9	32.8	230233	ND	ND	No
1433E	HLIPAANTGESK	Yes	619.33	987.5	7.96	80.9	29.8	72031	ND	ND	No
1433E	IISSIEQK	Yes	459.27	275.2	8.67	60.2	28.7	126673	ND	ND	No
1433E	IISSIEQK	Yes	459.27	604.3	8.67	60.2	22.7	52515	ND	ND	No
1433E	IISSIEQK	Yes	459.27	691.4	8.67	60.2	22.7	730425	ND	ND	No
1433E	IISSIEQK	Yes	459.27	804.4	8.67	60.2	22.7	80137	ND	ND	No
1433E	VFYYK	Yes	360.19	310.2	10.29	47.5	24.3	464492	ND	ND	No
1433E	VFYYK	Yes	360.19	473.2	10.29	47.5	18.3	384997	ND	ND	No
1433E	VFYYK	Yes	360.19	573.3	10.29	47.5	15.3	ND	ND	ND	No
1433E	VFYYK	Yes	360.19	620.3	10.29	47.5	18.3	253615	ND	ND	No
1433S	DNLTLWTADNAGEEGGEAPQEPQS	No									
1433S	EAGDAESR	Yes	417.68	262.2	5.24	54.9	20.9	59960	ND	ND	No
1433S	EAGDAESR	Yes	417.68	391.2	5.24	54.9	17.9	36302	ND	ND	No
1433S	EAGDAESR	Yes	417.68	462.2	5.24	54.9	17.9	29753	ND	ND	No
1433S	EAGDAESR	Yes	417.68	634.3	5.24	54.9	17.9	16749	ND	ND	No
1433S	LGLALNFSVFHYEIANSPEEAISLAK	No									
1433S	SNEEGSEEK	Yes	504.71	331.1	5.23	66.1	21.7	16881	ND	ND	No
1433S	SNEEGSEEK	Yes	504.71	549.3	5.23	66.1	24.7	65459	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
1433S	SNEEGSEEK	Yes	504.71	678.3	5.23	66.1	21.7	19026	ND	ND	No
1433S	SNEEGSEEK	Yes	504.71	807.3	5.23	66.1	24.7	50028	ND	ND	No
1433S	VLSSIEQK	Yes	452.26	517.3	8.22	59.3	31.4	42014	ND	31850	Yes (Based on Transition Ratios)
1433S	VLSSIEQK	Yes	452.26	604.3	8.22	59.3	22.4	76585	ND	7892	No
1433S	VLSSIEQK	Yes	452.26	691.4	8.22	59.3	22.4	702927	ND	155285	Yes (Based on Transition Ratios)
1433S	VLSSIEQK	Yes	452.26	804.4	8.22	59.3	22.4	99702	ND	6614	No
1433T	AVTEQGAELSNEER	Yes	766.9	1004.5	8.05	100	42.2	ND	ND	ND	No
1433T	AVTEQGAELSNEER	Yes	766.9	634.3	8.05	100	42.2	ND	ND	ND	No
1433T	AVTEQGAELSNEER	Yes	766.9	747.4	8.05	100	39.2	ND	ND	ND	No
1433T	AVTEQGAELSNEER	Yes	766.9	876.4	8.05	100	39.2	ND	ND	ND	No
1433T	EMQPTHPIR	Yes	554.8	360.7	9.80	100	29.9	ND	ND	ND	No
1433T	EMQPTHPIR	Yes	554.8	385.3	9.80	100	29.9	ND	ND	ND	No
1433T	EMQPTHPIR	Yes	554.8	522.3	9.80	100	29.9	ND	ND	ND	No
1433T	EMQPTHPIR	Yes	554.8	720.4	9.80	100	29.9	ND	ND	ND	No
1433T	QTIDNSQGAYQEAFDISK	Yes	1008	1100.5	17.80	100	49.9	ND	ND	ND	No
1433T	QTIDNSQGAYQEAFDISK	Yes	1008	1228.6	17.80	100	49.9	ND	ND	ND	No
1433T	QTIDNSQGAYQEAFDISK	Yes	1008	609.3	17.80	100	49.9	ND	ND	ND	No
1433T	QTIDNSQGAYQEAFDISK	Yes	1008	680.4	17.80	100	49.9	ND	ND	ND	No
1433T	TAFDEAIAELDTLNEDSYK	Yes	1073	1197.6	22.62	100	52.7	ND	7768	10484	No
1433T	TAFDEAIAELDTLNEDSYK	Yes	1073	748.352	22.62	100	46.7	ND	36045	22217	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
1433T	TAFDEAIAELDTLNEDSYK	Yes	1073	755.3	22.62	100	52.7	ND	33278	24614	No
1433T	TAFDEAIAELDTLNEDSYK	Yes	1073	969.453	22.62	100	58.7	ND	37538	20363	No
1433T	TAFDEAIAELDTLNEDSYK	Yes	715.7	1084.5	22.62	100	37	ND	ND	ND	No
1433T	TAFDEAIAELDTLNEDSYK	Yes	715.7	512.2	22.62	100	37	ND	ND	ND	No
1433T	TAFDEAIAELDTLNEDSYK	Yes	715.7	748.4	22.62	100	37	ND	ND	ND	No
1433T	TAFDEAIAELDTLNEDSYK	Yes	715.7	755.3	22.62	100	37	ND	ND	ND	No
1433T	YLIANATNPESK	Yes	660.8	1044.5	13.60	100	34.6	ND	ND	ND	No
1433T	YLIANATNPESK	Yes	660.8	675.3	13.60	100	34.6	ND	ND	ND	No
1433T	YLIANATNPESK	Yes	660.8	860.4	13.60	100	34.6	ND	ND	ND	No
1433T	YLIANATNPESK	Yes	660.8	931.4	13.60	100	34.6	ND	ND	ND	No
1433Z	FLIPNASQAESK	Yes	652.846	261.16	12.66	100	31.2	ND	33044	26867	No
1433Z	FLIPNASQAESK	Yes	652.846	466.2	12.66	100	34.2	ND	10712	25110	No
1433Z	FLIPNASQAESK	Yes	652.846	522.8	12.66	100	34.2	ND	2700	ND	No
1433Z	FLIPNASQAESK	Yes	652.846	931.448	12.66	100	28.2	ND	20492	18337	No
1433Z	GIVDQSQQAYQEAFEISK	Yes	1021	1114.5	20.50	100	50.4	ND	ND	ND	No
1433Z	GIVDQSQQAYQEAFEISK	Yes	1021	1185.6	20.50	100	50.4	ND	ND	ND	No
1433Z	GIVDQSQQAYQEAFEISK	Yes	1021	694.4	20.50	100	50.4	ND	ND	ND	No
1433Z	GIVDQSQQAYQEAFEISK	Yes	1021	951.5	20.50	100	50.4	ND	ND	ND	No
1433Z	SVTEQGAELSNEER	Yes	774.86	1004.46	8.32	100	39.6	ND	ND	ND	No
1433Z	SVTEQGAELSNEER	Yes	774.86	634.28	8.32	100	42.6	ND	ND	ND	No
1433Z	SVTEQGAELSNEER	Yes	774.86	747.4	8.32	100	39.6	ND	ND	ND	No
1433Z	SVTEQGAELSNEER	Yes	774.86	876.4	8.32	100	39.6	ND	ND	ND	No
1433Z	TAFDEAIAELDTLSEESYK	Yes	1066.5	1184.6	27.20	100	52.4	ND	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
1433Z	TAFDEAIAELDTLSEESYK	Yes	1066.5	655.3	27.20	100	52.4	ND	ND	ND	No
1433Z	TAFDEAIAELDTLSEESYK	Yes	1066.5	742.3	27.20	100	52.4	ND	ND	ND	No
1433Z	TAFDEAIAELDTLSEESYK	Yes	1066.5	956.5	27.20	100	52.4	ND	ND	ND	No
1433Z	TAFDEAIAELDTLSEESYK	Yes	711.3	639.3	27.20	100	36.8	ND	ND	ND	No
1433Z	TAFDEAIAELDTLSEESYK	Yes	711.3	655.3	27.20	100	36.8	ND	ND	ND	No
1433Z	TAFDEAIAELDTLSEESYK	Yes	711.3	742.3	27.20	100	36.8	ND	ND	ND	No
1433Z	TAFDEAIAELDTLSEESYK	Yes	711.3	748.4	27.20	100	36.8	ND	ND	ND	No
6PGD	AGQAVDDFIEK	Yes	596.796	523.7	11.96	100	31.8	ND	ND	5510	No
6PGD	AGQAVDDFIEK	Yes	596.796	766.4	11.96	100	31.8	ND	ND	3759	No
6PGD	AGQAVDDFIEK	Yes	596.796	865.431	11.96	100	28.8	ND	2995	7668	No
6PGD	AGQAVDDFIEK	Yes	596.796	936.468	11.96	100	28.8	ND	49595	42889	No
6PGD	HEMLPASLIQAQR	Yes	747.4	267.1	16.30	100	38.4	ND	ND	ND	No
6PGD	HEMLPASLIQAQR	Yes	747.4	398.2	16.30	100	38.4	ND	ND	ND	No
6PGD	HEMLPASLIQAQR	Yes	747.4	511.2	16.30	100	38.4	ND	ND	ND	No
6PGD	HEMLPASLIQAQR	Yes	747.4	983.6	16.30	100	38.4	ND	ND	ND	No
6PGD	LVPLLDTGDIIIDGGNSEYR	Yes	1080.56	1010.5	21.47	100	53	ND	11212	5787	No
6PGD	LVPLLDTGDIIIDGGNSEYR	Yes	1080.56	1123.5	21.47	100	53	ND	8014	8773	No
6PGD	LVPLLDTGDIIIDGGNSEYR	Yes	1080.56	897.37	21.47	100	53	ND	8601	18343	No
6PGD	LVPLLDTGDIIIDGGNSEYR	Yes	1080.56	974.487	21.47	100	47	ND	18249	11827	No
6PGD	YGPSLMPGGNK	Yes	560.8	450.7	14.10	100	30.2	ND	ND	ND	No
6PGD	YGPSLMPGGNK	Yes	560.8	472.3	14.10	100	30.2	ND	ND	ND	No
6PGD	YGPSLMPGGNK	Yes	560.8	603.3	14.10	100	30.2	ND	ND	ND	No
6PGD	YGPSLMPGGNK	Yes	560.8	803.4	14.10	100	30.2	ND	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
A1AG1	NWGLSVYADKPETTK	Yes	570.29	358.2	14.80	74.6	26.6	15161	ND	ND	No
A1AG1	NWGLSVYADKPETTK	Yes	570.29	703.4	14.80	74.6	35.6	19782	ND	ND	No
A1AG1	NWGLSVYADKPETTK	Yes	570.29	818.4	14.80	74.6	32.6	9017	ND	ND	No
A1AG1	NWGLSVYADKPETTK	Yes	570.29	889.5	14.80	74.6	32.6	13307	ND	ND	No
A1AG1	SVQEIQATFFYFTPNK	No									
A1AG1	TEDTIFLR	Yes	497.76	435.3	14.64	65.2	27.4	20543	ND	ND	No
A1AG1	TEDTIFLR	Yes	497.76	548.4	14.64	65.2	27.4	9853	ND	ND	No
A1AG1	TEDTIFLR	Yes	497.76	649.4	14.64	65.2	30.4	15459	ND	ND	No
A1AG1	TEDTIFLR	Yes	497.76	764.4	14.64	65.2	27.4	38060	ND	ND	No
A1AG1	WFYIASAFR	Yes	580.8	480.3	22.23	75.9	28.1	ND	7773	9038	Yes (Based on Manual Review)
A1AG1	WFYIASAFR	Yes	580.8	551.3	22.23	75.9	31.1	28779	22248	37207	No
A1AG1	WFYIASAFR	Yes	580.8	664.4	22.23	75.9	28.1	ND	12644	18958	Yes (Based on Manual Review)
A1AG1	WFYIASAFR	Yes	580.8	827.4	22.23	75.9	28.1	51249	30185	55344	No
A1AG1	YVGGQEHFAHLLILR	Yes	584.99	263.1	17.44	76.5	27.4	28795	36369	45277	No
A1AG1	YVGGQEHFAHLLILR	Yes	584.99	627.5	17.44	76.5	36.4	4721	12909	6516	No
A1AG1	YVGGQEHFAHLLILR	Yes	584.99	764.5	17.44	76.5	30.4	3629	8179	6390	No
A1AG1	YVGGQEHFAHLLILR	Yes	584.99	835.6	17.44	76.5	33.4	11539	10178	19375	No
ABCD1	DAGIALLSITHRPSLWK	Yes	626.69	357.2	20.27	81.8	26.5	16644	15695	26872	No
ABCD1	DAGIALLSITHRPSLWK	Yes	626.69	428.2	20.27	81.8	32.5	7326	64375	68949	Yes (Based on Transition Ratios)

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
ABCD1	DAGIALLSITHRPSLWK	Yes	626.69	741.4	20.27	81.8	32.5	1781	ND	5987	No
ABCD1	DAGIALLSITHRPSLWK	Yes	626.69	786.5	20.27	81.8	35.5	3234	5027	13975	No
ABCD1	ELEDAQAGSGTIGR	No									
ABCD1	GLQAPAGEPTQEASGVAAAK	Yes	618.32	370.2	10.56	80.8	26.1	48001	ND	ND	No
ABCD1	GLQAPAGEPTQEASGVAAAK	Yes	618.32	516.3	10.56	80.8	26.1	12249	ND	ND	No
ABCD1	GLQAPAGEPTQEASGVAAAK	Yes	618.32	674.4	10.56	80.8	38.1	11839	ND	ND	No
ABCD1	GLQAPAGEPTQEASGVAAAK	Yes	618.32	803.4	10.56	80.8	29.1	15535	ND	ND	No
ABCD1	NLLTAAADAIER	Yes	629.34	341.2	21.66	82.2	30.2	203667	ND	ND	No
ABCD1	NLLTAAADAIER	Yes	629.34	745.4	21.66	82.2	30.2	109727	ND	ND	No
ABCD1	NLLTAAADAIER	Yes	629.34	816.4	21.66	82.2	30.2	139616	ND	ND	No
ABCD1	NLLTAAADAIER	Yes	629.34	917.5	21.66	82.2	30.2	ND	ND	ND	Yes (Based on Manual Review)
ABCD1	YHTHLLQFDGEGGWK	Yes	596.62	447.2	15.82	78	28	26800	ND	ND	No
ABCD1	YHTHLLQFDGEGGWK	Yes	596.62	633.3	15.82	78	37	21885	ND	ND	No
ABCD1	YHTHLLQFDGEGGWK	Yes	596.62	748.3	15.82	78	28	17926	ND	ND	No
ABCD1	YHTHLLQFDGEGGWK	Yes	596.62	895.4	15.82	78	28	12723	ND	ND	No
ADA12	ADEVVSASVGSGDLWIPVK	Yes	965	316.1	19.65	125.5	51	7041	ND	ND	No
ADA12	ADEVVSASVGSGDLWIPVK	Yes	965	343.2	19.65	125.5	42	18438	ND	ND	No
ADA12	ADEVVSASVGSGDLWIPVK	Yes	965	415.2	19.65	125.5	51	4998	ND	ND	No
ADA12	ADEVVSASVGSGDLWIPVK	Yes	965	456.3	19.65	125.5	45	3289	ND	ND	No
ADA12	FGFGGSTDSGPIR	Yes	649.31	466.2	14.39	84.8	28.1	12510	ND	ND	No
ADA12	FGFGGSTDSGPIR	Yes	649.31	745.4	14.39	84.8	31.1	51191	ND	ND	No
ADA12	FGFGGSTDSGPIR	Yes	649.31	832.4	14.39	84.8	31.1	38987	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
ADA12	FGFGGSTDSGPIR	Yes	649.31	946.5	14.39	84.8	34.1	144144	ND	ND	No
ADA12	LIEIANHVDK	Yes	384.55	612.3	10.67	50.6	20.2	14646	ND	ND	No
ADA12	LIEIANHVDK	Yes	384.55	683.3	10.67	50.6	20.2	46832	ND	ND	No
ADA12	LIEIANHVDK	Yes	384.55	796.4	10.67	50.6	26.2	2603	ND	ND	No
ADA12	LIEIANHVDK	Yes	384.55	925.5	10.67	50.6	26.2	ND	ND	ND	No
ADA12	NHPEVLNIR	Yes	546.3	252.1	10.96	71.5	29.5	325509	ND	ND	No
ADA12	NHPEVLNIR	Yes	546.3	614.4	10.96	71.5	32.5	12196	ND	ND	No
ADA12	NHPEVLNIR	Yes	546.3	743.4	10.96	71.5	35.5	9577	ND	ND	No
ADA12	NHPEVLNIR	Yes	546.3	840.5	10.96	71.5	26.5	95971	ND	ND	No
ADA12	YVELVIVADNR	No									
ADML	LAHQIYQFTDK	Yes	455.24	363.2	12.05	59.7	20.8	197650	1284	7339	No
ADML	LAHQIYQFTDK	Yes	455.24	510.3	12.05	59.7	20.8	356558	6009	3578	No
ADML	LAHQIYQFTDK	Yes	455.24	563.3	12.05	59.7	20.8	174853	10798	5819	No
ADML	LAHQIYQFTDK	Yes	455.24	638.3	12.05	59.7	20.8	139796	ND	ND	No
ADML	SPEDSSPDAAR	Yes	566.25	529.3	5.66	74	33.4	58888	ND	ND	No
ADML	SPEDSSPDAAR	Yes	566.25	703.3	5.66	74	33.4	46261	ND	ND	No
ADML	SPEDSSPDAAR	Yes	566.25	818.4	5.66	74	27.4	41098	ND	ND	No
ADML	SPEDSSPDAAR	Yes	566.25	947.4	5.66	74	27.4	21671	ND	ND	No
ADML	TLVSSKPQAHGAPAPPSGSAPHFL	No									
AGR2	GWGDQLIWTQTYEEALYK	No									
AGR2	HLSPDGQYVPR	No									
AGR2	IPVSAFLLLVALSYTLAR	No									
AGR2	LAEQFVLLNLVYETTDK	No									

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
AGR2	LPQTLSR	No									
AIFM1	ALGTEVIQLFPEK	Yes	482.27	373.2	20.63	63.2	31.1	54144	ND	ND	No
AIFM1	ALGTEVIQLFPEK	Yes	482.27	520.3	20.63	63.2	19.1	15070	ND	ND	No
AIFM1	ALGTEVIQLFPEK	Yes	482.27	633.4	20.63	63.2	19.1	13609	ND	ND	No
AIFM1	ALGTEVIQLFPEK	Yes	482.27	761.4	20.63	63.2	22.1	15443	ND	ND	No
AIFM1	ELWFSDDPNVTK	Yes	725.85	429.2	17.45	94.6	31.4	140135	ND	ND	No
AIFM1	ELWFSDDPNVTK	Yes	725.85	558.3	17.45	94.6	43.4	348298	ND	ND	No
AIFM1	ELWFSDDPNVTK	Yes	725.85	788.4	17.45	94.6	34.4	73278	ND	ND	No
AIFM1	ELWFSDDPNVTK	Yes	725.85	875.4	17.45	94.6	34.4	232333	ND	ND	No
AIFM1	GVIFYLR	Yes	434.26	270.2	17.80	57	21.6	ND	ND	ND	Yes (Based on Manual Review)
AIFM1	GVIFYLR	Yes	434.26	288.2	17.80	57	21.6	ND	ND	ND	Yes (Based on Manual Review)
AIFM1	GVIFYLR	Yes	434.26	598.3	17.80	57	21.6	13864	6635	5858	No
AIFM1	GVIFYLR	Yes	434.26	711.4	17.80	57	18.6	8973	2165	670	No
AIFM1	LNDGSQITYEK	Yes	634.31	540.3	8.81	82.8	39.4	60447	ND	ND	No
AIFM1	LNDGSQITYEK	Yes	634.31	781.4	8.81	82.8	30.4	11909	ND	ND	No
AIFM1	LNDGSQITYEK	Yes	634.31	868.4	8.81	82.8	33.4	9914	ND	ND	No
AIFM1	LNDGSQITYEK	Yes	634.31	925.5	8.81	82.8	30.4	16224	ND	ND	No
AIFM1	TGGLEIDSDFGGFR	Yes	735.85	458.2	18.55	95.9	34.9	193086	ND	ND	No
AIFM1	TGGLEIDSDFGGFR	Yes	735.85	583.3	18.55	95.9	43.9	216289	ND	ND	No
AIFM1	TGGLEIDSDFGGFR	Yes	735.85	785.4	18.55	95.9	43.9	212035	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
AIFM1	TGGLEIDSDFGGFR	Yes	735.85	900.4	18.55	95.9	34.9	250017	ND	ND	No
ALDOA	ADDGRPFPQVIK	Yes	671.86	260.2	12.73	87.7	38.1	57232	ND	16752	No
ALDOA	ADDGRPFPQVIK	Yes	671.86	515.2	12.73	87.7	41.1	9951	ND	ND	No
ALDOA	ADDGRPFPQVIK	Yes	671.86	584.4	12.73	87.7	41.1	6634	ND	ND	No
ALDOA	ADDGRPFPQVIK	Yes	671.86	828.5	12.73	87.7	32.1	3715	ND	ND	No
ALDOA	ALQASALK	Yes	401.25	260.2	9.06	52.8	26.2	93337	ND	ND	No
ALDOA	ALQASALK	Yes	401.25	331.2	9.06	52.8	23.2	24128	2698	ND	No
ALDOA	ALQASALK	Yes	401.25	489.3	9.06	52.8	23.2	223049	16124	13040	No
ALDOA	ALQASALK	Yes	401.25	617.4	9.06	52.8	20.2	489365	32743	38710	No
ALDOA	GVVPLAGTNGETTTQGLDGLSER	No									
ALDOA	QLLLTADDR	Yes	522.79	355.2	12.69	68.4	25.5	25305	ND	ND	No
ALDOA	QLLLTADDR	Yes	522.79	577.3	12.69	68.4	25.5	57025	ND	ND	No
ALDOA	QLLLTADDR	Yes	522.79	690.3	12.69	68.4	28.5	38632	ND	ND	No
ALDOA	QLLLTADDR	Yes	522.79	803.4	12.69	68.4	25.5	34399	ND	ND	No
ALDOA	YTPSGQAGAAASESLFVSNHAY	No									
AMPN	ALEQALEK	Yes	451.25	276.2	9.58	59.2	31.4	216811	29554	24375	No
AMPN	ALEQALEK	Yes	451.25	389.2	9.58	59.2	31.4	188579	31830	24080	No
AMPN	ALEQALEK	Yes	451.25	588.3	9.58	59.2	22.4	228929	35778	16331	No
AMPN	ALEQALEK	Yes	451.25	717.4	9.58	59.2	22.4	821359	105037	77801	No
AMPN	DHSAIPVINR	Yes	374.54	402.2	10.85	49.3	19.7	116667	52211	38900	No
AMPN	DHSAIPVINR	Yes	374.54	411.2	10.85	49.3	19.7	84518	26157	38584	No
AMPN	DHSAIPVINR	Yes	374.54	524.2	10.85	49.3	16.7	92943	34489	29780	No
AMPN	DHSAIPVINR	Yes	374.54	598.4	10.85	49.3	25.7	20494	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
AMPN	ENSLLFDPLSSSSSNK	Yes	862.92	444.2	19.12	112.3	37.5	10118	ND	ND	No
AMPN	ENSLLFDPLSSSSSNK	Yes	862.92	557.3	19.12	112.3	37.5	11610	ND	ND	No
AMPN	ENSLLFDPLSSSSSNK	Yes	862.92	696.3	19.12	112.3	46.5	6571	ND	ND	No
AMPN	ENSLLFDPLSSSSSNK	Yes	862.92	906.5	19.12	112.3	43.5	30009	ND	ND	No
AMPN	EVVLQWFTENSK	Yes	740.38	348.2	21.23	96.5	44.1	9876	ND	ND	No
AMPN	EVVLQWFTENSK	Yes	740.38	477.2	21.23	96.5	44.1	5279	ND	ND	No
AMPN	EVVLQWFTENSK	Yes	740.38	578.3	21.23	96.5	35.1	13317	ND	ND	No
AMPN	EVVLQWFTENSK	Yes	740.38	911.4	21.23	96.5	35.1	20856	ND	1256	No
AMPN	SIQLPTTVR	Yes	507.8	329.2	13.27	66.5	24.8	100846	9370	10546	No
AMPN	SIQLPTTVR	Yes	507.8	573.3	13.27	66.5	24.8	92108	9816	18205	No
AMPN	SIQLPTTVR	Yes	507.8	686.4	13.27	66.5	24.8	29619	ND	ND	No
AMPN	SIQLPTTVR	Yes	507.8	814.5	13.27	66.5	24.8	36008	ND	ND	No
ANGP1	DAPHVEPDFSSQK	Yes	486.23	449.2	10.06	63.7	22.3	129411	ND	ND	No
ANGP1	DAPHVEPDFSSQK	Yes	486.23	596.3	10.06	63.7	22.3	121085	ND	ND	No
ANGP1	DAPHVEPDFSSQK	Yes	486.23	649.3	10.06	63.7	19.3	113401	ND	ND	No
ANGP1	DAPHVEPDFSSQK	Yes	486.23	808.4	10.06	63.7	22.3	41632	ND	ND	No
ANGP1	LEIQLLENSLSTYK	Yes	825.95	498.3	21.58	107.5	35.8	7726	ND	ND	No
ANGP1	LEIQLLENSLSTYK	Yes	825.95	597.4	21.58	107.5	38.8	11377	ND	ND	No
ANGP1	LEIQLLENSLSTYK	Yes	825.95	710.4	21.58	107.5	35.8	4332	ND	ND	No
ANGP1	LEIQLLENSLSTYK	Yes	825.95	941.5	21.58	107.5	38.8	10238	ND	ND	No
ANGP1	QLLQQTNEILK	Yes	664.38	355.2	14.79	86.7	31.7	13582	ND	ND	No
ANGP1	QLLQQTNEILK	Yes	664.38	616.4	14.79	86.7	28.7	5997	ND	ND	No
ANGP1	QLLQQTNEILK	Yes	664.38	717.4	14.79	86.7	31.7	8698	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
ANGP1	QLLQQTNEILK	Yes	664.38	973.5	14.79	86.7	34.7	5615	ND	ND	No
ANGP1	QSSLILHGADFSTK	Yes	501.93	335.2	13.86	65.7	29.1	17867	ND	ND	No
ANGP1	QSSLILHGADFSTK	Yes	501.93	597.3	13.86	65.7	32.1	7854	ND	ND	No
ANGP1	QSSLILHGADFSTK	Yes	501.93	725.3	13.86	65.7	26.1	23893	ND	ND	No
ANGP1	QSSLILHGADFSTK	Yes	501.93	862.4	13.86	65.7	32.1	10466	ND	ND	No
ANGP1	QTYIIQELEK	Yes	632.84	506.3	16.78	82.6	30.3	9552	ND	ND	No
ANGP1	QTYIIQELEK	Yes	632.84	518.3	16.78	82.6	39.3	37203	ND	ND	No
ANGP1	QTYIIQELEK	Yes	632.84	759.4	16.78	82.6	33.3	102064	ND	ND	No
ANGP1	QTYIIQELEK	Yes	632.84	872.5	16.78	82.6	30.3	26215	ND	ND	No
ANGP2	DAPLEYDDSVQR	Yes	704.32	284.1	10.77	91.9	36.5	57077	ND	ND	No
ANGP2	DAPLEYDDSVQR	Yes	704.32	303.2	10.77	91.9	30.5	9948	ND	ND	No
ANGP2	DAPLEYDDSVQR	Yes	704.32	604.3	10.77	91.9	42.5	22642	ND	ND	No
ANGP2	DAPLEYDDSVQR	Yes	704.32	882.4	10.77	91.9	33.5	26897	ND	ND	No
ANGP2	DQLQVLVSK	Yes	515.3	446.3	13.23	67.5	34.2	12065	ND	ND	No
ANGP2	DQLQVLVSK	Yes	515.3	545.4	13.23	67.5	25.2	17644	ND	ND	No
ANGP2	DQLQVLVSK	Yes	515.3	673.4	13.23	67.5	25.2	18383	ND	ND	No
ANGP2	DQLQVLVSK	Yes	515.3	786.5	13.23	67.5	25.2	24421	ND	ND	No
ANGP2	ISSISQPGNDFSTK	Yes	740.87	335.2	11.05	96.6	41.1	69610	1535	ND	No
ANGP2	ISSISQPGNDFSTK	Yes	740.87	616.3	11.05	96.6	32.1	133125	1528	ND	No
ANGP2	ISSISQPGNDFSTK	Yes	740.87	865.4	11.05	96.6	35.1	470480	3046	ND	No
ANGP2	ISSISQPGNDFSTK	Yes	740.87	993.5	11.05	96.6	35.1	24718	ND	ND	No
ANGP2	QILDQTSEINK	Yes	644.84	261.2	10.45	84.2	36.9	88150	ND	ND	No
ANGP2	QILDQTSEINK	Yes	644.84	691.4	10.45	84.2	30.9	27326	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
ANGP2	QILDQTSEINK	Yes	644.84	819.4	10.45	84.2	30.9	13209	ND	ND	No
ANGP2	QILDQTSEINK	Yes	644.84	934.4	10.45	84.2	30.9	13511	ND	ND	No
ANGP2	SSSSPYVSNAVQR	Yes	691.34	303.2	8.67	90.2	35.9	14376	ND	ND	No
ANGP2	SSSSPYVSNAVQR	Yes	691.34	402.2	8.67	90.2	38.9	8626	ND	ND	No
ANGP2	SSSSPYVSNAVQR	Yes	691.34	773.4	8.67	90.2	38.9	28945	ND	ND	No
ANGP2	SSSSPYVSNAVQR	Yes	691.34	936.5	8.67	90.2	38.9	10852	ND	ND	No
APOA1	AELQEGAR	Yes	437.23	303.2	6.08	57.4	30.7	32779	ND	ND	No
APOA1	AELQEGAR	Yes	437.23	314.2	6.08	57.4	21.7	18768	ND	ND	No
APOA1	AELQEGAR	Yes	437.23	560.3	6.08	57.4	21.7	41545	ND	ND	No
APOA1	AELQEGAR	Yes	437.23	673.4	6.08	57.4	21.7	42721	ND	ND	No
APOA1	AKPALEDLR	Yes	506.79	288.2	10.23	66.4	33.8	67547	413771	304672	No
APOA1	AKPALEDLR	Yes	506.79	645.4	10.23	66.4	33.8	6217	50728	54768	No
APOA1	AKPALEDLR	Yes	506.79	716.4	10.23	66.4	33.8	6215	44134	45365	No
APOA1	AKPALEDLR	Yes	506.79	813.4	10.23	66.4	24.8	27001	229473	181571	No
APOA1	ATEHLSTLSEK	Yes	405.88	363.2	8.09	53.4	24.2	152014	406460	283988	No
APOA1	ATEHLSTLSEK	Yes	405.88	577.3	8.09	53.4	21.2	43077	121335	100207	No
APOA1	ATEHLSTLSEK	Yes	405.88	664.4	8.09	53.4	24.2	63143	179229	136387	No
APOA1	ATEHLSTLSEK	Yes	405.88	777.4	8.09	53.4	18.2	24423	78358	64430	No
APOA1	LAEYHAK	Yes	277.82	355.2	5.91	36.8	17.7	12865	61357	53448	Yes (Based on Transition Ratios)
APOA1	LAEYHAK	Yes	277.82	518.3	5.91	36.8	14.7	90636	259261	199228	Yes (Based on Transition Ratios)

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
APOA1	LAEYHAK	Yes	277.82	647.3	5.91	36.8	20.7	ND	ND	ND	No
APOA1	LHELQEK	Yes	448.75	251.2	6.34	58.9	25.2	605787	205526	130878	No
APOA1	LHELQEK	Yes	448.75	380.2	6.34	58.9	31.2	206361	46453	34554	No
APOA1	LHELQEK	Yes	448.75	646.3	6.34	58.9	22.2	240611	48307	57299	No
APOA1	LHELQEK	Yes	448.75	750.4	6.34	58.9	22.2	23628	7049	ND	No
APOE	AATVGSLAGQPLQER	Yes	749.4	600.3	13.82	97.7	32.5	193679	433217	288301	No
APOE	AATVGSLAGQPLQER	Yes	749.4	642.4	13.82	97.7	35.5	917391	2100808	1423198	No
APOE	AATVGSLAGQPLQER	Yes	749.4	827.4	13.82	97.7	44.5	658628	1673309	1041481	No
APOE	AATVGSLAGQPLQER	Yes	749.4	898.5	13.82	97.7	38.5	588960	1516934	947242	No
APOE	ALMDETMK	Yes	469.72	508.2	12.19	61.6	32.2	324047	31280	30829	No
APOE	ALMDETMK	Yes	469.72	623.3	12.19	61.6	26.2	860928	86062	91743	No
APOE	ALMDETMK	Yes	469.72	754.3	12.19	61.6	23.2	3039940	316318	322057	No
APOE	ALMDETMK	Yes	469.72	867.4	12.19	61.6	26.2	132175	17359	15998	No
APOE	FWDYLR	No									
APOE	GEVQAMLGQSTEELR	Yes	824.4	616.3	17.92	107.3	38.8	160359	62735	51936	No
APOE	GEVQAMLGQSTEELR	Yes	824.4	729.4	17.92	107.3	38.8	172436	60538	57131	No
APOE	GEVQAMLGQSTEELR	Yes	824.4	734.4	17.92	107.3	41.8	128340	43162	66023	No
APOE	GEVQAMLGQSTEELR	Yes	824.4	919.4	17.92	107.3	47.8	329516	123116	112134	No
APOE	LAVYQAGAR	Yes	474.77	502.3	10.55	62.2	32.4	464439	1875459	1407023	No
APOE	LAVYQAGAR	Yes	474.77	665.3	10.55	62.2	26.4	858280	3581457	2409376	No
APOE	LAVYQAGAR	Yes	474.77	764.4	10.55	62.2	23.4	579284	2469472	1785851	No
APOE	LAVYQAGAR	Yes	474.77	835.4	10.55	62.2	26.4	272824	970277	670810	No
APOE	LGPLVEQGR	Yes	484.78	588.3	12.27	63.5	29.8	1255147	8739975	5413619	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
APOE	LGPLVEQGR	Yes	484.78	701.4	12.27	63.5	32.8	548143	3552824	2229051	No
APOE	LGPLVEQGR	Yes	484.78	798.4	12.27	63.5	32.8	153891	971776	653830	No
APOE	LGPLVEQGR	Yes	484.78	855.5	12.27	63.5	32.8	245430	1710796	1027637	No
APOE	SELEEQLTPVAEETR	Yes	865.93	459.2	15.38	112.7	46.6	98957	41157	37671	No
APOE	SELEEQLTPVAEETR	Yes	865.93	801.4	15.38	112.7	40.6	480014	182608	232636	No
APOE	SELEEQLTPVAEETR	Yes	865.93	902.5	15.38	112.7	40.6	282948	111473	128210	No
APOE	SELEEQLTPVAEETR	Yes	865.93	930.4	15.38	112.7	37.6	110336	38737	44588	No
APOE	SWFEPLVEDMQR	Yes	768.86	274.1	23.75	100.2	45.3	890677	451999	340770	No
APOE	SWFEPLVEDMQR	Yes	768.86	421.2	23.75	100.2	36.3	334159	193086	151397	No
APOE	SWFEPLVEDMQR	Yes	768.86	678.3	23.75	100.2	39.3	146920	88778	58862	No
APOE	SWFEPLVEDMQR	Yes	768.86	987.5	23.75	100.2	45.3	480159	235966	169565	No
APOE	WELALGR	Yes	422.74	316.1	18.36	55.5	21.1	403709	887870	1003357	No
APOE	WELALGR	Yes	422.74	345.2	18.36	55.5	30.1	137633	217482	265039	No
APOE	WELALGR	Yes	422.74	529.3	18.36	55.5	21.1	531586	1582080	1347490	No
APOE	WELALGR	Yes	422.74	658.4	18.36	55.5	30.1	276357	664598	673060	No
APOE	WVQTLSEQVQEELLSSQVTQELR	No									
ASM3B	EIEPEPDFILWTGDDTPHVPDEK	Yes	893.75	276.2	21.52	116.3	40.1	4054	ND	ND	No
ASM3B	EIEPEPDFILWTGDDTPHVPDEK	Yes	893.75	372.2	21.52	116.3	43.1	3423	ND	ND	No
ASM3B	EIEPEPDFILWTGDDTPHVPDEK	Yes	893.75	488.2	21.52	116.3	46.1	14160	ND	ND	No
ASM3B	EIEPEPDFILWTGDDTPHVPDEK	Yes	893.75	821.4	21.52	116.3	49.1	2901	ND	ND	No
ASM3B	FWHIADLHLDPDYK	Yes	885.44	310.2	19.64	115.2	50.5	15815	ND	ND	No
ASM3B	FWHIADLHLDPDYK	Yes	885.44	471.2	19.64	115.2	44.5	15824	ND	ND	No
ASM3B	FWHIADLHLDPDYK	Yes	885.44	522.3	19.64	115.2	47.5	23658	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
ASM3B	FWHIADLHLDPDYK	Yes	885.44	637.3	19.64	115.2	47.5	3772	ND	ND	No
ASM3B	IAGDQSTLQR	Yes	544.79	604.3	6.99	71.3	35.5	13771	ND	ND	No
ASM3B	IAGDQSTLQR	Yes	544.79	732.4	6.99	71.3	35.5	10240	ND	ND	No
ASM3B	IAGDQSTLQR	Yes	544.79	904.4	6.99	71.3	26.5	25293	ND	ND	No
ASM3B	IAGDQSTLQR	Yes	544.79	975.5	6.99	71.3	26.5	11561	ND	ND	No
ASM3B	LGEAAVLEIVER	Yes	649.87	999.6	19.54	84.8	37.1	13209	ND	ND	No
ASM3B	LGEAAVLEIVER	Yes	649.87	516.3	19.54	84.8	28.1	10637	ND	ND	No
ASM3B	LGEAAVLEIVER	Yes	649.87	758.4	19.54	84.8	31.1	45939	ND	ND	No
ASM3B	LGEAAVLEIVER	Yes	649.87	857.5	19.54	84.8	31.1	28698	ND	ND	No
ASM3B	VIAGQFFGHHHTDSFR	No									
AT2A2	AEIGIAMGSGTAVAK	Yes	688.4	555.3	15.70	100	35.8	ND	ND	ND	No
AT2A2	AEIGIAMGSGTAVAK	Yes	688.4	633.4	15.70	100	35.8	ND	ND	ND	No
AT2A2	AEIGIAMGSGTAVAK	Yes	688.4	821.4	15.70	100	35.8	ND	ND	ND	No
AT2A2	AEIGIAMGSGTAVAK	Yes	688.4	892.5	15.70	100	35.8	ND	ND	ND	No
AT2A2	IGIFGQDEDVTSK	Yes	704.9	1125.5	17.20	100	36.5	ND	ND	ND	No
AT2A2	IGIFGQDEDVTSK	Yes	704.9	335.2	17.20	100	36.5	ND	25549	ND	No
AT2A2	IGIFGQDEDVTSK	Yes	704.9	793.4	17.20	100	36.5	ND	171814	ND	No
AT2A2	IGIFGQDEDVTSK	Yes	704.9	978.4	17.20	100	36.5	ND	2018	ND	No
AT2A2	NMLFSGTNIAAGK	Yes	662.3	359.2	17.70	100	34.6	ND	ND	ND	No
AT2A2	NMLFSGTNIAAGK	Yes	662.3	731.4	17.70	100	34.6	ND	ND	ND	No
AT2A2	NMLFSGTNIAAGK	Yes	662.3	818.4	17.70	100	34.6	ND	ND	ND	No
AT2A2	NMLFSGTNIAAGK	Yes	662.3	965.5	17.70	100	34.6	ND	ND	ND	No
ATS1	ASFGSGPAVEWIPK	Yes	723.38	357.3	18.43	94.3	34.3	104905	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
ATS1	ASFGSGPAVEWIPK	Yes	723.38	543.3	18.43	94.3	34.3	38197	ND	ND	No
ATS1	ASFGSGPAVEWIPK	Yes	723.38	939.5	18.43	94.3	34.3	89861	ND	ND	No
ATS1	ASFGSGPAVEWIPK	Yes	723.38	996.6	18.43	94.3	34.3	86229	ND	ND	No
ATS1	GAFYLLGEAYFIQPLPAASER	Yes	1157.1	552.3	24.55	150.3	50.4	24102	ND	ND	No
ATS1	GAFYLLGEAYFIQPLPAASER	Yes	1157.1	630.3	24.55	150.3	50.4	48873	ND	ND	No
ATS1	GAFYLLGEAYFIQPLPAASER	Yes	1157.1	840.5	24.55	150.3	53.4	88743	ND	ND	No
ATS1	GAFYLLGEAYFIQPLPAASER	Yes	1157.1	968.5	24.55	150.3	50.4	41295	ND	ND	No
ATS1	GIGYFFVLQPK	Yes	634.86	485.3	22.47	82.9	30.4	23844	ND	ND	No
ATS1	GIGYFFVLQPK	Yes	634.86	584.4	22.47	82.9	30.4	33265	ND	ND	No
ATS1	GIGYFFVLQPK	Yes	634.86	731.4	22.47	82.9	30.4	49849	ND	ND	No
ATS1	GIGYFFVLQPK	Yes	634.86	878.5	22.47	82.9	27.4	65175	ND	ND	No
ATS1	GPEVTSNAALTLR	Yes	664.86	284.1	12.86	86.8	37.8	83180	ND	ND	No
ATS1	GPEVTSNAALTLR	Yes	664.86	758.5	12.86	86.8	31.8	7469	ND	ND	No
ATS1	GPEVTSNAALTLR	Yes	664.86	845.5	12.86	86.8	34.8	12494	ND	ND	No
ATS1	GPEVTSNAALTLR	Yes	664.86	946.5	12.86	86.8	31.8	13212	ND	ND	No
ATS1	HYLLTLFSVAAR	No									
ATS12	EGSGYVDIGLIPK	Yes	674.36	357.3	17.33	88	29.2	217810	ND	ND	No
ATS12	EGSGYVDIGLIPK	Yes	674.36	527.4	17.33	88	32.2	179513	ND	ND	No
ATS12	EGSGYVDIGLIPK	Yes	674.36	755.5	17.33	88	32.2	315214	ND	ND	No
ATS12	EGSGYVDIGLIPK	Yes	674.36	854.5	17.33	88	32.2	192788	ND	ND	No
ATS12	LILLEEEEQGLK	Yes	707.4	340.3	17.76	92.3	33.6	324526	ND	ND	No
ATS12	LILLEEEEQGLK	Yes	707.4	574.3	17.76	92.3	42.6	47451	ND	ND	No
ATS12	LILLEEEEQGLK	Yes	707.4	832.4	17.76	92.3	33.6	93496	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
ATS12	LILLEEEEQGLK	Yes	707.4	961.4	17.76	92.3	33.6	121003	ND	ND	No
ATS12	QLQYDPTPLTWSK	Yes	788.9	370.2	16.73	102.8	37.2	61555	ND	ND	No
ATS12	QLQYDPTPLTWSK	Yes	788.9	521.3	16.73	102.8	46.2	30947	ND	ND	No
ATS12	QLQYDPTPLTWSK	Yes	788.9	731.4	16.73	102.8	46.2	51537	ND	ND	No
ATS12	QLQYDPTPLTWSK	Yes	788.9	929.5	16.73	102.8	37.2	55517	ND	ND	No
ATS12	QWQDSSTQPELSSR	Yes	824.88	315.1	10.37	107.4	47.8	3016	ND	ND	No
ATS12	QWQDSSTQPELSSR	Yes	824.88	349.2	10.37	107.4	38.8	6269	ND	ND	No
ATS12	QWQDSSTQPELSSR	Yes	824.88	688.4	10.37	107.4	44.8	13909	ND	ND	No
ATS12	QWQDSSTQPELSSR	Yes	824.88	917.5	10.37	107.4	38.8	1500	ND	ND	No
ATS12	WVETLVVADTK	Yes	630.85	286.2	15.87	82.4	30.3	40124	28863	35082	Yes (Based on Transition Ratios)
ATS12	WVETLVVADTK	Yes	630.85	533.3	15.87	82.4	39.3	11647	28346	22495	Yes (Based on Transition Ratios)
ATS12	WVETLVVADTK	Yes	630.85	846.5	15.87	82.4	30.3	4577	ND	ND	No
ATS12	WVETLVVADTK	Yes	630.85	975.5	15.87	82.4	30.3	7920	ND	ND	No
ATS19	EQPILLSEK	Yes	528.8	258.1	12.44	69.2	25.8	644654	ND	ND	No
ATS19	EQPILLSEK	Yes	528.8	476.3	12.44	69.2	25.8	165208	ND	ND	No
ATS19	EQPILLSEK	Yes	528.8	589.4	12.44	69.2	34.8	326760	ND	ND	No
ATS19	EQPILLSEK	Yes	528.8	799.5	12.44	69.2	25.8	833853	ND	ND	No
ATS19	GQNLGDVSWSR	No									
ATS19	LRPPPPSEGEEDEELESQELPR	Yes	845.07	270.2	12.90	110	43.6	45680	ND	ND	No
ATS19	LRPPPPSEGEEDEELESQELPR	Yes	845.07	272.2	12.90	110	37.6	106618	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
ATS19	LRPPPPSEGEEDEELESQELPR	Yes	845.07	642.4	12.90	110	43.6	6934	ND	ND	No
ATS19	LRPPPPSEGEEDEELESQELPR	Yes	845.07	971.5	12.90	110	43.6	10641	ND	ND	No
ATS19	NISIVDNEK	Yes	516.27	390.2	10.17	67.6	34.2	30211	ND	ND	No
ATS19	NISIVDNEK	Yes	516.27	604.3	10.17	67.6	25.2	31720	ND	ND	No
ATS19	NISIVDNEK	Yes	516.27	717.4	10.17	67.6	22.2	15456	ND	ND	No
ATS19	NISIVDNEK	Yes	516.27	804.4	10.17	67.6	25.2	138315	ND	ND	No
ATS19	SVAPVPLEEPVEGR	Yes	739.9	355.2	13.49	96.4	38.1	41872	ND	ND	No
ATS19	SVAPVPLEEPVEGR	Yes	739.9	454.3	13.49	96.4	32.1	62181	ND	ND	No
ATS19	SVAPVPLEEPVEGR	Yes	739.9	557.3	13.49	96.4	44.1	46254	ND	ND	No
ATS19	SVAPVPLEEPVEGR	Yes	739.9	815.4	13.49	96.4	44.1	36042	ND	ND	No
BAGE1	AVFLALSAQLLQAR	No									
BAGE1	EESPVVSWR	Yes	544.77	448.2	13.13	71.3	26.5	14288	ND	ND	No
BAGE1	EESPVVSWR	Yes	544.77	646.4	13.13	71.3	23.5	2497	ND	ND	No
BAGE1	EESPVVSWR	Yes	544.77	743.4	13.13	71.3	35.5	6164	ND	ND	No
BAGE1	EESPVVSWR	Yes	544.77	830.5	13.13	71.3	35.5	2621	ND	ND	No
BAGE2	EESPVVSWR	Yes	544.77	448.2	13.13	71.3	26.5	14288	ND	ND	No
BAGE2	EESPVVSWR	Yes	544.77	646.4	13.13	71.3	23.5	2497	ND	ND	No
BAGE2	EESPVVSWR	Yes	544.77	743.4	13.13	71.3	35.5	6164	ND	ND	No
BAGE2	EESPVVSWR	Yes	544.77	830.5	13.13	71.3	35.5	2621	ND	ND	No
BAGE3	EESPVVSWR	Yes	544.77	448.2	13.13	71.3	26.5	14288	ND	ND	No
BAGE3	EESPVVSWR	Yes	544.77	646.4	13.13	71.3	23.5	2497	ND	ND	No
BAGE3	EESPVVSWR	Yes	544.77	743.4	13.13	71.3	35.5	6164	ND	ND	No
BAGE3	EESPVVSWR	Yes	544.77	830.5	13.13	71.3	35.5	2621	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
BAGE4	EESPVVSWWLEPEDGTAL	No									
BAGE5	EESPVVSWR	Yes	544.77	448.2	13.13	71.3	26.5	14288	ND	ND	No
BAGE5	EESPVVSWR	Yes	544.77	646.4	13.13	71.3	23.5	2497	ND	ND	No
BAGE5	EESPVVSWR	Yes	544.77	743.4	13.13	71.3	35.5	6164	ND	ND	No
BAGE5	EESPVVSWR	Yes	544.77	830.5	13.13	71.3	35.5	2621	ND	ND	No
BASP1	AAEAAAAPAESAAPAAGEEPSK	Yes	983.97	414.2	9.12	127.9	51.8	143621	ND	ND	No
BASP1	AAEAAAAPAESAAPAAGEEPSK	Yes	983.97	485.2	9.12	127.9	48.8	329148	ND	ND	No
BASP1	AAEAAAAPAESAAPAAGEEPSK	Yes	983.97	556.3	9.12	127.9	42.8	580012	ND	ND	No
BASP1	AAEAAAAPAESAAPAAGEEPSK	Yes	983.97	885.4	9.12	127.9	54.8	148879	ND	ND	No
BASP1	AEGAATEEEGTPK	Yes	645.3	258.1	6.68	84.2	39.9	577396	ND	ND	No
BASP1	AEGAATEEEGTPK	Yes	645.3	789.4	6.68	84.2	33.9	210898	ND	ND	No
BASP1	AEGAATEEEGTPK	Yes	645.3	890.4	6.68	84.2	30.9	341863	ND	ND	No
BASP1	AEGAATEEEGTPK	Yes	645.3	961.4	6.68	84.2	30.9	234980	ND	ND	No
BASP1	APEQEQAAPGPAAGGEAPK	Yes	592.62	629.3	8.19	77.4	33.8	134390	ND	ND	No
BASP1	APEQEQAAPGPAAGGEAPK	Yes	592.62	754.3	8.19	77.4	27.8	109555	ND	ND	No
BASP1	APEQEQAAPGPAAGGEAPK	Yes	592.62	825.4	8.19	77.4	24.8	350900	ND	ND	No
BASP1	APEQEQAAPGPAAGGEAPK	Yes	592.62	951.5	8.19	77.4	27.8	94107	ND	ND	No
BASP1	AQGPAASAEEPKPVEAPAANSDQTVTVK	No									
BASP1	EKPDQDAEGK	Yes	558.76	404.2	5.86	73.1	36.1	58731	ND	ND	No
BASP1	EKPDQDAEGK	Yes	558.76	647.3	5.86	73.1	36.1	40234	ND	ND	No
BASP1	EKPDQDAEGK	Yes	558.76	859.4	5.86	73.1	30.1	452533	ND	ND	No
BASP1	EKPDQDAEGK	Yes	558.76	913.4	5.86	73.1	30.1	8714	ND	ND	No
BASP1	ESEPQAAAEPAEAK	Yes	714.34	515.3	7.80	93.1	42.9	499201	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
BASP1	ESEPQAAAEPAEAK	Yes	714.34	644.3	7.80	93.1	36.9	125610	ND	ND	No
BASP1	ESEPQAAAEPAEAK	Yes	714.34	786.4	7.80	93.1	33.9	308021	ND	ND	No
BASP1	ESEPQAAAEPAEAK	Yes	714.34	857.4	7.80	93.1	42.9	310099	ND	ND	No
BASP1	ETPAATEAPSSTPK	Yes	693.84	616.3	7.70	90.5	42	528487	2285	1294	No
BASP1	ETPAATEAPSSTPK	Yes	693.84	816.4	7.70	90.5	33	312266	656	970	No
BASP1	ETPAATEAPSSTPK	Yes	693.84	917.5	7.70	90.5	33	528706	1763	1960	No
BASP1	ETPAATEAPSSTPK	Yes	693.84	988.5	7.70	90.5	39	292104	705	863	No
BASP1	GYNVNDEK	Yes	469.71	276.2	7.25	61.6	32.2	188398	ND	ND	No
BASP1	GYNVNDEK	Yes	469.71	505.2	7.25	61.6	26.2	259493	ND	ND	No
BASP1	GYNVNDEK	Yes	469.71	604.3	7.25	61.6	23.2	275282	ND	ND	No
BASP1	GYNVNDEK	Yes	469.71	718.3	7.25	61.6	23.2	659710	ND	ND	No
BASP1	SDGAPASDSKPGSSEAAPSSK	Yes	644.96	260.1	6.28	84.2	36.4	52850	ND	ND	No
BASP1	SDGAPASDSKPGSSEAAPSSK	Yes	644.96	331.1	6.28	84.2	27.4	38204	ND	ND	No
BASP1	SDGAPASDSKPGSSEAAPSSK	Yes	644.96	418.2	6.28	84.2	36.4	15204	ND	ND	No
BASP1	SDGAPASDSKPGSSEAAPSSK	Yes	644.96	586.2	6.28	84.2	33.4	7243	ND	ND	No
BASP1	TEAPAAPAAQETK	Yes	642.83	541.3	7.39	83.9	27.8	1121835	ND	ND	No
BASP1	TEAPAAPAAQETK	Yes	642.83	744.4	7.39	83.9	33.8	2198989	ND	ND	No
BASP1	TEAPAAPAAQETK	Yes	642.83	815.4	7.39	83.9	39.8	677726	ND	ND	No
BASP1	TEAPAAPAAQETK	Yes	642.83	983.5	7.39	83.9	30.8	1128052	ND	ND	No
BAX	TGALLLQGFIQDR	Yes	716.4	343.2	21.64	93.4	34	15777	ND	ND	No
BAX	TGALLLQGFIQDR	Yes	716.4	456.3	21.64	93.4	34	14444	ND	ND	No
BAX	TGALLLQGFIQDR	Yes	716.4	863.4	21.64	93.4	34	16541	ND	ND	No
BAX	TGALLLQGFIQDR	Yes	716.4	976.5	21.64	93.4	34	12140	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
BAX	VPELIR	Yes	363.73	288.2	11.73	47.9	27.5	11353	ND	ND	No
BAX	VPELIR	Yes	363.73	401.3	11.73	47.9	27.5	67820	ND	ND	No
BAX	VPELIR	Yes	363.73	530.3	11.73	47.9	21.5	37218	ND	ND	No
BAX	VPELIR	Yes	363.73	627.4	11.73	47.9	18.5	35485	ND	ND	No
BAX	VVALFYFASK	Yes	572.82	270.2	21.69	74.9	24.7	9531	ND	ND	No
BAX	VVALFYFASK	Yes	572.82	762.4	21.69	74.9	27.7	4998	ND	ND	No
BAX	VVALFYFASK	Yes	572.82	875.5	21.69	74.9	27.7	3626	ND	ND	No
BAX	VVALFYFASK	Yes	572.82	946.5	21.69	74.9	27.7	7553	ND	ND	No
BDNF	DADLYTSR	Yes	470.72	363.2	8.19	61.7	20.2	57153	ND	ND	No
BDNF	DADLYTSR	Yes	470.72	526.3	8.19	61.7	20.2	86079	ND	ND	No
BDNF	DADLYTSR	Yes	470.72	639.3	8.19	61.7	23.2	24078	ND	ND	No
BDNF	DADLYTSR	Yes	470.72	754.4	8.19	61.7	20.2	52638	ND	ND	No
BDNF	GLTSLADTFEHVIEELLDEDQK	No									
BDNF	GQGGLAYPGVR	No									
BDNF	QYFYETK	Yes	489.73	377.2	10.86	64.2	24	60836	ND	ND	No
BDNF	QYFYETK	Yes	489.73	540.3	10.86	64.2	24	83319	ND	ND	No
BDNF	QYFYETK	Yes	489.73	687.3	10.86	64.2	24	42666	ND	ND	No
BDNF	QYFYETK	Yes	489.73	850.4	10.86	64.2	27	6672	ND	ND	No
BDNF	THGTLESVNGPK	Yes	413.88	301.2	7.36	54.4	15.7	67027	4909	ND	No
BDNF	THGTLESVNGPK	Yes	413.88	510.3	7.36	54.4	18.7	67543	2892	ND	No
BDNF	THGTLESVNGPK	Yes	413.88	601.3	7.36	54.4	18.7	98557	1911	ND	No
BDNF	THGTLESVNGPK	Yes	413.88	726.3	7.36	54.4	18.7	12288	6676	12782	Yes (Based on Transition Ratios)

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
BGH3	ADHHATNGVVHLIDK	Yes	542.95	262.1	10.26	71	34.2	28820	ND	ND	No
BGH3	ADHHATNGVVHLIDK	Yes	542.95	488.3	10.26	71	28.2	12521	ND	ND	No
BGH3	ADHHATNGVVHLIDK	Yes	542.95	625.4	10.26	71	28.2	17203	ND	ND	No
BGH3	ADHHATNGVVHLIDK	Yes	542.95	724.4	10.26	71	28.2	13432	ND	ND	No
BGH3	DILATNGVIHYIDELLIPDSAK	Yes	804.1	305.2	24.70	104.7	47.6	11267	ND	ND	No
BGH3	DILATNGVIHYIDELLIPDSAK	Yes	804.1	514.3	24.70	104.7	41.6	4269	ND	ND	No
BGH3	DILATNGVIHYIDELLIPDSAK	Yes	804.1	517.3	24.70	104.7	41.6	35541	ND	ND	No
BGH3	DILATNGVIHYIDELLIPDSAK	Yes	804.1	630.3	24.70	104.7	38.6	14272	ND	ND	No
BGH3	EGVYTVFAPTNEAFR	No									
BGH3	LTLLAPLNSVFK	Yes	658.4	328.2	24.36	85.9	28.5	365500	25531	16110	No
BGH3	LTLLAPLNSVFK	Yes	658.4	804.5	24.36	85.9	31.5	1113116	47343	33102	No
BGH3	LTLLAPLNSVFK	Yes	658.4	875.5	24.36	85.9	31.5	558825	24161	29607	No
BGH3	LTLLAPLNSVFK	Yes	658.4	988.6	24.36	85.9	31.5	202592	11767	11877	No
BGH3	SPYQLVLQHSR	Yes	443.24	527.3	13.01	58.2	23.2	18749	73709	77319	No
BGH3	SPYQLVLQHSR	Yes	443.24	589.3	13.01	58.2	23.2	5117	19906	19298	No
BGH3	SPYQLVLQHSR	Yes	443.24	640.4	13.01	58.2	26.2	21391	100486	104425	No
BGH3	SPYQLVLQHSR	Yes	443.24	852.5	13.01	58.2	29.2	5538	22051	24502	No
BMP2	INIYEIIKPATANSK	Yes	558.99	633.3	18.23	73.1	29.1	6734	ND	ND	No
BMP2	INIYEIIKPATANSK	Yes	558.99	688.4	18.23	73.1	29.1	37408	ND	ND	No
BMP2	INIYEIIKPATANSK	Yes	558.99	816.5	18.23	73.1	35.1	13041	ND	ND	No
BMP2	INIYEIIKPATANSK	Yes	558.99	929.5	18.23	73.1	35.1	3967	ND	ND	No
BMP2	LVNQNASR	Yes	451.25	333.2	5.48	59.2	31.4	9208	1450	ND	No
BMP2	LVNQNASR	Yes	451.25	575.3	5.48	59.2	22.4	12431	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
BMP2	LVNQNASR	Yes	451.25	689.3	5.48	59.2	22.4	73899	ND	ND	No
BMP2	LVNQNASR	Yes	451.25	788.4	5.48	59.2	25.4	12363	ND	ND	No
BMP2	SFHHEESLEELPETSGK	Yes	978.45	372.2	11.14	127.2	48.6	5663	ND	ND	No
BMP2	SFHHEESLEELPETSGK	Yes	978.45	509.2	11.14	127.2	51.6	2913	ND	ND	No
BMP2	SFHHEESLEELPETSGK	Yes	978.45	618.3	11.14	127.2	51.6	9441	ND	ND	No
BMP2	SFHHEESLEELPETSGK	Yes	978.45	638.3	11.14	127.2	54.6	3741	ND	ND	No
BMP2	SLHQDEHSWSQIRPLLVTFGHDGK	No									
BMP2	WTAQGHANHGFVVEVAHLEEK	No									
BST1	AGLIIPLFLVLASR	No									
BST1	ALLSPEQR	No									
BST1	DIFLGR	No									
BST1	GEGTSAHLR	Yes	464.24	425.3	7.68	60.9	19.9	ND	ND	ND	No
BST1	GEGTSAHLR	Yes	464.24	496.3	7.68	60.9	19.9	ND	ND	ND	No
BST1	GEGTSAHLR	Yes	464.24	583.3	7.68	60.9	25.9	ND	ND	ND	No
BST1	GEGTSAHLR	Yes	464.24	741.4	7.68	60.9	28.9	ND	ND	ND	No
BST1	GFFADYEIPNLQK	Yes	771.39	352.2	20.02	100.5	33.4	191481	9485	21580	No
BST1	GFFADYEIPNLQK	Yes	771.39	599.4	20.02	100.5	36.4	337667	24688	26520	No
BST1	GFFADYEIPNLQK	Yes	771.39	712.4	20.02	100.5	36.4	ND	ND	7642	Yes (Based on Manual Review)
BST1	GFFADYEIPNLQK	Yes	771.39	841.5	20.02	100.5	33.4	109775	ND	11836	No
C163A	EAEFGQGTGPIWLNEVK	Yes	937.97	489.3	19.66	122	40.8	33563	ND	ND	No
C163A	EAEFGQGTGPIWLNEVK	Yes	937.97	602.4	19.66	122	43.8	29802	ND	ND	No
C163A	EAEFGQGTGPIWLNEVK	Yes	937.97	788.4	19.66	122	40.8	40477	ND	ND	No

Table S5. MRM assay of individual proteins.											
Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
C163A	EAEFGQGTGPIWLNEVK	Yes	937.97	998.6	19.66	122	43.8	11610	ND	ND	No
C163A	GENLVHQIQYR	Yes	678.85	301.1	11.60	88.6	41.4	12455	ND	ND	No
C163A	GENLVHQIQYR	Yes	678.85	414.2	11.60	88.6	41.4	3665	ND	ND	No
C163A	GENLVHQIQYR	Yes	678.85	707.4	11.60	88.6	35.4	ND	ND	ND	No
C163A	GENLVHQIQYR	Yes	678.85	844.4	11.60	88.6	35.4	3301	ND	ND	No
C163A	INPASLDK	Yes	429.24	462.3	9.15	56.4	27.4	ND	13797	12386	Yes (Based on Manual Review)
C163A	INPASLDK	Yes	429.24	533.3	9.15	56.4	30.4	ND	14940	25923	Yes (Based on Manual Review)
C163A	INPASLDK	Yes	429.24	630.3	9.15	56.4	21.4	1226484	107772	132639	No
C163A	INPASLDK	Yes	429.24	744.4	9.15	56.4	21.4	120340	11977	12440	No
C163A	LEVFYNGAWGTVGK	Yes	770.89	303.2	18.50	100.4	33.4	21426	ND	ND	No
C163A	LEVFYNGAWGTVGK	Yes	770.89	342.2	18.50	100.4	33.4	100985	ND	ND	No
C163A	LEVFYNGAWGTVGK	Yes	770.89	461.3	18.50	100.4	36.4	45845	ND	ND	No
C163A	LEVFYNGAWGTVGK	Yes	770.89	889.5	18.50	100.4	36.4	36643	ND	ND	No
C163A	TSYQVYSK	Yes	488.24	397.2	7.96	64	30	231389	18361	20952	No
C163A	TSYQVYSK	Yes	488.24	624.3	7.96	64	24	103422	4839	5961	No
C163A	TSYQVYSK	Yes	488.24	787.4	7.96	64	21	284944	13388	16732	No
C163A	TSYQVYSK	Yes	488.24	874.4	7.96	64	24	74208	3359	5586	No
C4BPA	EDVYVVGTVLR	No									
C4BPA	GYILVGQAK	Yes	474.78	403.2	11.99	62.2	23.4	275966	ND	ND	No
C4BPA	GYILVGQAK	Yes	474.78	502.3	11.99	62.2	23.4	315211	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
C4BPA	GYILVGQAK	Yes	474.78	615.4	11.99	62.2	23.4	376472	ND	ND	No
C4BPA	GYILVGQAK	Yes	474.78	728.5	11.99	62.2	23.4	92533	ND	ND	No
C4BPA	IAHGHYK	Yes	413.22	504.3	5.29	54.3	26.7	32289	ND	ND	No
C4BPA	IAHGHYK	Yes	413.22	516.3	5.29	54.3	23.7	9545	ND	ND	No
C4BPA	IAHGHYK	Yes	413.22	641.3	5.29	54.3	23.7	29837	ND	ND	No
C4BPA	IAHGHYK	Yes	413.22	712.4	5.29	54.3	23.7	15452	ND	ND	No
C4BPA	LSLEIEQLELQR	Yes	490.94	416.3	19.19	64.3	19.6	6999	ND	ND	No
C4BPA	LSLEIEQLELQR	Yes	490.94	443.3	19.19	64.3	25.6	4951	ND	ND	No
C4BPA	LSLEIEQLELQR	Yes	490.94	545.3	19.19	64.3	19.6	10489	ND	ND	No
C4BPA	LSLEIEQLELQR	Yes	490.94	658.4	19.19	64.3	31.6	3613	ND	ND	No
C4BPA	TWYPEVPK	Yes	340.51	288.1	14.29	44.9	20.9	1184	ND	ND	No
C4BPA	TWYPEVPK	Yes	340.51	451.2	14.29	44.9	17.9	ND	ND	ND	No
C4BPA	TWYPEVPK	Yes	340.51	569.3	14.29	44.9	20.9	ND	ND	ND	No
C4BPA	TWYPEVPK	Yes	340.51	677.3	14.29	44.9	23.9	ND	ND	ND	No
CAH9	FPAEIHVVHLSTAFAR	Yes	598.99	565.3	16.95	78.3	31.1	8639	ND	ND	No
CAH9	FPAEIHVVHLSTAFAR	Yes	598.99	652.3	16.95	78.3	37.1	20013	ND	ND	No
CAH9	FPAEIHVVHLSTAFAR	Yes	598.99	765.4	16.95	78.3	37.1	14317	ND	ND	No
CAH9	FPAEIHVVHLSTAFAR	Yes	598.99	902.5	16.95	78.3	37.1	10838	ND	ND	No
CAH9	GGVSYRPAEVAETGA	No									
CAH9	LEEIAEEGSETQVPGLDISALLPSDFSR	Yes	1001.5	409.2	24.37	130.2	57.6	5094	ND	ND	No
CAH9	LEEIAEEGSETQVPGLDISALLPSDFSR	Yes	1001.5	708.3	24.37	130.2	45.6	11601	ND	ND	No
CAH9	LEEIAEEGSETQVPGLDISALLPSDFSR	Yes	1001.5	821.4	24.37	130.2	48.6	5113	ND	ND	No
CAH9	LEEIAEEGSETQVPGLDISALLPSDFSR	Yes	1001.5	934.5	24.37	130.2	48.6	3497	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
CAH9	VIEASFPAGVDSSPR	Yes	511.26	446.2	13.71	67	23.6	33060	ND	ND	No
CAH9	VIEASFPAGVDSSPR	Yes	511.26	561.3	13.71	67	23.6	80788	ND	ND	No
CAH9	VIEASFPAGVDSSPR	Yes	511.26	717.4	13.71	67	26.6	23819	ND	ND	No
CAH9	VIEASFPAGVDSSPR	Yes	511.26	885.4	13.71	67	32.6	10197	ND	ND	No
CAH9	YGGDPPWPR	Yes	522.75	393.1	12.41	68.4	22.5	59158	ND	ND	No
CAH9	YGGDPPWPR	Yes	522.75	555.3	12.41	68.4	34.5	22777	ND	ND	No
CAH9	YGGDPPWPR	Yes	522.75	652.4	12.41	68.4	31.5	65075	ND	ND	No
CAH9	YGGDPPWPR	Yes	522.75	881.4	12.41	68.4	25.5	5620	ND	ND	No
CALR	DDEFTHLYTLIVRPDNTYEVK	No									
CALR	DPDASKPEDWDER	Yes	520.56	304.2	9.51	68.2	30.1	50454	ND	ND	No
CALR	DPDASKPEDWDER	Yes	520.56	328.1	9.51	68.2	24.1	18158	ND	ND	No
CALR	DPDASKPEDWDER	Yes	520.56	720.3	9.51	68.2	33.1	5607	ND	ND	No
CALR	DPDASKPEDWDER	Yes	520.56	946.4	9.51	68.2	30.1	17472	ND	ND	No
CALR	FYGDEEK	Yes	444.19	276.2	7.52	58.3	31	83392	ND	ND	No
CALR	FYGDEEK	Yes	444.19	405.2	7.52	58.3	28	40000	5042	3667	Yes (Based on Transition Ratios)
CALR	FYGDEEK	Yes	444.19	577.2	7.52	58.3	22	405161	10816	11944	Yes (Based on Transition Ratios)
CALR	FYGDEEK	Yes	444.19	740.3	7.52	58.3	22	121217	ND	ND	No
CALR	GLQTSQDAR	No									
CALR	GQTLVVQFTVK	No									
CALU	DWILPSDYDHAEAEAR	No									

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
CALU	EQFVEFR	Yes	477.74	322.2	13.76	62.6	32.5	66982	ND	ND	No
CALU	EQFVEFR	Yes	477.74	451.2	13.76	62.6	23.5	64272	ND	ND	No
CALU	EQFVEFR	Yes	477.74	550.3	13.76	62.6	23.5	30534	ND	ND	No
CALU	EQFVEFR	Yes	477.74	697.4	13.76	62.6	23.5	39899	ND	ND	No
CALU	GHDLNEDGLVSWEEYK	Yes	945.93	423.2	16.50	123	47.1	3128	ND	ND	No
CALU	GHDLNEDGLVSWEEYK	Yes	945.93	568.3	16.50	123	50.1	2709	ND	ND	No
CALU	GHDLNEDGLVSWEEYK	Yes	945.93	666.3	16.50	123	50.1	1323	ND	ND	No
CALU	GHDLNEDGLVSWEEYK	Yes	945.93	841.4	16.50	123	53.1	5599	ND	ND	No
CALU	TFDQLTPEESK	Yes	647.81	364.2	11.25	84.6	31	141796	ND	ND	No
CALU	TFDQLTPEESK	Yes	647.81	589.3	11.25	84.6	40	264251	ND	ND	No
CALU	TFDQLTPEESK	Yes	647.81	690.3	11.25	84.6	31	129105	ND	ND	No
CALU	TFDQLTPEESK	Yes	647.81	931.5	11.25	84.6	28	14458	ND	ND	No
CALU	VHNDAQSFDYDHDAFLGAEEAK	No									
CALX	AEEDEILNR	Yes	544.76	402.2	10.34	71.3	26.5	36469	ND	ND	No
CALX	AEEDEILNR	Yes	544.76	515.3	10.34	71.3	35.5	12681	ND	ND	No
CALX	AEEDEILNR	Yes	544.76	759.4	10.34	71.3	35.5	12934	ND	ND	No
CALX	AEEDEILNR	Yes	544.76	888.4	10.34	71.3	26.5	14638	ND	ND	No
CALX	APVPTGEVYFADSFDR	Yes	590.95	524.2	18.33	77.2	30.7	26819	ND	ND	No
CALX	APVPTGEVYFADSFDR	Yes	590.95	639.3	18.33	77.2	27.7	30572	ND	ND	No
CALX	APVPTGEVYFADSFDR	Yes	590.95	710.3	18.33	77.2	27.7	33171	ND	ND	No
CALX	APVPTGEVYFADSFDR	Yes	590.95	751.4	18.33	77.2	27.7	19688	ND	ND	No
CALX	GTLSGWILSK	Yes	531.3	347.2	18.64	69.5	31.9	131575	5536	9531	No
CALX	GTLSGWILSK	Yes	531.3	703.4	18.64	69.5	25.9	99393	5188	3643	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
CALX	GTLSGWILSK	Yes	531.3	790.4	18.64	69.5	25.9	193462	8175	8902	No
CALX	GTLSGWILSK	Yes	531.3	903.5	18.64	69.5	25.9	39342	ND	ND	No
CALX	IPDPEAVKPDDWDEDAPAK	Yes	703.33	315.2	13.98	91.7	42.4	217605	ND	ND	No
CALX	IPDPEAVKPDDWDEDAPAK	Yes	703.33	326.2	13.98	91.7	33.4	134150	ND	ND	No
CALX	IPDPEAVKPDDWDEDAPAK	Yes	703.33	386.2	13.98	91.7	39.4	152743	ND	ND	No
CALX	IPDPEAVKPDDWDEDAPAK	Yes	703.33	931.4	13.98	91.7	42.4	14743	ND	ND	No
CALX	TGIYEEK	Yes	420.21	276.2	7.40	55.2	27	292573	11388	11011	Yes (Based on Transition Ratios)
CALX	TGIYEEK	Yes	420.21	568.3	7.40	55.2	21	462933	2301	4334	No
CALX	TGIYEEK	Yes	420.21	681.3	7.40	55.2	21	148154	1651	ND	No
CALX	TGIYEEK	Yes	420.21	738.4	7.40	55.2	21	155145	836	1825	No
CAP7	DWIDGVLNNPGPGPA	Yes	761.37	302.1	19.95	99.2	42	21756	ND	ND	No
CAP7	DWIDGVLNNPGPGPA	Yes	761.37	341.2	19.95	99.2	45	26377	ND	ND	No
CAP7	DWIDGVLNNPGPGPA	Yes	761.37	495.3	19.95	99.2	39	47196	ND	ND	No
CAP7	DWIDGVLNNPGPGPA	Yes	761.37	686.3	19.95	99.2	33	14015	ND	ND	No
CAP7	EANLTSSVTILPLPLQNATVEAGTR	No									
CAP7	GPDFFTR	No									
CAP7	LTVLALLAGLLASSR	No									
CAP7	QFPFLASIQNQGR	Yes	753.4	276.1	20.48	98.2	38.6	27250	ND	ND	No
CAP7	QFPFLASIQNQGR	Yes	753.4	633.3	20.48	98.2	32.6	3032	ND	ND	No
CAP7	QFPFLASIQNQGR	Yes	753.4	802.4	20.48	98.2	35.6	21997	ND	ND	No
CAP7	QFPFLASIQNQGR	Yes	753.4	873.5	20.48	98.2	44.6	24685	ND	ND	No
CATB	HYGYNSYSVSNSEK	Yes	545.57	301.1	8.74	71.4	31.4	14645	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
CATB	HYGYNSYSVSNSEK	Yes	545.57	635.3	8.74	71.4	28.4	6159	ND	ND	No
CATB	HYGYNSYSVSNSEK	Yes	545.57	722.3	8.74	71.4	25.4	11762	ND	ND	No
CATB	HYGYNSYSVSNSEK	Yes	545.57	750.4	8.74	71.4	25.4	22210	ND	ND	No
CATB	ILGWGVENGTPYWLVANSWNTDWGDNGFFK	No									
CATB	LPASFDAR	Yes	438.73	508.3	10.66	57.6	21.8	12873	ND	ND	No
CATB	LPASFDAR	Yes	438.73	595.3	10.66	57.6	24.8	80849	4844	5829	No
CATB	LPASFDAR	Yes	438.73	666.3	10.66	57.6	24.8	85179	4845	4353	No
CATB	LPASFDAR	Yes	438.73	763.4	10.66	57.6	21.8	37955	2920	908	No
CATB	NGPVEGAFSVYSDFLLYK	No									
CATB	TDQYWEK	Yes	485.22	462.2	9.35	63.6	32.8	58137	ND	ND	No
CATB	TDQYWEK	Yes	485.22	625.3	9.35	63.6	23.8	38336	ND	ND	No
CATB	TDQYWEK	Yes	485.22	753.4	9.35	63.6	23.8	52981	ND	ND	No
CATB	TDQYWEK	Yes	485.22	868.4	9.35	63.6	23.8	23189	ND	ND	No
CATG	HPQYNQR	Yes	471.73	417.2	5.36	61.9	20.3	1132	ND	ND	No
CATG	HPQYNQR	Yes	471.73	580.3	5.36	61.9	26.3	1268	ND	ND	No
CATG	HPQYNQR	Yes	471.73	708.3	5.36	61.9	26.3	1430	ND	ND	No
CATG	HPQYNQR	Yes	471.73	805.4	5.36	61.9	29.3	3909	ND	ND	No
CATG	NVNPVALPR	Yes	490.29	385.3	11.68	64.2	24.1	19036	ND	ND	No
CATG	NVNPVALPR	Yes	490.29	456.3	11.68	64.2	33.1	91377	ND	ND	No
CATG	NVNPVALPR	Yes	490.29	652.4	11.68	64.2	24.1	78887	ND	ND	No
CATG	NVNPVALPR	Yes	490.29	766.5	11.68	64.2	24.1	98931	ND	ND	No
CATG	SSGVPPEVFTR	Yes	588.31	331.2	12.20	76.9	25.4	69543	ND	ND	No
CATG	SSGVPPEVFTR	Yes	588.31	423.2	12.20	76.9	28.4	97461	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
CATG	SSGVPPEVFTR	Yes	588.31	748.4	12.20	76.9	37.4	12061	ND	ND	No
CATG	SSGVPPEVFTR	Yes	588.31	845.5	12.20	76.9	28.4	45332	ND	ND	No
CATG	VSSFLPWIR	Yes	552.81	474.3	22.78	72.3	32.8	6965	ND	ND	No
CATG	VSSFLPWIR	Yes	552.81	684.4	22.78	72.3	26.8	24577	ND	ND	No
CATG	VSSFLPWIR	Yes	552.81	831.5	22.78	72.3	26.8	16656	ND	ND	No
CATG	VSSFLPWIR	Yes	552.81	918.5	22.78	72.3	23.8	27914	ND	ND	No
CBPB2	ASASYYEQYHSLNEIYSWIEFITER	Yes	1033.82	405.2	25.22	134.4	56.3	8520	26423	16502	No
CBPB2	ASASYYEQYHSLNEIYSWIEFITER	Yes	1033.82	665.4	25.22	134.4	50.3	10394	13390	14641	No
CBPB2	ASASYYEQYHSLNEIYSWIEFITER	Yes	1033.82	794.4	25.22	134.4	53.3	18007	23751	14760	No
CBPB2	ASASYYEQYHSLNEIYSWIEFITER	Yes	1033.82	907.5	25.22	134.4	47.3	9883	11687	13892	No
CBPB2	AYISMHSYSQHIVFPYSYTR	Yes	817.39	689.3	18.96	106.4	36.2	3675	13098	13695	No
CBPB2	AYISMHSYSQHIVFPYSYTR	Yes	817.39	703.3	18.96	106.4	42.2	10467	33972	25052	No
CBPB2	AYISMHSYSQHIVFPYSYTR	Yes	817.39	786.4	18.96	106.4	45.2	64467	289608	250220	No
CBPB2	AYISMHSYSQHIVFPYSYTR	Yes	817.39	933.4	18.96	106.4	48.2	32682	144446	95679	No
CBPB2	DHEELSLVASEAVR	Yes	777.89	253.1	16.01	101.3	45.7	187337	47739	69282	No
CBPB2	DHEELSLVASEAVR	Yes	777.89	382.1	16.01	101.3	42.7	78040	21357	23997	No
CBPB2	DHEELSLVASEAVR	Yes	777.89	511.2	16.01	101.3	39.7	64477	17226	19272	No
CBPB2	DHEELSLVASEAVR	Yes	777.89	931.5	16.01	101.3	42.7	48749	7212	11690	No
CBPB2	DTGTYGFLLPER	Yes	684.84	401.2	19.81	89.3	29.6	3049030	1475914	1786415	No
CBPB2	DTGTYGFLLPER	Yes	684.84	627.4	19.81	89.3	32.6	744094	396643	435417	No
CBPB2	DTGTYGFLLPER	Yes	684.84	831.5	19.81	89.3	32.6	1469213	776450	922854	No
CBPB2	DTGTYGFLLPER	Yes	684.84	994.5	19.81	89.3	32.6	539383	239942	277008	No
CBPB2	EAFAAVSK	Yes	411.72	333.2	10.10	54.1	20.6	1090016	785735	643444	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
CBPB2	EAFAAVSK	Yes	411.72	475.3	10.10	54.1	23.6	1363434	1264100	1084422	No
CBPB2	EAFAAVSK	Yes	411.72	622.4	10.10	54.1	20.6	742094	713478	626234	No
CBPB2	EAFAAVSK	Yes	411.72	693.4	10.10	54.1	23.6	61111	61419	52119	No
CBPB2	IHIGSSFEK	Yes	339.85	251.2	12.24	44.8	23.9	785124	100918	141450	No
CBPB2	IHIGSSFEK	Yes	339.85	421.3	12.24	44.8	20.9	181595	22730	29656	No
CBPB2	IHIGSSFEK	Yes	339.85	423.2	12.24	44.8	14.9	615216	83638	138320	No
CBPB2	IHIGSSFEK	Yes	339.85	510.3	12.24	44.8	14.9	295811	36748	51757	No
CBPB2	LVDFYVMPVVNVDGYDYSWK	No									
CBPB2	QVHFFVNASDVDNVK	Yes	573.62	659.3	17.15	75	26.8	13389	ND	ND	No
CBPB2	QVHFFVNASDVDNVK	Yes	573.62	689.3	17.15	75	23.8	78363	ND	ND	No
CBPB2	QVHFFVNASDVDNVK	Yes	573.62	776.4	17.15	75	26.8	76368	ND	ND	No
CBPB2	QVHFFVNASDVDNVK	Yes	573.62	847.4	17.15	75	29.8	22609	ND	ND	No
CBPB2	YPLYVLK	Yes	448.27	522.3	17.48	58.8	31.2	393410	48162	99701	No
CBPB2	YPLYVLK	Yes	448.27	635.4	17.48	58.8	22.2	567585	78707	150558	No
CBPB2	YPLYVLK	Yes	448.27	636.3	17.48	58.8	22.2	123713	13549	34360	No
CBPB2	YPLYVLK	Yes	448.27	732.5	17.48	58.8	22.2	1088839	120547	219721	No
CBPB2	YTHGHGSETLYLAPGGGDDWIYDLGIK	No									
CCL22	No peptide										
CD14	AFPALTSLDLSDNPGLGER	Yes	987	500.3	22.14	128.3	48.9	55070	171904	130555	No
CD14	AFPALTSLDLSDNPGLGER	Yes	987	628.3	22.14	128.3	42.9	101483	308186	221877	No
CD14	AFPALTSLDLSDNPGLGER	Yes	987	742.4	22.14	128.3	51.9	64027	212728	163731	No
CD14	AFPALTSLDLSDNPGLGER	Yes	987	944.4	22.14	128.3	51.9	61136	175453	128926	No
CD14	ATVNPSAPR	Yes	456.75	386.2	7.30	59.9	22.6	1112667	548678	395588	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
CD14	ATVNPSAPR	Yes	456.75	430.2	7.30	59.9	31.6	471728	257556	171485	No
CD14	ATVNPSAPR	Yes	456.75	527.3	7.30	59.9	25.6	3728867	2008363	1433545	No
CD14	ATVNPSAPR	Yes	456.75	740.4	7.30	59.9	22.6	541278	282188	201515	No
CD14	ELTLEDLK	Yes	480.77	260.2	17.35	63	32.7	3616963	ND	ND	No
CD14	ELTLEDLK	Yes	480.77	504.3	17.35	63	23.7	4064128	ND	ND	No
CD14	ELTLEDLK	Yes	480.77	617.4	17.35	63	23.7	2474104	ND	ND	No
CD14	ELTLEDLK	Yes	480.77	718.4	17.35	63	23.7	2942134	ND	ND	No
CD14	FPAIQNLALR	Yes	571.84	714.4	19.65	74.8	36.7	4587824	51378	41996	No
CD14	FPAIQNLALR	Yes	571.84	827.5	19.65	74.8	36.7	3350648	35713	34047	No
CD14	FPAIQNLALR	Yes	571.84	898.5	19.65	74.8	36.7	3574228	31362	33321	No
CD14	FPAIQNLALR	Yes	571.84	995.6	19.65	74.8	36.7	532547	5286	5179	No
CD14	ITGTMPPLPLEATGLALSSLR	No									
CD14	LTVGAAQVPAQLLVGALR	Yes	593.03	416.3	24.17	77.5	24.8	172705	375000	340842	No
CD14	LTVGAAQVPAQLLVGALR	Yes	593.03	515.3	24.17	77.5	24.8	157643	299445	278333	No
CD14	LTVGAAQVPAQLLVGALR	Yes	593.03	628.4	24.17	77.5	27.8	73655	137055	146301	No
CD14	LTVGAAQVPAQLLVGALR	Yes	593.03	740.4	24.17	77.5	24.8	42884	101973	107306	No
CD14	NVSWATGR	Yes	445.73	301.2	11.56	58.5	25.1	163450	ND	ND	No
CD14	NVSWATGR	Yes	445.73	404.2	11.56	58.5	31.1	477894	ND	ND	No
CD14	NVSWATGR	Yes	445.73	590.3	11.56	58.5	22.1	505147	ND	ND	No
CD14	NVSWATGR	Yes	445.73	677.3	11.56	58.5	22.1	2117910	ND	ND	No
CD14	STLSVGVSGTLVLLQGAR	Yes	879.51	431.2	23.07	114.5	38.2	3375	22851	17961	No
CD14	STLSVGVSGTLVLLQGAR	Yes	879.51	544.3	23.07	114.5	50.2	ND	17545	20433	No
CD14	STLSVGVSGTLVLLQGAR	Yes	879.51	657.4	23.07	114.5	38.2	ND	39851	27070	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
CD14	STLSVGVSGTLVLLQGAR	Yes	879.51	970.6	23.07	114.5	38.2	ND	6549	5847	No
CD14	SWLAELQQWLKPGLK	Yes	599.67	274.1	25.16	78.4	25.1	1302125	549305	555118	No
CD14	SWLAELQQWLKPGLK	Yes	599.67	414.3	25.16	78.4	37.1	543676	241156	260259	No
CD14	SWLAELQQWLKPGLK	Yes	599.67	542.4	25.16	78.4	37.1	155425	73405	75307	No
CD14	SWLAELQQWLKPGLK	Yes	599.67	841.5	25.16	78.4	34.1	98179	41988	42402	No
CD14	VDADADPR	Yes	429.7	272.2	6.41	56.4	30.4	631974	137433	107556	No
CD14	VDADADPR	Yes	429.7	573.3	6.41	56.4	18.4	49328	10484	8138	No
CD14	VDADADPR	Yes	429.7	644.3	6.41	56.4	21.4	127647	35181	28784	No
CD14	VDADADPR	Yes	429.7	759.3	6.41	56.4	21.4	66276	15580	11308	No
CD24	AAGGALQSTASLFVVSLSLLHLYS	No									
CD2A2	HSHPTR	Yes	367.69	276.2	5.61	48.4	24.7	63679	ND	ND	No
CD2A2	HSHPTR	Yes	367.69	510.3	5.61	48.4	15.7	ND	ND	ND	No
CD2A2	HSHPTR	Yes	367.69	597.3	5.61	48.4	27.7	1612	ND	ND	No
CD2A2	VFVVHIPR	Yes	483.8	346.2	16.60	63.4	32.8	ND	ND	ND	No
CD2A2	VFVVHIPR	Yes	483.8	522.3	16.60	63.4	20.8	21500	ND	ND	No
CD2A2	VFVVHIPR	Yes	483.8	621.4	16.60	63.4	32.8	ND	ND	ND	No
CD2A2	VFVVHIPR	Yes	483.8	720.5	16.60	63.4	23.8	408532	ND	ND	No
CD38	DLAHQFTQVQR	No									
CD38	ILLWSR	Yes	394.25	262.2	16.95	51.9	25.8	5588	ND	ND	No
CD38	ILLWSR	Yes	394.25	448.2	16.95	51.9	22.8	5665	ND	ND	No
CD38	ILLWSR	Yes	394.25	561.3	16.95	51.9	16.8	2603	ND	ND	No
CD38	ILLWSR	Yes	394.25	674.4	16.95	51.9	19.8	3106	ND	ND	No
CD38	NIYRPDK	Yes	453.25	515.3	6.41	59.5	31.4	33773	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
CD38	NIYRPDK	Yes	453.25	678.4	6.41	59.5	22.4	227558	ND	ND	No
CD38	NIYRPDK	Yes	453.25	759.4	6.41	59.5	19.4	9379	ND	ND	No
CD38	NIYRPDK	Yes	453.25	791.4	6.41	59.5	25.4	26256	ND	ND	No
CD38	NSTFGSVEVHNLQPEK	Yes	595.96	373.2	12.80	77.9	33.9	75429	ND	ND	No
CD38	NSTFGSVEVHNLQPEK	Yes	595.96	728.4	12.80	77.9	36.9	6613	ND	ND	No
CD38	NSTFGSVEVHNLQPEK	Yes	595.96	865.5	12.80	77.9	36.9	8584	ND	ND	No
CD38	NSTFGSVEVHNLQPEK	Yes	595.96	964.5	12.80	77.9	30.9	3017	ND	ND	No
CD38	VQTLEAWVIHGGR	Yes	489.27	426.2	18.29	64.1	25.5	27811	ND	ND	No
CD38	VQTLEAWVIHGGR	Yes	489.27	539.3	18.29	64.1	28.5	51574	ND	ND	No
CD38	VQTLEAWVIHGGR	Yes	489.27	638.4	18.29	64.1	31.5	23690	ND	ND	No
CD38	VQTLEAWVIHGGR	Yes	489.27	824.5	18.29	64.1	25.5	13652	ND	ND	No
CD40L	GDQNPQIAAHVISEASSK	Yes	617.98	415.2	12.81	80.7	26.1	16115	ND	ND	No
CD40L	GDQNPQIAAHVISEASSK	Yes	617.98	721.4	12.81	80.7	38.1	10259	ND	ND	No
CD40L	GDQNPQIAAHVISEASSK	Yes	617.98	753.4	12.81	80.7	26.1	1975	ND	ND	No
CD40L	GDQNPQIAAHVISEASSK	Yes	617.98	957.5	12.81	80.7	35.1	2831	ND	ND	No
CD40L	SQFEGFVK	No									
CD40L	TTSVLQWAEK	Yes	581.81	533.3	16.01	76.1	37.1	107088	ND	ND	No
CD40L	TTSVLQWAEK	Yes	581.81	774.4	16.01	76.1	28.1	111057	ND	ND	No
CD40L	TTSVLQWAEK	Yes	581.81	873.5	16.01	76.1	28.1	14338	ND	ND	No
CD40L	TTSVLQWAEK	Yes	581.81	960.5	16.01	76.1	28.1	91329	ND	ND	No
CD44	FAGVFHVEK	Yes	517.28	815.4	12.69	67.7	25.3	31240	63087	45891	No
CD44	FAGVFHVEK	Yes	517.28	886.5	12.69	67.7	25.3	6968	11483	12501	No
CD44	FAGVFHVEK	Yes	517.28	887.4	12.69	67.7	25.3	3390	3671	1563	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
CD44	HLSFSGSGIDDDEDFISSTISTTPR	No									
CD44	KPSGLNGEASK	Yes	544.29	783.4	5.59	71.2	35.4	5912	ND	ND	No
CD44	KPSGLNGEASK	Yes	544.29	854.4	5.59	71.2	26.4	4186	ND	ND	No
CD44	KPSGLNGEASK	Yes	544.29	862.4	5.59	71.2	29.4	18078	ND	ND	No
CD44	KPSGLNGEASK	Yes	544.29	959.5	5.59	71.2	26.4	19867	ND	ND	No
CD44	TNPEDIYPSNPTDDDVSSGSSSER	No									
CD44	YGFIEGHVVIPR	Yes	462.92	272.2	16.06	60.7	30.2	163831	515656	485910	No
CD44	YGFIEGHVVIPR	Yes	462.92	484.3	16.06	60.7	30.2	182263	564470	500258	No
CD44	YGFIEGHVVIPR	Yes	462.92	583.4	16.06	60.7	21.2	90376	357617	319546	No
CD44	YGFIEGHVVIPR	Yes	462.92	777.5	16.06	60.7	30.2	95958	299807	265247	No
CD59	AGLQVVYNK	Yes	446.75	424.2	9.04	58.6	22.2	206079	30067	29658	No
CD59	AGLQVVYNK	Yes	446.75	523.3	9.04	58.6	22.2	232038	44188	27540	No
CD59	AGLQVVYNK	Yes	446.75	651.3	9.04	58.6	22.2	244798	36203	31423	No
CD59	AGLQVVYNK	Yes	446.75	821.5	9.04	58.6	22.2	75752	8496	11084	No
CD59	TVLLLVTPFLAAAWSLHP	Yes	975.07	314.2	25.03	126.8	48.4	4179	ND	ND	No
CD59	TVLLLVTPFLAAAWSLHP	Yes	975.07	427.3	25.03	126.8	42.4	3264	ND	ND	No
CD59	TVLLLVTPFLAAAWSLHP	Yes	975.07	540.4	25.03	126.8	42.4	2755	ND	ND	No
CD59	TVLLLVTPFLAAAWSLHP	Yes	975.07	740.5	25.03	126.8	42.4	1569	ND	ND	No
CD97	ELNSPILFAFSHLESSDGEAGR	No									
CD97	FIPEDPK	No									
CD97	TSSAEVTIQNVIK	Yes	463.92	347.2	23.54	60.8	18.2	ND	ND	ND	No
CD97	TSSAEVTIQNVIK	Yes	463.92	359.3	23.54	60.8	18.2	28955	ND	ND	No
CD97	TSSAEVTIQNVIK	Yes	463.92	601.4	23.54	60.8	21.2	10658	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
CD97	TSSAEVTIQNVIK	Yes	463.92	714.5	23.54	60.8	24.2	5221	ND	ND	No
CD97	VFQGQGLSTR	Yes	546.79	276.2	9.40	71.5	32.6	16431	ND	ND	No
CD97	VFQGQGLSTR	Yes	546.79	661.4	9.40	71.5	23.6	4073	ND	ND	No
CD97	VFQGQGLSTR	Yes	546.79	718.4	9.40	71.5	35.6	31596	ND	ND	No
CD97	VFQGQGLSTR	Yes	546.79	846.4	9.40	71.5	26.6	14960	ND	ND	No
CD97	YSEFTSTTSGTGHNQTR	Yes	625.28	518.3	7.98	81.7	38.4	12379	ND	ND	No
CD97	YSEFTSTTSGTGHNQTR	Yes	625.28	712.3	7.98	81.7	38.4	8352	ND	ND	No
CD97	YSEFTSTTSGTGHNQTR	Yes	625.28	813.4	7.98	81.7	35.4	3544	ND	ND	No
CD97	YSEFTSTTSGTGHNQTR	Yes	625.28	957.5	7.98	81.7	38.4	5899	ND	ND	No
CDCP1	EEGVFTVTPDTK	Yes	661.83	460.2	12.81	86.4	40.6	600204	44976	30026	No
CDCP1	EEGVFTVTPDTK	Yes	661.83	561.3	12.81	86.4	31.6	273282	ND	ND	No
CDCP1	EEGVFTVTPDTK	Yes	661.83	761.4	12.81	86.4	31.6	320469	ND	ND	No
CDCP1	EEGVFTVTPDTK	Yes	661.83	908.5	12.81	86.4	31.6	418538	ND	ND	No
CDCP1	IYVVDLSNER	Yes	604.32	376.2	14.28	79	26.1	93152	ND	ND	No
CDCP1	IYVVDLSNER	Yes	604.32	733.3	14.28	79	29.1	82512	ND	ND	No
CDCP1	IYVVDLSNER	Yes	604.32	832.4	14.28	79	29.1	73990	ND	ND	No
CDCP1	IYVVDLSNER	Yes	604.32	931.5	14.28	79	29.1	64818	ND	ND	No
CDCP1	LSLVLVPAQK	Yes	534.35	443.3	16.84	69.9	32	1373873	ND	ND	No
CDCP1	LSLVLVPAQK	Yes	534.35	655.4	16.84	69.9	26	391822	ND	ND	No
CDCP1	LSLVLVPAQK	Yes	534.35	754.5	16.84	69.9	26	253531	ND	ND	No
CDCP1	LSLVLVPAQK	Yes	534.35	867.6	16.84	69.9	26	67163	ND	ND	No
CDCP1	SPPESESEPYTFSHPNNGDVSSK	No									
CDCP1	VEYYIPGSTTNPEVFK	Yes	922.46	392.2	16.63	120	49.1	155039	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
CDCP1	VEYYIPGSTTNPEVFK	Yes	922.46	555.2	16.63	120	40.1	93615	ND	ND	No
CDCP1	VEYYIPGSTTNPEVFK	Yes	922.46	619.3	16.63	120	52.1	50922	ND	ND	No
CDCP1	VEYYIPGSTTNPEVFK	Yes	922.46	668.3	16.63	120	40.1	67737	ND	ND	No
CDK4	APPPGLPAETIK	Yes	397.56	420.2	12.00	52.3	14.8	62272	ND	ND	No
CDK4	APPPGLPAETIK	Yes	397.56	533.3	12.00	52.3	17.8	47241	ND	ND	No
CDK4	APPPGLPAETIK	Yes	397.56	561.3	12.00	52.3	20.8	19957	ND	ND	No
CDK4	APPPGLPAETIK	Yes	397.56	658.4	12.00	52.3	17.8	34709	ND	ND	No
CDK4	DLKPENILVTSGGTVK	No									
CDK4	IFDLIGLPPEDDWPR	Yes	594.97	458.3	24.36	77.8	36.9	58289	ND	ND	No
CDK4	IFDLIGLPPEDDWPR	Yes	594.97	489.3	24.36	77.8	27.9	12947	ND	ND	No
CDK4	IFDLIGLPPEDDWPR	Yes	594.97	659.4	24.36	77.8	24.9	36596	ND	ND	No
CDK4	IFDLIGLPPEDDWPR	Yes	594.97	914.4	24.36	77.8	24.9	41235	ND	ND	No
CDK4	VPNGGGGGGGLPISTVR	Yes	747.91	462.3	12.49	97.5	38.4	12038	ND	ND	No
CDK4	VPNGGGGGGGLPISTVR	Yes	747.91	672.4	12.49	97.5	38.4	31260	ND	ND	No
CDK4	VPNGGGGGGGLPISTVR	Yes	747.91	899.5	12.49	97.5	41.4	4321	ND	ND	No
CDK4	VPNGGGGGGGLPISTVR	Yes	747.91	956.6	12.49	97.5	44.4	7293	ND	ND	No
CDK4	VTLVFEHVDQDLR	Yes	524.28	288.2	16.99	68.6	30.3	247606	ND	ND	No
CDK4	VTLVFEHVDQDLR	Yes	524.28	646.3	16.99	68.6	33.3	45718	ND	ND	No
CDK4	VTLVFEHVDQDLR	Yes	524.28	745.4	16.99	68.6	33.3	36723	ND	ND	No
CDK4	VTLVFEHVDQDLR	Yes	524.28	882.4	16.99	68.6	33.3	26479	ND	ND	No
CEAM5	EVLLLVHNLPQHLFGYSWYK	Yes	819.44	310.2	24.27	106.7	42.3	4815	ND	ND	No
CEAM5	EVLLLVHNLPQHLFGYSWYK	Yes	819.44	342.2	24.27	106.7	45.3	8770	ND	ND	No
CEAM5	EVLLLVHNLPQHLFGYSWYK	Yes	819.44	455.3	24.27	106.7	42.3	5309	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
CEAM5	EVLLLVHNLPQHLFGYSWYK	Yes	819.44	950.4	24.27	106.7	39.3	3947	ND	ND	No
CEAM5	INGIPQQHTQVLFIAK	No									
CEAM5	LTIESTPFNVAEGK	Yes	753.4	404.2	16.58	98.2	44.6	74712	ND	ND	No
CEAM5	LTIESTPFNVAEGK	Yes	753.4	457.3	16.58	98.2	35.6	80732	ND	ND	No
CEAM5	LTIESTPFNVAEGK	Yes	753.4	861.4	16.58	98.2	35.6	166575	ND	ND	No
CEAM5	LTIESTPFNVAEGK	Yes	753.4	962.5	16.58	98.2	35.6	35164	ND	ND	No
CEAM5	QIIGYVIGTQQATPGPAYSGR	Yes	726.38	319.2	16.24	94.7	40.6	ND	ND	ND	No
CEAM5	QIIGYVIGTQQATPGPAYSGR	Yes	726.38	804.4	16.24	94.7	31.6	51332	ND	ND	No
CEAM5	QIIGYVIGTQQATPGPAYSGR	Yes	726.38	905.4	16.24	94.7	37.6	8187	ND	ND	No
CEAM5	QIIGYVIGTQQATPGPAYSGR	Yes	726.38	976.5	16.24	94.7	34.6	4709	ND	ND	No
CEAM5	SDLVNEEATGQFR	Yes	733.35	316.2	12.37	95.6	37.8	178652	ND	ND	No
CEAM5	SDLVNEEATGQFR	Yes	733.35	679.4	12.37	95.6	40.8	44726	ND	ND	No
CEAM5	SDLVNEEATGQFR	Yes	733.35	808.4	12.37	95.6	34.8	26119	ND	ND	No
CEAM5	SDLVNEEATGQFR	Yes	733.35	937.4	12.37	95.6	34.8	9826	ND	ND	No
CEAM8	EVLLLVHNLPQDPR	No									
CEAM8	GYNWYK	No									
CEAM8	LFIPNITTK	Yes	523.82	261.2	17.09	68.6	25.5	2931811	ND	ND	No
CEAM8	LFIPNITTK	Yes	523.82	673.4	17.09	68.6	25.5	1383799	ND	ND	No
CEAM8	LFIPNITTK	Yes	523.82	786.5	17.09	68.6	25.5	616824	ND	ND	No
CEAM8	LFIPNITTK	Yes	523.82	933.5	17.09	68.6	25.5	53239	ND	ND	No
CEAM8	TLTLLSVTR	Yes	502.31	462.3	16.94	65.8	27.6	9731	ND	ND	No
CEAM8	TLTLLSVTR	Yes	502.31	575.4	16.94	65.8	24.6	9076	ND	ND	No
CEAM8	TLTLLSVTR	Yes	502.31	688.4	16.94	65.8	33.6	3973	ND	ND	No

Table S5. MRM assay of individual proteins.											
Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
CEAM8	TLTLLSVTR	Yes	502.31	789.5	16.94	65.8	24.6	14135	ND	ND	No
CERU	GAYPLSIEPIGVR	Yes	686.39	502.3	17.91	89.5	29.7	3267	99542	40472	Yes (Based on Transition Ratios)
CERU	GAYPLSIEPIGVR	Yes	686.39	541.3	17.91	89.5	32.7	11058	821576	295104	No
CERU	GAYPLSIEPIGVR	Yes	686.39	870.5	17.91	89.5	41.7	6416	617660	209269	No
CERU	GAYPLSIEPIGVR	Yes	686.39	983.6	17.91	89.5	41.7	2317	145152	66620	No
CERU	GPEEEHLGILGPVIWAEVGDTIR	Yes	829.77	561.3	24.53	108	36.9	27339	63776	39820	No
CERU	GPEEEHLGILGPVIWAEVGDTIR	Yes	829.77	660.4	24.53	108	48.9	12449	39626	18428	No
CERU	GPEEEHLGILGPVIWAEVGDTIR	Yes	829.77	789.4	24.53	108	39.9	27804	86417	36624	No
CERU	GPEEEHLGILGPVIWAEVGDTIR	Yes	829.77	860.4	24.53	108	39.9	30845	85765	46367	No
CERU	IYHSHIDAPK	Yes	394.21	315.2	7.05	51.9	26.7	78706	52909	23256	No
CERU	IYHSHIDAPK	Yes	394.21	430.2	7.05	51.9	20.7	38348	22790	9958	No
CERU	IYHSHIDAPK	Yes	394.21	680.4	7.05	51.9	23.7	21285	11028	6429	No
CERU	IYHSHIDAPK	Yes	394.21	767.4	7.05	51.9	17.7	31642	19163	7560	No
CERU	NNEGTYYSPNYNPQSR	Yes	952.41	487.3	10.15	123.9	44.4	18886	32406	9242	No
CERU	NNEGTYYSPNYNPQSR	Yes	952.41	516.2	10.15	123.9	41.4	ND	4518	ND	Yes (Based on Manual Review)
CERU	NNEGTYYSPNYNPQSR	Yes	952.41	601.3	10.15	123.9	41.4	11667	16977	4899	No
CERU	NNEGTYYSPNYNPQSR	Yes	952.41	975.5	10.15	123.9	50.4	17215	28442	10869	No
CERU	SVPPSASHVAPTETFTYEWTVPK	No									
CH10	DGDILGK	Yes	359.19	317.2	8.99	47.3	21.3	691996	ND	ND	No
CH10	DGDILGK	Yes	359.19	430.3	8.99	47.3	15.3	163507	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
CH10	DGDILGK	Yes	359.19	545.3	8.99	47.3	18.3	239135	ND	ND	No
CH10	DGDILGK	Yes	359.19	602.4	8.99	47.3	15.3	71944	ND	ND	No
CH10	DYFLFR	Yes	430.72	279.1	19.42	56.6	18.5	333355	ND	ND	No
CH10	DYFLFR	Yes	430.72	322.2	19.42	56.6	21.5	117471	ND	ND	No
CH10	DYFLFR	Yes	430.72	582.3	19.42	56.6	21.5	444679	ND	ND	No
CH10	DYFLFR	Yes	430.72	745.4	19.42	56.6	24.5	4260	ND	ND	No
CH10	GGEIQPVSVK	Yes	507.29	357.2	9.37	66.4	21.8	379199	ND	ND	No
CH10	GGEIQPVSVK	Yes	507.29	529.3	9.37	66.4	24.8	731486	ND	ND	No
CH10	GGEIQPVSVK	Yes	507.29	657.4	9.37	66.4	24.8	228452	ND	ND	No
CH10	GGEIQPVSVK	Yes	507.29	770.5	9.37	66.4	24.8	123445	ND	ND	No
CH10	VLLPEYGGTK	Yes	538.8	305.2	12.97	70.5	35.2	199640	ND	ND	No
CH10	VLLPEYGGTK	Yes	538.8	654.3	12.97	70.5	32.2	165814	ND	ND	No
CH10	VLLPEYGGTK	Yes	538.8	751.4	12.97	70.5	26.2	1740986	ND	ND	No
CH10	VLLPEYGGTK	Yes	538.8	864.4	12.97	70.5	26.2	330672	ND	ND	No
CH10	VLQATVVAVGSGSK	Yes	658.38	534.3	11.54	85.9	40.5	15772	ND	ND	No
CH10	VLQATVVAVGSGSK	Yes	658.38	605.3	11.54	85.9	40.5	25048	ND	ND	No
CH10	VLQATVVAVGSGSK	Yes	658.38	704.4	11.54	85.9	31.5	15387	ND	ND	No
CH10	VLQATVVAVGSGSK	Yes	658.38	975.5	11.54	85.9	31.5	5258	ND	ND	No
CH60	GIIDPTK	Yes	372.22	345.2	9.12	49	21.9	112744	ND	ND	No
CH60	GIIDPTK	Yes	372.22	399.2	9.12	49	18.9	3727	ND	ND	No
CH60	GIIDPTK	Yes	372.22	460.2	9.12	49	18.9	21472	ND	ND	No
CH60	GIIDPTK	Yes	372.22	573.3	9.12	49	18.9	116549	ND	ND	No
CH60	GYISPYFINTSK	Yes	695.36	421.2	16.43	90.7	30.1	208246	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
CH60	GYISPYFINTSK	Yes	695.36	449.2	16.43	90.7	42.1	90581	ND	ND	No
CH60	GYISPYFINTSK	Yes	695.36	872.5	16.43	90.7	42.1	34718	ND	ND	No
CH60	GYISPYFINTSK	Yes	695.36	969.5	16.43	90.7	33.1	191136	ND	ND	No
CH60	LVQDVANNTNEEAGDGTTTATVLAR	Yes	854.09	555.3	12.60	111.2	41.1	ND	ND	ND	No
CH60	LVQDVANNTNEEAGDGTTTATVLAR	Yes	854.09	630.4	12.60	111.2	41.1	ND	ND	ND	No
CH60	LVQDVANNTNEEAGDGTTTATVLAR	Yes	854.09	832.5	12.60	111.2	38.1	ND	ND	ND	No
CH60	LVQDVANNTNEEAGDGTTTATVLAR	Yes	854.09	990.6	12.60	111.2	41.1	ND	ND	ND	No
CH60	TALLDAAGVASLLTTAEVVVTEIPK	Yes	828.14	286.2	25.09	107.8	39.8	14290	ND	ND	No
CH60	TALLDAAGVASLLTTAEVVVTEIPK	Yes	828.14	486.3	25.09	107.8	39.8	5679	ND	ND	No
CH60	TALLDAAGVASLLTTAEVVVTEIPK	Yes	828.14	686.4	25.09	107.8	36.8	9083	ND	ND	No
CH60	TALLDAAGVASLLTTAEVVVTEIPK	Yes	828.14	785.5	25.09	107.8	36.8	14912	ND	ND	No
CH60	TVIIEQSWGSPK	Yes	672.86	314.2	14.28	87.8	32.1	59452	ND	ND	No
CH60	TVIIEQSWGSPK	Yes	672.86	331.2	14.28	87.8	32.1	20125	ND	ND	No
CH60	TVIIEQSWGSPK	Yes	672.86	789.4	14.28	87.8	41.1	8565	ND	ND	No
CH60	TVIIEQSWGSPK	Yes	672.86	918.4	14.28	87.8	32.1	24053	ND	ND	No
CKAP4	DFTSLENTVEER	Yes	720.34	304.2	15.90	93.9	40.2	34379	ND	ND	No
CKAP4	DFTSLENTVEER	Yes	720.34	747.4	15.90	93.9	34.2	35437	ND	ND	No
CKAP4	DFTSLENTVEER	Yes	720.34	876.4	15.90	93.9	34.2	37945	ND	ND	No
CKAP4	DFTSLENTVEER	Yes	720.34	989.5	15.90	93.9	34.2	9635	ND	ND	No
CKAP4	IETNENNLESAK	Yes	681.33	305.2	7.95	88.9	29.5	26083	ND	ND	No
CKAP4	IETNENNLESAK	Yes	681.33	434.2	7.95	88.9	41.5	21425	ND	ND	No
CKAP4	IETNENNLESAK	Yes	681.33	775.4	7.95	88.9	35.5	22525	ND	ND	No
CKAP4	IETNENNLESAK	Yes	681.33	904.4	7.95	88.9	38.5	11899	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
CKAP4	LEGLGSSEADQDGLASTVR	Yes	952.96	300.2	13.78	123.9	50.4	50307	ND	ND	No
CKAP4	LEGLGSSEADQDGLASTVR	Yes	952.96	462.3	13.78	123.9	44.4	19072	ND	ND	No
CKAP4	LEGLGSSEADQDGLASTVR	Yes	952.96	533.3	13.78	123.9	47.4	21066	ND	ND	No
CKAP4	LEGLGSSEADQDGLASTVR	Yes	952.96	818.4	13.78	123.9	53.4	12526	ND	ND	No
CKAP4	LPPQDFLDR	No									
CKAP4	VQSLQATFGTFESILR	No									
CL041	ASAPLSQSGLATANGKPEPTSIS	Yes	1092.56	504.3	12.57	141.9	56.6	3446	ND	ND	No
CL041	ASAPLSQSGLATANGKPEPTSIS	Yes	1092.56	730.4	12.57	141.9	50.6	3125	ND	ND	No
CL041	ASAPLSQSGLATANGKPEPTSIS	Yes	1092.56	912.5	12.57	141.9	56.6	ND	ND	ND	No
CL041	ASAPLSQSGLATANGKPEPTSIS	Yes	1092.56	915.5	12.57	141.9	59.6	2841	ND	ND	No
CL041	GDPDSEADSIDSDQEDPLK	Yes	1016.93	357.3	12.42	132.2	50.2	10331	ND	ND	No
CL041	GDPDSEADSIDSDQEDPLK	Yes	1016.93	672.2	12.42	132.2	47.2	3980	ND	ND	No
CL041	GDPDSEADSIDSDQEDPLK	Yes	1016.93	729.4	12.42	132.2	53.2	3279	ND	ND	No
CL041	GDPDSEADSIDSDQEDPLK	Yes	1016.93	931.4	12.42	132.2	47.2	4480	ND	ND	No
CL041	ILDEDSWSDGEQEPITVDQTWR	No									
CL041	TELGSQTPESSR	Yes	646.31	575.3	7.03	84.4	33.9	72293	ND	3693	No
CL041	TELGSQTPESSR	Yes	646.31	676.3	7.03	84.4	33.9	40866	ND	4196	No
CL041	TELGSQTPESSR	Yes	646.31	891.4	7.03	84.4	33.9	16930	3662	3165	No
CL041	TELGSQTPESSR	Yes	646.31	948.4	7.03	84.4	30.9	32117	ND	ND	No
CL041	YGVEALLHR	Yes	353.2	312.2	14.66	46.6	24.6	80008	ND	ND	No
CL041	YGVEALLHR	Yes	353.2	425.3	14.66	46.6	18.6	41884	ND	ND	No
CL041	YGVEALLHR	Yes	353.2	609.4	14.66	46.6	24.6	24999	ND	ND	No
CL041	YGVEALLHR	Yes	353.2	738.4	14.66	46.6	24.6	ND	ND	ND	Yes (Based on

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference** Manual Review)
CLCA1	ASVTALIESVNGK	Yes	644.86	504.3	17.85	84.2	39.9	26063	ND	ND	No
CLCA1	ASVTALIESVNGK	Yes	644.86	746.4	17.85	84.2	30.9	35386	ND	ND	No
CLCA1	ASVTALIESVNGK	Yes	644.86	859.5	17.85	84.2	30.9	16063	ND	ND	No
CLCA1	ASVTALIESVNGK	Yes	644.86	930.5	17.85	84.2	30.9	9999	ND	ND	No
CLCA1	SEISNIAR	No									
CLCA1	TSSGGSFVASDVPNAPIPDLFPPGQITDLK	No									
CLCA1	TVTLELLDNGAGADATK	Yes	844.94	302.2	17.16	110	39.7	34268	ND	ND	No
CLCA1	TVTLELLDNGAGADATK	Yes	844.94	690.3	17.16	110	39.7	14930	ND	ND	No
CLCA1	TVTLELLDNGAGADATK	Yes	844.94	804.4	17.16	110	48.7	18762	ND	ND	No
CLCA1	TVTLELLDNGAGADATK	Yes	844.94	919.4	17.16	110	39.7	29879	ND	ND	No
CLCA1	WGVFDEYNNDEK	No									
CLIC1	FSAYIK	Yes	364.7	260.2	10.84	48	24.5	595472	ND	ND	No
CLIC1	FSAYIK	Yes	364.7	423.3	10.84	48	27.5	101951	ND	ND	No
CLIC1	FSAYIK	Yes	364.7	494.3	10.84	48	18.5	718926	ND	ND	No
CLIC1	FSAYIK	Yes	364.7	581.3	10.84	48	18.5	954036	ND	ND	No
CLIC1	GFTIPEAFR	No									
CLIC1	LAALNPESNTAGLDIFAK	Yes	922.99	256.2	20.11	120.1	46.1	251074	24648	35646	Yes (Based on Transition Ratios)
CLIC1	LAALNPESNTAGLDIFAK	Yes	922.99	478.3	20.11	120.1	52.1	32561	ND	ND	No
CLIC1	LAALNPESNTAGLDIFAK	Yes	922.99	483.3	20.11	120.1	40.1	131558	ND	2907	Yes (Based on Transition Ratios)

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
CLIC1	LAALNPESNTAGLDIFAK	Yes	922.99	593.3	20.11	120.1	43.1	34385	ND	ND	No
CLIC1	NSNPALNDNLEK	Yes	664.83	316.1	9.48	86.8	28.8	197486	1502	ND	No
CLIC1	NSNPALNDNLEK	Yes	664.83	732.4	9.48	86.8	31.8	96972	1130	ND	No
CLIC1	NSNPALNDNLEK	Yes	664.83	845.4	9.48	86.8	40.8	98520	ND	ND	No
CLIC1	NSNPALNDNLEK	Yes	664.83	916.5	9.48	86.8	31.8	28861	ND	ND	No
CLIC1	YLSNAYAR	Yes	479.24	409.2	8.63	62.8	26.6	7272	ND	ND	No
CLIC1	YLSNAYAR	Yes	479.24	594.3	8.63	62.8	32.6	5315	ND	ND	No
CLIC1	YLSNAYAR	Yes	479.24	681.3	8.63	62.8	20.6	36170	ND	ND	No
CLIC1	YLSNAYAR	Yes	479.24	794.4	8.63	62.8	29.6	6873	ND	ND	No
CLUS	ASSIIDELFQDR	Yes	465.24	418.2	22.96	61	21.3	49973	276207	299523	No
CLUS	ASSIIDELFQDR	Yes	465.24	565.3	22.96	61	21.3	36875	225494	240691	No
CLUS	ASSIIDELFQDR	Yes	465.24	678.4	22.96	61	18.3	5657	39256	45385	No
CLUS	ASSIIDELFQDR	Yes	465.24	807.4	22.96	61	27.3	4947	22753	22626	No
CLUS	EIQNAVNGVK	Yes	536.29	417.2	8.40	70.2	23.1	21019	121356	95814	No
CLUS	EIQNAVNGVK	Yes	536.29	587.4	8.40	70.2	32.1	13887	77194	76501	No
CLUS	EIQNAVNGVK	Yes	536.29	701.4	8.40	70.2	26.1	21989	116214	109011	No
CLUS	EIQNAVNGVK	Yes	536.29	829.5	8.40	70.2	26.1	17366	95497	77738	No
CLUS	IDSLLENDR	Yes	537.78	646.3	11.84	70.4	26.2	63530	ND	ND	No
CLUS	IDSLLENDR	Yes	537.78	759.4	11.84	70.4	26.2	18675	ND	ND	No
CLUS	IDSLLENDR	Yes	537.78	846.4	11.84	70.4	26.2	39885	ND	ND	No
CLUS	IDSLLENDR	Yes	537.78	961.5	11.84	70.4	26.2	20410	ND	ND	No
CLUS	LANLTQGEDQYYLR	Yes	842.42	299.2	15.01	109.7	39.6	156005	15195	8822	No
CLUS	LANLTQGEDQYYLR	Yes	842.42	412.3	15.01	109.7	39.6	46631	6453	4504	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
CLUS	LANLTQGEDQYYLR	Yes	842.42	451.3	15.01	109.7	39.6	29979	ND	5067	No
CLUS	LANLTQGEDQYYLR	Yes	842.42	742.4	15.01	109.7	48.6	45149	ND	5127	No
CLUS	VTTVASHTSDSDVPSGVTEVVVK	No									
CMGA	AEGNNQAPGEEEEEEEEATNTHPPASLPSQK	No									
CMGA	EAVEEPSSK	Yes	488.24	418.2	5.78	64	24	240271	ND	ND	No
CMGA	EAVEEPSSK	Yes	488.24	547.3	5.78	64	21	125345	ND	ND	No
CMGA	EAVEEPSSK	Yes	488.24	676.3	5.78	64	21	122989	ND	ND	No
CMGA	EAVEEPSSK	Yes	488.24	775.4	5.78	64	21	48704	ND	ND	No
CMGA	SEALAVDGAGKPGAEEAQDPEGK	Yes	742.69	288.1	9.62	96.8	38.4	38315	ND	ND	No
CMGA	SEALAVDGAGKPGAEEAQDPEGK	Yes	742.69	401.2	9.62	96.8	35.4	7531	ND	ND	No
CMGA	SEALAVDGAGKPGAEEAQDPEGK	Yes	742.69	430.2	9.62	96.8	44.4	17732	ND	ND	No
CMGA	SEALAVDGAGKPGAEEAQDPEGK	Yes	742.69	472.2	9.62	96.8	32.4	11210	ND	ND	No
CMGA	SGELEQEEER	Yes	603.27	690.3	7.00	78.8	29	31569	ND	ND	No
CMGA	SGELEQEEER	Yes	603.27	819.3	7.00	78.8	32	51021	ND	ND	No
CMGA	SGELEQEEER	Yes	603.27	902.4	7.00	78.8	29	40548	ND	ND	No
CMGA	SGELEQEEER	Yes	603.27	932.4	7.00	78.8	32	17744	ND	ND	No
CMGA	YPGPQAEGDSEGLSQGLVDR	Yes	1037.99	743.3	13.69	134.9	57.2	4357	ND	ND	No
CMGA	YPGPQAEGDSEGLSQGLVDR	Yes	1037.99	774.4	13.69	134.9	54.2	4979	ND	ND	No
CMGA	YPGPQAEGDSEGLSQGLVDR	Yes	1037.99	915.4	13.69	134.9	54.2	3438	ND	ND	No
CMGA	YPGPQAEGDSEGLSQGLVDR	Yes	1037.99	944.5	13.69	134.9	57.2	4095	ND	ND	No
CNTN1	AHSDGGDGVVSQVK	Yes	452.56	525.2	7.33	59.4	29.6	41322	7305	2962	No
CNTN1	AHSDGGDGVVSQVK	Yes	452.56	560.3	7.33	59.4	20.6	332139	29001	32250	No
CNTN1	AHSDGGDGVVSQVK	Yes	452.56	697.3	7.33	59.4	17.6	180384	12732	17667	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
CNTN1	AHSDGGDGVVSQVK	Yes	452.56	796.3	7.33	59.4	20.6	64702	7580	3631	No
CNTN1	DGEYVVEVR	Yes	533.26	274.2	11.47	69.8	35	ND	32365	35099	Yes (Based on Manual Review)
CNTN1	DGEYVVEVR	Yes	533.26	502.3	11.47	69.8	29	ND	18432	18887	Yes (Based on Manual Review)
CNTN1	DGEYVVEVR	Yes	533.26	601.4	11.47	69.8	26	75018	21021	17935	No
CNTN1	DGEYVVEVR	Yes	533.26	764.4	11.47	69.8	26	59811	9617	13138	No
CNTN1	HSIEVPIPR	No									
CNTN1	STEATLSFGYLDPFPPEERPEVR	Yes	879.77	389.2	22.10	114.5	42.4	ND	ND	ND	
CNTN1	TTKPYPADIVVQFK	Yes	536.3	591.3	16.26	70.2	24.9	67046	ND	ND	No
CNTN1	TTKPYPADIVVQFK	Yes	536.3	620.4	16.26	70.2	24.9	211362	ND	ND	No
CNTN1	TTKPYPADIVVQFK	Yes	536.3	848.5	16.26	70.2	24.9	60973	ND	ND	No
CNTN1	TTKPYPADIVVQFK	Yes	536.3	874.4	16.26	70.2	24.9	70651	ND	ND	No
CO4A1	GDPGTPGVPGK	Yes	491.25	301.2	7.15	64.4	33.1	397555	ND	ND	No
CO4A1	GDPGTPGVPGK	Yes	491.25	428.2	7.15	64.4	21.1	86532	ND	ND	No
CO4A1	GDPGTPGVPGK	Yes	491.25	554.3	7.15	64.4	24.1	134917	ND	ND	No
CO4A1	GDPGTPGVPGK	Yes	491.25	712.4	7.15	64.4	21.1	11490	ND	ND	No
CO4A1	GEPGVGLPGLK	Yes	512.3	414.3	14.28	67.1	34	721898	ND	ND	No
CO4A1	GEPGVGLPGLK	Yes	512.3	584.4	14.28	67.1	34	159954	ND	ND	No
CO4A1	GEPGVGLPGLK	Yes	512.3	740.5	14.28	67.1	31	176274	ND	ND	No
CO4A1	GEPGVGLPGLK	Yes	512.3	837.5	14.28	67.1	25	98626	ND	ND	No
CO4A1	GPPGGVGFPGSR	No									

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
CO4A1	GPPGPQGPPGEIGFPGQPGAK	Yes	971.49	372.2	14.08	126.3	51.2	86151	ND	ND	No
CO4A1	GPPGPQGPPGEIGFPGQPGAK	Yes	971.49	591.3	14.08	126.3	54.2	16781	ND	ND	No
CO4A1	GPPGPQGPPGEIGFPGQPGAK	Yes	971.49	654.4	14.08	126.3	54.2	28435	ND	ND	No
CO4A1	GPPGPQGPPGEIGFPGQPGAK	Yes	971.49	858.4	14.08	126.3	54.2	5320	ND	ND	No
CO4A1	ILYHGYSLLYVQGNER	Yes	963	475.2	16.77	125.2	47.9	ND	ND	ND	No
CO4A1	ILYHGYSLLYVQGNER	Yes	963	527.3	16.77	125.2	44.9	ND	ND	ND	No
CO4A1	ILYHGYSLLYVQGNER	Yes	963	702.4	16.77	125.2	47.9	ND	ND	ND	No
CO4A1	ILYHGYSLLYVQGNER	Yes	963	747.4	16.77	125.2	50.9	ND	ND	ND	No
CO5A2	DGEVGPSGPVGPPGLAGER	Yes	874.43	361.2	12.70	113.8	44	12553	ND	ND	No
CO5A2	DGEVGPSGPVGPPGLAGER	Yes	874.43	458.2	12.70	113.8	38	5937	ND	ND	No
CO5A2	DGEVGPSGPVGPPGLAGER	Yes	874.43	853.5	12.70	113.8	41	28409	ND	ND	No
CO5A2	DGEVGPSGPVGPPGLAGER	Yes	874.43	895.4	12.70	113.8	41	6993	ND	ND	No
CO5A2	GPEGPPGKPGEDGEPGR	Yes	544.93	284.1	8.81	71.3	25.3	ND	ND	ND	No
CO5A2	GPEGPPGKPGEDGEPGR	Yes	544.93	438.2	8.81	71.3	31.3	ND	ND	ND	No
CO5A2	GPEGPPGKPGEDGEPGR	Yes	544.93	515.3	8.81	71.3	25.3	ND	ND	ND	No
CO5A2	GPEGPPGKPGEDGEPGR	Yes	544.93	913.4	8.81	71.3	31.3	ND	ND	ND	No
CO5A2	GTQGPPGATGFPGSAGR	Yes	757.87	344.2	10.46	98.8	35.8	6641	ND	ND	No
CO5A2	GTQGPPGATGFPGSAGR	Yes	757.87	544.3	10.46	98.8	35.8	18617	ND	ND	No
CO5A2	GTQGPPGATGFPGSAGR	Yes	757.87	849.4	10.46	98.8	41.8	7045	ND	ND	No
CO5A2	GTQGPPGATGFPGSAGR	Yes	757.87	977.5	10.46	98.8	44.8	2035	ND	ND	No
CO5A2	LGPLGAPGEDGRPGPPGSIGIR	No									
CO5A2	VGPPGPAGAPGPAGPLGEPGK	Yes	593.98	697.4	11.86	77.6	27.8	32430	ND	ND	No
CO5A2	VGPPGPAGAPGPAGPLGEPGK	Yes	593.98	704.4	11.86	77.6	27.8	57361	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
CO5A2	VGPPGPAGAPGPAGPLGEPGK	Yes	593.98	754.4	11.86	77.6	24.8	33471	ND	ND	No
CO5A2	VGPPGPAGAPGPAGPLGEPGK	Yes	593.98	858.4	11.86	77.6	36.8	14965	ND	ND	No
CO6A3	ALGSAIEYTIENVFESAPNPR	Yes	760.05	483.3	24.61	99	36.3	29935	ND	12426	No
CO6A3	ALGSAIEYTIENVFESAPNPR	Yes	760.05	554.3	24.61	99	36.3	12272	ND	ND	No
CO6A3	ALGSAIEYTIENVFESAPNPR	Yes	760.05	641.3	24.61	99	33.3	ND	ND	9091	Yes (Based on Manual Review)
CO6A3	ALGSAIEYTIENVFESAPNPR	Yes	760.05	917.4	24.61	99	39.3	18692	ND	3763	No
CO6A3	IGDLHPQIVNLLK	Yes	487.29	536.3	18.33	63.9	22.4	11276	3587	5448	No
CO6A3	IGDLHPQIVNLLK	Yes	487.29	761.4	18.33	63.9	31.4	ND	4684	6846	Yes (Based on Manual Review)
CO6A3	IGDLHPQIVNLLK	Yes	487.29	924.6	18.33	63.9	25.4	43184	22358	17009	No
CO6A3	IGDLHPQIVNLLK	Yes	487.29	973.5	18.33	63.9	19.4	ND	ND	ND	No
CO6A3	NADPAELEQIVLSPAFILAAESLPK	Yes	879.48	598.2	24.71	114.5	51.4	7384	ND	ND	No
CO6A3	NADPAELEQIVLSPAFILAAESLPK	Yes	879.48	711.3	24.71	114.5	42.4	5738	ND	ND	No
CO6A3	NADPAELEQIVLSPAFILAAESLPK	Yes	879.48	828.5	24.71	114.5	42.4	12266	ND	ND	No
CO6A3	NADPAELEQIVLSPAFILAAESLPK	Yes	879.48	941.6	24.71	114.5	45.4	3799	ND	ND	No
CO6A3	VAVVQYSDR	Yes	518.77	668.3	8.90	67.9	25.3	36578	16925	12421	No
CO6A3	VAVVQYSDR	Yes	518.77	767.4	8.90	67.9	28.3	34106	12685	16170	No
CO6A3	VAVVQYSDR	Yes	518.77	866.4	8.90	67.9	25.3	14429	5963	4705	No
CO6A3	VAVVQYSDR	Yes	518.77	937.5	8.90	67.9	28.3	15640	2096	2986	No
CO6A3	WYYDPNTK	Yes	543.75	459.3	11.80	71.1	32.4	184505	ND	ND	No
CO6A3	WYYDPNTK	Yes	543.75	574.3	11.80	71.1	26.4	38014	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
CO6A3	WYYDPNTK	Yes	543.75	737.3	11.80	71.1	26.4	128266	ND	ND	No
CO6A3	WYYDPNTK	Yes	543.75	900.4	11.80	71.1	26.4	33055	ND	ND	No
COCA1	GPGDLEAPSNLVISER	Yes	827.43	327.1	15.53	107.7	47.9	115985	ND	ND	No
COCA1	GPGDLEAPSNLVISER	Yes	827.43	391.2	15.53	107.7	41.9	42169	ND	ND	No
COCA1	GPGDLEAPSNLVISER	Yes	827.43	440.2	15.53	107.7	41.9	35588	ND	ND	No
COCA1	GPGDLEAPSNLVISER	Yes	827.43	640.3	15.53	107.7	38.9	54523	ND	ND	No
COCA1	ITVDPTTDGPTK	Yes	622.82	402.2	9.06	81.3	38.9	489472	ND	ND	No
COCA1	ITVDPTTDGPTK	Yes	622.82	429.2	9.06	81.3	29.9	284347	ND	ND	No
COCA1	ITVDPTTDGPTK	Yes	622.82	816.4	9.06	81.3	29.9	427932	ND	ND	No
COCA1	ITVDPTTDGPTK	Yes	622.82	931.4	9.06	81.3	29.9	131790	ND	ND	No
COCA1	SLYDDVDTGEK	Yes	621.28	333.2	10.96	81.1	38.8	65911	ND	ND	No
COCA1	SLYDDVDTGEK	Yes	621.28	549.3	10.96	81.1	38.8	87076	ND	ND	No
COCA1	SLYDDVDTGEK	Yes	621.28	763.3	10.96	81.1	29.8	80140	ND	ND	No
COCA1	SLYDDVDTGEK	Yes	621.28	878.4	10.96	81.1	29.8	69051	ND	ND	No
COCA1	SQDEVEIPAR	Yes	572.29	343.2	10.01	74.8	24.7	193420	ND	ND	No
COCA1	SQDEVEIPAR	Yes	572.29	684.4	10.01	74.8	36.7	49376	ND	ND	No
COCA1	SQDEVEIPAR	Yes	572.29	813.4	10.01	74.8	27.7	21953	ND	ND	No
COCA1	SQDEVEIPAR	Yes	572.29	928.5	10.01	74.8	27.7	51798	ND	ND	No
COCA1	VTDETTDSFK	Yes	571.76	597.3	8.11	74.8	33.7	57318	ND	ND	No
COCA1	VTDETTDSFK	Yes	571.76	698.3	8.11	74.8	36.7	47120	ND	ND	No
COCA1	VTDETTDSFK	Yes	571.76	827.4	8.11	74.8	27.7	53434	ND	ND	No
COCA1	VTDETTDSFK	Yes	571.76	942.4	8.11	74.8	27.7	167492	ND	ND	No
COF1	EILVGDVGQTVDDPYATFVK	Yes	1083.55	356.2	20.03	140.8	53.2	26457	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
COF1	EILVGDVGQTVDDPYATFVK	Yes	1083.55	627.3	20.03	140.8	50.2	9667	ND	ND	No
COF1	EILVGDVGQTVDDPYATFVK	Yes	1083.55	825.5	20.03	140.8	56.2	29037	ND	ND	No
COF1	EILVGDVGQTVDDPYATFVK	Yes	1083.55	940.5	20.03	140.8	59.2	4703	ND	ND	No
COF1	LGGSAVISLEGKPL	Yes	670.89	414.3	17.23	87.5	41	ND	ND	ND	No
COF1	LGGSAVISLEGKPL	Yes	670.89	485.3	17.23	87.5	38	21078	ND	ND	No
COF1	LGGSAVISLEGKPL	Yes	670.89	743.4	17.23	87.5	32	25603	ND	ND	No
COF1	LGGSAVISLEGKPL	Yes	670.89	856.5	17.23	87.5	32	21956	ND	ND	No
COF1	YALYDATYETK	Yes	669.32	641.3	12.93	87.3	40.9	17157	3181	6530	Yes (Based on Transition Ratios)
COF1	YALYDATYETK	Yes	669.32	712.4	12.93	87.3	40.9	37165	ND	3600	No
COF1	YALYDATYETK	Yes	669.32	827.4	12.93	87.3	31.9	95002	5147	7677	No
COF1	YALYDATYETK	Yes	669.32	990.4	12.93	87.3	31.9	50507	2058	2055	No
COIA1	ADDILASPPR	Yes	527.78	302.1	11.37	69.1	31.7	64978	ND	ND	No
COIA1	ADDILASPPR	Yes	527.78	369.2	11.37	69.1	22.7	30226	ND	ND	No
COIA1	ADDILASPPR	Yes	527.78	456.3	11.37	69.1	25.7	18372	ND	ND	No
COIA1	ADDILASPPR	Yes	527.78	640.4	11.37	69.1	25.7	25580	ND	ND	No
COIA1	AVGLAGTFR	Yes	446.26	480.3	12.95	58.6	22.1	106939	25505	18437	No
COIA1	AVGLAGTFR	Yes	446.26	551.3	12.95	58.6	22.1	189558	32038	21513	No
COIA1	AVGLAGTFR	Yes	446.26	664.4	12.95	58.6	22.1	14494	2036	2037	No
COIA1	AVGLAGTFR	Yes	446.26	721.4	12.95	58.6	22.1	254985	29053	22315	No
COIA1	DELLFPSWEALFSGSEGPLKPGAR	No									
COIA1	LSGVQDGHQDISLLYTEPGAGQTHTAASFR	No									
COIA1	TEAPSATGQASSLLGGR	Yes	801.91	289.2	13.02	104.4	37.8	83374	3715	4565	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
COIA1	TEAPSATGQASSLLGGR	Yes	801.91	302.1	13.02	104.4	37.8	59638	3553	2971	No
COIA1	TEAPSATGQASSLLGGR	Yes	801.91	760.4	13.02	104.4	46.8	40838	3555	ND	No
COIA1	TEAPSATGQASSLLGGR	Yes	801.91	945.5	13.02	104.4	40.8	46084	4045	4072	No
COX5A	EIYPYVIQELRPTLNELGISTPEELGLDK	No									
COX5A	GLLHSAR	Yes	377.22	284.2	7.03	49.7	16.1	ND	ND	ND	No
COX5A	GLLHSAR	Yes	377.22	333.2	7.03	49.7	25.1	ND	ND	ND	No
COX5A	GLLHSAR	Yes	377.22	470.2	7.03	49.7	22.1	ND	ND	ND	No
COX5A	GLLHSAR	Yes	377.22	583.3	7.03	49.7	19.1	46861	ND	ND	No
COX5A	IIDAALR	Yes	386.24	359.2	10.38	50.8	19.5	7154	ND	ND	No
COX5A	IIDAALR	Yes	386.24	430.3	10.38	50.8	28.5	46988	ND	ND	No
COX5A	IIDAALR	Yes	386.24	545.3	10.38	50.8	19.5	143162	ND	ND	No
COX5A	IIDAALR	Yes	386.24	658.4	10.38	50.8	28.5	15898	ND	ND	No
COX5A	ILEVVK	Yes	350.73	455.3	10.67	46.2	17.9	15946	ND	ND	No
COX5A	ILEVVK	Yes	350.73	474.3	10.67	46.2	17.9	681903	ND	ND	No
COX5A	ILEVVK	Yes	350.73	554.4	10.67	46.2	14.9	4303	ND	ND	No
COX5A	ILEVVK	Yes	350.73	587.4	10.67	46.2	17.9	435901	ND	ND	No
COX5A	TPGPAVAIQSVR	No									
CRP	APLTKPLK	Yes	434.29	357.3	7.31	57	30.6	280845	1577327	1908902	Yes (Based on Transition Ratios)
CRP	APLTKPLK	Yes	434.29	586.4	7.31	57	24.6	84437	617737	617997	Yes (Based on Transition Ratios)
CRP	APLTKPLK	Yes	434.29	699.5	7.31	57	24.6	100933	ND	51133	Yes (Based on Transition

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
											Ratios)
CRP	APLTKPLK	Yes	434.29	796.5	7.31	57	21.6	15825	10533	ND	Yes (Based on Transition Ratios)
CRP	ESDTSYVSLK	Yes	564.77	347.2	10.75	73.9	27.4	359646	175461	70274	No
CRP	ESDTSYVSLK	Yes	564.77	446.3	10.75	73.9	27.4	130551	70944	22325	No
CRP	ESDTSYVSLK	Yes	564.77	609.4	10.75	73.9	27.4	125689	66445	31824	No
CRP	ESDTSYVSLK	Yes	564.77	696.4	10.75	73.9	27.4	144853	73836	23902	No
CRP	YEVQGEVFTKPQLWP	Yes	910.96	293.1	20.66	118.5	45.6	7092	77998	39706	No
CRP	YEVQGEVFTKPQLWP	Yes	910.96	302.2	20.66	118.5	39.6	5640	47999	17822	No
CRP	YEVQGEVFTKPQLWP	Yes	910.96	392.2	20.66	118.5	39.6	3329	13149	9645	No
CRP	YEVQGEVFTKPQLWP	Yes	910.96	520.2	20.66	118.5	39.6	2108	14527	7644	No
CS051	AQADLLAHLVPEPDR	Yes	548.96	387.2	18.69	71.8	34.5	145950	ND	ND	No
CS051	AQADLLAHLVPEPDR	Yes	548.96	613.3	18.69	71.8	22.5	300098	ND	ND	No
CS051	AQADLLAHLVPEPDR	Yes	548.96	712.4	18.69	71.8	34.5	96273	ND	ND	No
CS051	AQADLLAHLVPEPDR	Yes	548.96	825.4	18.69	71.8	31.5	78434	ND	ND	No
CS051	DTGVAFELR	Yes	504.26	288.2	14.71	66	33.7	151577	ND	ND	No
CS051	DTGVAFELR	Yes	504.26	564.3	14.71	66	24.7	110051	ND	ND	No
CS051	DTGVAFELR	Yes	504.26	635.4	14.71	66	24.7	225223	ND	ND	No
CS051	DTGVAFELR	Yes	504.26	791.4	14.71	66	24.7	113411	ND	ND	No
CS051	GYWGDIATGPFVAFGIEADDESLLR	No									
CS051	LEEQLPWLSLR	Yes	692.39	500.2	22.58	90.3	33	76609	ND	ND	No
CS051	LEEQLPWLSLR	Yes	692.39	613.3	22.58	90.3	30	126926	ND	ND	No
CS051	LEEQLPWLSLR	Yes	692.39	771.5	22.58	90.3	33	360035	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
CS051	LEEQLPWLSLR	Yes	692.39	884.5	22.58	90.3	30	48049	ND	ND	No
CS051	TAGEITQHNVTELLR	Yes	561.3	401.3	15.32	73.4	32.2	10655	ND	ND	No
CS051	TAGEITQHNVTELLR	Yes	561.3	631.4	15.32	73.4	23.2	4626	ND	ND	No
CS051	TAGEITQHNVTELLR	Yes	561.3	730.4	15.32	73.4	32.2	5899	ND	ND	No
CS051	TAGEITQHNVTELLR	Yes	561.3	981.5	15.32	73.4	32.2	3279	ND	ND	No
CSF1	DNTPNAIAIVQLQELSLR	No									
CSF1	DPPEPGSPR	Yes	476.23	310.1	6.06	62.4	29.5	11703	ND	ND	No
CSF1	DPPEPGSPR	Yes	476.23	439.2	6.06	62.4	20.5	24628	ND	ND	No
CSF1	DPPEPGSPR	Yes	476.23	513.3	6.06	62.4	23.5	50299	ND	ND	No
CSF1	DPPEPGSPR	Yes	476.23	739.4	6.06	62.4	23.5	70429	ND	ND	No
CSF1	FNSVPLTDTGHER	Yes	491.58	262.1	10.58	64.4	22.6	ND	8988	4415	Yes (Based on Manual Review)
CSF1	FNSVPLTDTGHER	Yes	491.58	599.3	10.58	64.4	31.6	ND	8732	2411	Yes (Based on Manual Review)
CSF1	FNSVPLTDTGHER	Yes	491.58	714.3	10.58	64.4	31.6	19974	ND	ND	No
CSF1	FNSVPLTDTGHER	Yes	491.58	815.4	10.58	64.4	31.6	ND	4449	3944	Yes (Based on Manual Review)
CSF1	ISSLRPQGLSNPSTLSAQPQLSR	Yes	813.11	999.6	13.87	105.9	39	6180	ND	ND	No
CSF1	ISSLRPQGLSNPSTLSAQPQLSR	Yes	813.11	600.3	13.87	105.9	42	37252	ND	ND	No
CSF1	ISSLRPQGLSNPSTLSAQPQLSR	Yes	813.11	728.4	13.87	105.9	36	13067	ND	ND	No
CSF1	ISSLRPQGLSNPSTLSAQPQLSR	Yes	813.11	886.5	13.87	105.9	48	18025	ND	ND	No
CSF1	TFYETPLQLLEK	No									

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
CSF2	No peptide										
CT085	IELPER	Yes	378.72	304.2	10.36	49.9	28.2	4194	ND	ND	No
CT085	IELPER	Yes	378.72	401.2	10.36	49.9	22.2	24918	ND	ND	No
CT085	IELPER	Yes	378.72	514.3	10.36	49.9	19.2	19958	ND	ND	No
CT085	IELPER	Yes	378.72	643.3	10.36	49.9	19.2	10792	ND	ND	No
CT085	IRPVTPVEK	Yes	346.88	375.2	7.74	45.7	21.2	70236	ND	ND	No
CT085	IRPVTPVEK	Yes	346.88	466.3	7.74	45.7	18.2	183212	ND	ND	No
CT085	IRPVTPVEK	Yes	346.88	472.3	7.74	45.7	15.2	282122	ND	ND	No
CT085	IRPVTPVEK	Yes	346.88	567.4	7.74	45.7	15.2	92847	ND	ND	No
CT085	QNWPQNWGFLTTPFEELIK	Yes	1174.59	373.3	24.67	152.5	57.2	2811	ND	ND	No
CT085	QNWPQNWGFLTTPFEELIK	Yes	1174.59	429.2	24.67	152.5	51.2	5527	ND	ND	No
CT085	QNWPQNWGFLTTPFEELIK	Yes	1174.59	526.2	24.67	152.5	60.2	3068	ND	ND	No
CT085	QNWPQNWGFLTTPFEELIK	Yes	1174.59	875.5	24.67	152.5	60.2	6913	ND	ND	No
CT085	SAVPGLNK	Yes	393.23	261.2	8.77	51.7	25.8	157451	ND	ND	No
CT085	SAVPGLNK	Yes	393.23	431.3	8.77	51.7	28.8	62691	ND	ND	No
CT085	SAVPGLNK	Yes	393.23	528.3	8.77	51.7	19.8	632582	ND	ND	No
CT085	SAVPGLNK	Yes	393.23	627.4	8.77	51.7	19.8	71132	ND	ND	No
CT085	VFPSPPVPQTTQGFIGWR	Yes	1007.53	344.2	20.53	131	55.8	4750	ND	ND	No
CT085	VFPSPPVPQTTQGFIGWR	Yes	1007.53	418.2	20.53	131	46.8	4370	ND	ND	No
CT085	VFPSPPVPQTTQGFIGWR	Yes	1007.53	431.2	20.53	131	43.8	4335	ND	ND	No
CT085	VFPSPPVPQTTQGFIGWR	Yes	1007.53	724.4	20.53	131	43.8	9779	ND	ND	No
CTGF	DQTVVGPALAAYR	Yes	680.86	345.1	14.39	88.8	32.5	146090	ND	ND	No
CTGF	DQTVVGPALAAYR	Yes	680.86	761.4	14.39	88.8	32.5	85815	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
CTGF	DQTVVGPALAAYR	Yes	680.86	818.5	14.39	88.8	32.5	245458	ND	ND	No
CTGF	DQTVVGPALAAYR	Yes	680.86	917.5	14.39	88.8	32.5	149236	ND	ND	No
CTGF	TTTLPVEFK	Yes	518.29	294.2	14.51	67.9	31.3	414553	ND	ND	No
CTGF	TTTLPVEFK	Yes	518.29	619.3	14.51	67.9	25.3	603333	ND	ND	No
CTGF	TTTLPVEFK	Yes	518.29	732.4	14.51	67.9	25.3	144773	ND	ND	No
CTGF	TTTLPVEFK	Yes	518.29	833.5	14.51	67.9	25.3	453384	ND	ND	No
CYR61	ALALVVTLLHLTR	No									
CYR61	ELGFDASEVELTR	Yes	733.36	518.3	16.83	95.6	31.8	32196	ND	ND	No
CYR61	ELGFDASEVELTR	Yes	733.36	617.4	16.83	95.6	43.8	27170	ND	ND	No
CYR61	ELGFDASEVELTR	Yes	733.36	833.4	16.83	95.6	37.8	56202	ND	ND	No
CYR61	ELGFDASEVELTR	Yes	733.36	904.5	16.83	95.6	34.8	29225	ND	ND	No
CYR61	ILYNPLQGQK	No									
CYR61	LFNDIHK	Yes	296.16	397.3	9.61	39.2	15.7	18408	ND	ND	No
CYR61	LFNDIHK	Yes	296.16	490.2	9.61	39.2	12.7	18359	ND	ND	No
CYR61	LFNDIHK	Yes	296.16	512.3	9.61	39.2	15.7	5197	ND	ND	No
CYR61	LFNDIHK	Yes	296.16	626.3	9.61	39.2	21.7	887	ND	ND	No
CYR61	NNELIAVGK	Yes	479.27	303.2	11.01	62.8	32.6	156552	ND	ND	No
CYR61	NNELIAVGK	Yes	479.27	374.2	11.01	62.8	32.6	222206	ND	ND	No
CYR61	NNELIAVGK	Yes	479.27	600.4	11.01	62.8	23.6	113403	ND	ND	No
CYR61	NNELIAVGK	Yes	479.27	729.5	11.01	62.8	23.6	67990	ND	ND	No
CYTA	LEAVQYK	Yes	425.74	314.2	8.59	55.9	21.2	132368	ND	ND	No
CYTA	LEAVQYK	Yes	425.74	537.3	8.59	55.9	21.2	143964	ND	ND	No
CYTA	LEAVQYK	Yes	425.74	541.3	8.59	55.9	21.2	7411	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
CYTA	LEAVQYK	Yes	425.74	608.3	8.59	55.9	21.2	1126130	ND	ND	No
CYTA	SLPGQNEDLVLTGYQVDK	Yes	659.34	709.4	16.55	86.1	31.2	21427	ND	ND	No
CYTA	SLPGQNEDLVLTGYQVDK	Yes	659.34	810.4	16.55	86.1	31.2	18038	ND	ND	No
CYTA	SLPGQNEDLVLTGYQVDK	Yes	659.34	841.4	16.55	86.1	37.2	1575	ND	ND	No
CYTA	SLPGQNEDLVLTGYQVDK	Yes	659.34	923.5	16.55	86.1	31.2	7488	ND	ND	No
CYTA	TNETYGK	Yes	406.69	367.2	5.49	53.5	23.4	134783	ND	ND	No
CYTA	TNETYGK	Yes	406.69	468.2	5.49	53.5	20.4	62722	ND	ND	No
CYTA	TNETYGK	Yes	406.69	597.3	5.49	53.5	20.4	182225	ND	ND	No
CYTA	TNETYGK	Yes	406.69	711.3	5.49	53.5	20.4	56539	ND	ND	No
CYTA	TQVVAGTNYYIK	No									
CYTA	VKPQLEEK	Yes	324.19	276.2	6.41	42.8	23.1	54061	ND	ND	No
CYTA	VKPQLEEK	Yes	324.19	405.2	6.41	42.8	14.1	57757	ND	ND	No
CYTA	VKPQLEEK	Yes	324.19	453.3	6.41	42.8	17.1	21071	ND	ND	No
CYTA	VKPQLEEK	Yes	324.19	518.3	6.41	42.8	17.1	68589	ND	ND	No
CYTB	HDELTYF	No									
CYTB	SQLEEK	Yes	367.19	276.2	5.62	48.4	21.7	202094	ND	ND	No
CYTB	SQLEEK	Yes	367.19	405.2	5.62	48.4	18.7	104033	ND	ND	No
CYTB	SQLEEK	Yes	367.19	518.3	5.62	48.4	15.7	424574	ND	ND	No
CYTB	SQLEEK	Yes	367.19	646.3	5.62	48.4	18.7	21234	ND	ND	No
CYTB	SQVVAGTNYFIK	Yes	663.86	315.2	14.75	86.6	31.7	206912	ND	ND	No
CYTB	SQVVAGTNYFIK	Yes	663.86	414.2	14.75	86.6	31.7	42269	ND	ND	No
CYTB	SQVVAGTNYFIK	Yes	663.86	842.4	14.75	86.6	31.7	53227	ND	ND	No
CYTB	SQVVAGTNYFIK	Yes	663.86	913.5	14.75	86.6	28.7	63325	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
CYTB	VFQSLPHENKPLTLSNYQTNK	Yes	820.1	362.2	13.47	106.8	48.4	15542	ND	ND	No
CYTB	VFQSLPHENKPLTLSNYQTNK	Yes	820.1	375.2	13.47	106.8	45.4	10480	ND	ND	No
CYTB	VFQSLPHENKPLTLSNYQTNK	Yes	820.1	462.2	13.47	106.8	45.4	6202	ND	ND	No
CYTB	VFQSLPHENKPLTLSNYQTNK	Yes	820.1	854.4	13.47	106.8	39.4	6099	ND	ND	No
CYTB	VHVGDEDFVHLR	Yes	474.91	288.2	13.27	62.3	27.8	14529	ND	ND	No
CYTB	VHVGDEDFVHLR	Yes	474.91	336.2	13.27	62.3	24.8	14416	ND	ND	No
CYTB	VHVGDEDFVHLR	Yes	474.91	425.3	13.27	62.3	27.8	40991	ND	ND	No
CYTB	VHVGDEDFVHLR	Yes	474.91	752.3	13.27	62.3	21.8	5301	ND	ND	No
DDX17	DWVLNEFR	Yes	539.77	302.1	19.61	70.6	23.2	158378	ND	ND	No
DDX17	DWVLNEFR	Yes	539.77	565.3	19.61	70.6	26.2	48898	ND	ND	No
DDX17	DWVLNEFR	Yes	539.77	678.4	19.61	70.6	26.2	89998	ND	ND	No
DDX17	DWVLNEFR	Yes	539.77	777.4	19.61	70.6	23.2	77768	ND	ND	No
DDX17	FVINYDYPNSSEDYVHR	Yes	706.66	312.2	15.39	92.2	36.6	17514	13345	7552	No
DDX17	FVINYDYPNSSEDYVHR	Yes	706.66	574.3	15.39	92.2	42.6	30860	9479	12436	No
DDX17	FVINYDYPNSSEDYVHR	Yes	706.66	752.4	15.39	92.2	33.6	1742	ND	371	No
DDX17	FVINYDYPNSSEDYVHR	Yes	706.66	992.4	15.39	92.2	36.6	6197	512	ND	Yes (Based on Transition Ratios)
DDX17	LIDFLESGK	Yes	511.28	420.2	17.67	67	34	34527	ND	ND	No
DDX17	LIDFLESGK	Yes	511.28	680.4	17.67	67	28	12355	ND	ND	No
DDX17	LIDFLESGK	Yes	511.28	795.4	17.67	67	25	113429	ND	ND	No
DDX17	LIDFLESGK	Yes	511.28	908.5	17.67	67	25	8800	ND	ND	No
DDX17	SSQSSSQQFSGIGR	Yes	728.35	489.3	9.76	95	34.5	20963	ND	ND	No
DDX17	SSQSSSQQFSGIGR	Yes	728.35	636.3	9.76	95	34.5	14095	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
DDX17	SSQSSSQQFSGIGR	Yes	728.35	764.4	9.76	95	43.5	17394	ND	ND	No
DDX17	SSQSSSQQFSGIGR	Yes	728.35	979.5	9.76	95	43.5	14209	ND	ND	No
DDX17	VLEEANQAINPK	Yes	663.36	342.2	9.86	86.6	31.7	87304	ND	ND	No
DDX17	VLEEANQAINPK	Yes	663.36	358.2	9.86	86.6	31.7	241606	ND	ND	No
DDX17	VLEEANQAINPK	Yes	663.36	968.5	9.86	86.6	31.7	12683	ND	ND	No
DDX17	VLEEANQAINPK	Yes	663.36	984.5	9.86	86.6	31.7	43739	ND	ND	No
DEFB1	No peptide										
DESP	IQSQFTDAQK	Yes	583.3	242.2	10.90	100	31.2	ND	71370	ND	No
DESP	IQSQFTDAQK	Yes	583.3	562.3	10.90	100	31.2	ND	4504	ND	No
DESP	IQSQFTDAQK	Yes	583.3	709.4	10.90	100	31.2	ND	16893	ND	No
DESP	IQSQFTDAQK	Yes	583.3	924.4	10.90	100	31.2	ND	ND	ND	No
DESP	ITNLTQQLEQASIVK	Yes	843.5	1015.6	20.10	100	42.6	ND	ND	ND	No
DESP	ITNLTQQLEQASIVK	Yes	843.5	1143.6	20.10	100	42.6	ND	ND	ND	No
DESP	ITNLTQQLEQASIVK	Yes	843.5	774.4	20.10	100	42.6	ND	ND	ND	No
DESP	ITNLTQQLEQASIVK	Yes	843.5	887.5	20.10	100	42.6	ND	ND	ND	No
DESP	NMPLQHLLEQIK	Yes	732.4	1218.7	22.00	100	37.7	ND	ND	ND	No
DESP	NMPLQHLLEQIK	Yes	732.4	609.9	22.00	100	37.7	ND	ND	ND	No
DESP	NMPLQHLLEQIK	Yes	732.4	630.4	22.00	100	37.7	ND	ND	ND	No
DESP	NMPLQHLLEQIK	Yes	732.4	880.5	22.00	100	37.7	ND	ND	ND	No
DESP	YGDGIQLTR	Yes	511.767	221.093	10.50	100	28	ND	41209	28990	No
DESP	YGDGIQLTR	Yes	511.767	687.415	10.50	100	34	ND	8886	ND	No
DESP	YGDGIQLTR	Yes	511.767	802.4	10.50	100	28	ND	2930	1610	No
DESP	YGDGIQLTR	Yes	511.767	859.5	10.50	100	28	ND	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
DFB4A	No peptide										
DHI1L	ALPSLTDSK	Yes	466.26	349.2	11.37	61.1	32	76967	ND	ND	No
DHI1L	ALPSLTDSK	Yes	466.26	563.3	11.37	61.1	32	93018	ND	ND	No
DHI1L	ALPSLTDSK	Yes	466.26	650.3	11.37	61.1	26	134715	ND	ND	No
DHI1L	ALPSLTDSK	Yes	466.26	747.4	11.37	61.1	23	385131	2454	5438	No
DHI1L	GSLVVVSSLLGR	No									
DHI1L	LGGLDYLVLNHIGGAPAGTR	Yes	665.37	456.2	19.82	86.8	28.5	74912	ND	ND	No
DHI1L	LGGLDYLVLNHIGGAPAGTR	Yes	665.37	686.4	19.82	86.8	40.5	344370	ND	ND	No
DHI1L	LGGLDYLVLNHIGGAPAGTR	Yes	665.37	799.4	19.82	86.8	40.5	158863	ND	ND	No
DHI1L	LGGLDYLVLNHIGGAPAGTR	Yes	665.37	936.5	19.82	86.8	40.5	58319	ND	ND	No
DHI1L	NDGHLEPVTAWEVQVPR	Yes	649.66	272.2	17.59	84.8	30.7	121144	50070	36516	No
DHI1L	NDGHLEPVTAWEVQVPR	Yes	649.66	598.4	17.59	84.8	33.7	26378	5013	6152	No
DHI1L	NDGHLEPVTAWEVQVPR	Yes	649.66	727.4	17.59	84.8	27.7	17353	ND	ND	No
DHI1L	NDGHLEPVTAWEVQVPR	Yes	649.66	913.5	17.59	84.8	27.7	5969	ND	ND	No
DHI1L	VPTSFSTPYSAAK	Yes	678.35	532.3	12.25	88.5	32.3	48478	ND	ND	No
DHI1L	VPTSFSTPYSAAK	Yes	678.35	636.3	12.25	88.5	41.3	241729	ND	ND	No
DHI1L	VPTSFSTPYSAAK	Yes	678.35	824.4	12.25	88.5	35.3	153089	ND	ND	No
DHI1L	VPTSFSTPYSAAK	Yes	678.35	971.5	12.25	88.5	41.3	60933	ND	ND	No
DMBT1	FGQGSGPIVLDDVR	Yes	730.38	274.2	15.09	100	37.6	ND	ND	ND	No
DMBT1	FGQGSGPIVLDDVR	Yes	730.38	617.3	15.09	100	37.6	ND	ND	ND	No
DMBT1	FGQGSGPIVLDDVR	Yes	730.38	926.531	15.09	100	37.6	ND	ND	ND	No
DMBT1	FGQGSGPIVLDDVR	Yes	730.38	983.553	15.09	100	34.6	ND	ND	ND	No
DMBT1	INLGFSNLK	Yes	503.291	228.135	15.50	100	24.6	ND	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
DMBT1	INLGFSNLK	Yes	503.291	608.3	15.50	100	27.6	ND	ND	ND	No
DMBT1	INLGFSNLK	Yes	503.291	665.362	15.50	100	24.6	ND	ND	ND	No
DMBT1	INLGFSNLK	Yes	503.291	778.4	15.50	100	27.6	ND	ND	ND	No
DMBT1	VDVVLGPIQLQTPPR	Yes	816.5	1049.6	22.60	100	41.4	ND	ND	ND	No
DMBT1	VDVVLGPIQLQTPPR	Yes	816.5	1106.6	22.60	100	41.4	ND	ND	ND	No
DMBT1	VDVVLGPIQLQTPPR	Yes	816.5	1219.7	22.60	100	41.4	ND	ND	ND	No
DMBT1	VDVVLGPIQLQTPPR	Yes	816.5	369.2	22.60	100	41.4	ND	ND	ND	No
DMKN	GGVSPSSSASR	No									
DMKN	LGFINWDAINK	No									
DMKN	QVPGFGVADALGNR	Yes	700.87	346.2	16.42	91.4	36.3	13044	ND	ND	No
DMKN	QVPGFGVADALGNR	Yes	700.87	530.3	16.42	91.4	42.3	44882	ND	ND	No
DMKN	QVPGFGVADALGNR	Yes	700.87	645.3	16.42	91.4	42.3	11449	ND	ND	No
DMKN	QVPGFGVADALGNR	Yes	700.87	872.5	16.42	91.4	36.3	12328	ND	ND	No
DMKN	VGEAAHALGNTGHEIGR	Yes	563.62	286.1	9.09	73.7	35.3	9951	ND	ND	No
DMKN	VGEAAHALGNTGHEIGR	Yes	563.62	474.3	9.09	73.7	32.3	19401	ND	ND	No
DMKN	VGEAAHALGNTGHEIGR	Yes	563.62	611.3	9.09	73.7	35.3	7755	ND	ND	No
DMKN	VGEAAHALGNTGHEIGR	Yes	563.62	668.3	9.09	73.7	35.3	6808	ND	ND	No
DMKN	VSEALGQGTR	Yes	509.27	631.4	7.11	66.7	24.9	73307	ND	ND	No
DMKN	VSEALGQGTR	Yes	509.27	702.4	7.11	66.7	27.9	60628	ND	ND	No
DMKN	VSEALGQGTR	Yes	509.27	831.4	7.11	66.7	24.9	57457	ND	ND	No
DMKN	VSEALGQGTR	Yes	509.27	918.5	7.11	66.7	33.9	38564	ND	ND	No
DPP4	LGTFEVEDQIEAAR	Yes	789.4	1030.5	18.70	100	40.2	ND	14706	16193	No
DPP4	LGTFEVEDQIEAAR	Yes	789.4	446.2	18.70	100	40.2	ND	9761	14262	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
DPP4	LGTFEVEDQIEAAR	Yes	789.4	802.4	18.70	100	40.2	ND	13413	9179	No
DPP4	LGTFEVEDQIEAAR	Yes	789.4	931.4	18.70	100	40.2	ND	17430	16865	No
DPP4	MLQNVQMPSK	Yes	588.3	331.2	13.70	100	31.4	ND	ND	ND	No
DPP4	MLQNVQMPSK	Yes	588.3	462.2	13.70	100	31.4	ND	ND	ND	No
DPP4	MLQNVQMPSK	Yes	588.3	803.4	13.70	100	31.4	ND	ND	ND	No
DPP4	MLQNVQMPSK	Yes	588.3	931.5	13.70	100	31.4	ND	ND	ND	No
DPP4	WEYYDSVYTER	Yes	755.8	1032.5	14.13	100	38.8	ND	ND	ND	No
DPP4	WEYYDSVYTER	Yes	755.8	1195.5	14.13	100	32.8	ND	ND	ND	No
DPP4	WEYYDSVYTER	Yes	755.8	316.1	14.13	100	35.8	ND	ND	ND	No
DPP4	WEYYDSVYTER	Yes	755.8	869.4	14.13	100	38.8	ND	ND	ND	No
DPP4	WISDHEYLYK	Yes	451.9	310.2	13.21	100	23.5	ND	ND	ND	No
DPP4	WISDHEYLYK	Yes	451.9	423.3	13.21	100	23.5	ND	ND	ND	No
DPP4	WISDHEYLYK	Yes	451.9	426.7	13.21	100	23.5	ND	ND	ND	No
DPP4	WISDHEYLYK	Yes	451.9	586.3	13.21	100	23.5	ND	ND	ND	No
DPP4	WISDHEYLYK	Yes	677.3	1054.5	13.21	100	35.3	ND	ND	ND	No
DPP4	WISDHEYLYK	Yes	677.3	527.7	13.21	100	35.3	ND	ND	ND	No
DPP4	WISDHEYLYK	Yes	677.3	584.3	13.21	100	35.3	ND	ND	ND	No
DPP4	WISDHEYLYK	Yes	677.3	852.4	13.21	100	35.3	ND	ND	ND	No
DPP4	YMGLPTPEDNLDHYR	Yes	607.6	295.1	18.40	100	31.5	ND	ND	ND	No
DPP4	YMGLPTPEDNLDHYR	Yes	607.6	352.1	18.40	100	31.5	ND	ND	ND	No
DPP4	YMGLPTPEDNLDHYR	Yes	607.6	579.8	18.40	100	31.5	ND	ND	ND	No
DPP4	YMGLPTPEDNLDHYR	Yes	910.9	1158.5	18.40	100	45.6	ND	ND	ND	No
DPP4	YMGLPTPEDNLDHYR	Yes	910.9	352.1	18.40	100	45.6	ND	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
DPP4	YMGLPTPEDNLDHYR	Yes	910.9	678.8	18.40	100	45.6	ND	ND	ND	No
DSG2	GNNVEKPLELR	No									
DSG2	GQIIGNFQAFDEDTGLPAHAR	Yes	753.04	299.2	18.19	98.1	33	59741	26553	40065	No
DSG2	GQIIGNFQAFDEDTGLPAHAR	Yes	753.04	551.3	18.19	98.1	42	60555	22581	16687	No
DSG2	GQIIGNFQAFDEDTGLPAHAR	Yes	753.04	721.4	18.19	98.1	33	4877	ND	ND	No
DSG2	GQIIGNFQAFDEDTGLPAHAR	Yes	753.04	937.5	18.19	98.1	42	4335	ND	ND	No
DSG2	ILDVNDNIPVVENK	Yes	791.43	342.2	15.34	103.1	43.3	159085	11428	15120	No
DSG2	ILDVNDNIPVVENK	Yes	791.43	489.3	15.34	103.1	37.3	43864	ND	3260	No
DSG2	ILDVNDNIPVVENK	Yes	791.43	685.4	15.34	103.1	46.3	188161	9363	13092	No
DSG2	ILDVNDNIPVVENK	Yes	791.43	897.5	15.34	103.1	34.3	33601	ND	ND	No
DSG2	NLDFSVIVANK	Yes	610.34	431.3	17.88	79.7	35.4	95923	ND	ND	No
DSG2	NLDFSVIVANK	Yes	610.34	730.4	17.88	79.7	29.4	60999	ND	ND	No
DSG2	NLDFSVIVANK	Yes	610.34	877.5	17.88	79.7	29.4	45163	ND	ND	No
DSG2	NLDFSVIVANK	Yes	610.34	992.5	17.88	79.7	29.4	91436	ND	ND	No
DSG2	VYAPASTLVDQPYANEGTVVVTER	Yes	860.44	405.2	16.59	112	41.4	9975	ND	ND	No
DSG2	VYAPASTLVDQPYANEGTVVVTER	Yes	860.44	504.3	16.59	112	44.4	11474	ND	ND	No
DSG2	VYAPASTLVDQPYANEGTVVVTER	Yes	860.44	603.3	16.59	112	38.4	7390	ND	ND	No
DSG2	VYAPASTLVDQPYANEGTVVVTER	Yes	860.44	702.4	16.59	112	38.4	3740	ND	ND	No
DX39A	DFLLKPELLR	Yes	415.25	288.2	19.46	54.6	27.7	5684	ND	ND	No
DX39A	DFLLKPELLR	Yes	415.25	530.3	19.46	54.6	27.7	18948	ND	ND	No
DX39A	DFLLKPELLR	Yes	415.25	627.4	19.46	54.6	24.7	255482	ND	ND	No
DX39A	DFLLKPELLR	Yes	415.25	755.5	19.46	54.6	27.7	31238	ND	ND	No
DX39A	FEVNVAELPEEIDISTYIEQSR	Yes	861.09	519.3	24.28	112.1	41.5	6595	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
DX39A	FEVNVAELPEEIDISTYIEQSR	Yes	861.09	795.4	24.28	112.1	41.5	7402	ND	ND	No
DX39A	FEVNVAELPEEIDISTYIEQSR	Yes	861.09	896.4	24.28	112.1	38.5	3400	ND	ND	No
DX39A	FEVNVAELPEEIDISTYIEQSR	Yes	861.09	983.5	24.28	112.1	38.5	7487	ND	ND	No
DX39A	GLAITFVSDENDAK	No									
DX39A	ILNDVQDR	Yes	486.76	418.2	8.34	63.8	26.9	6350	ND	ND	No
DX39A	ILNDVQDR	Yes	486.76	632.3	8.34	63.8	32.9	5435	ND	ND	No
DX39A	ILNDVQDR	Yes	486.76	746.3	8.34	63.8	23.9	32212	ND	ND	No
DX39A	ILNDVQDR	Yes	486.76	859.4	8.34	63.8	29.9	4830	ND	ND	No
DX39A	LTPHEK	Yes	362.7	276.2	5.35	47.8	27.5	79705	ND	ND	No
DX39A	LTPHEK	Yes	362.7	413.2	5.35	47.8	24.5	183462	ND	ND	No
DX39A	LTPHEK	Yes	362.7	510.3	5.35	47.8	18.5	739789	ND	ND	No
DX39A	LTPHEK	Yes	362.7	611.3	5.35	47.8	18.5	52986	ND	ND	No
DX39B	DFLLKPELLR	Yes	415.25	288.2	19.46	54.6	27.7	5684	ND	ND	No
DX39B	DFLLKPELLR	Yes	415.25	530.3	19.46	54.6	27.7	18948	ND	ND	No
DX39B	DFLLKPELLR	Yes	415.25	627.4	19.46	54.6	24.7	255482	ND	ND	No
DX39B	DFLLKPELLR	Yes	415.25	755.5	19.46	54.6	27.7	31238	ND	ND	No
DX39B	ELAFQISK	Yes	468.26	347.2	14.16	61.4	23.1	406175	ND	ND	No
DX39B	ELAFQISK	Yes	468.26	622.4	14.16	61.4	23.1	174446	ND	ND	No
DX39B	ELAFQISK	Yes	468.26	693.4	14.16	61.4	23.1	214847	ND	ND	No
DX39B	ELAFQISK	Yes	468.26	806.5	14.16	61.4	23.1	6359	ND	ND	No
DX39B	FEVNISELPDEIDISSYIEQTR	Yes	866.43	277.1	24.29	112.8	50.7	9373	ND	ND	No
DX39B	FEVNISELPDEIDISSYIEQTR	Yes	866.43	646.4	24.29	112.8	38.7	7591	ND	ND	No
DX39B	FEVNISELPDEIDISSYIEQTR	Yes	866.43	809.4	24.29	112.8	41.7	7252	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
DX39B	FEVNISELPDEIDISSYIEQTR	Yes	866.43	983.5	24.29	112.8	44.7	7151	ND	ND	No
DX39B	GLAITFVSDENDAK	No									
DX39B	ILNDVQDR	Yes	486.76	418.2	8.34	63.8	26.9	6350	ND	ND	No
DX39B	ILNDVQDR	Yes	486.76	632.3	8.34	63.8	32.9	5435	ND	ND	No
DX39B	ILNDVQDR	Yes	486.76	746.3	8.34	63.8	23.9	32212	ND	ND	No
DX39B	ILNDVQDR	Yes	486.76	859.4	8.34	63.8	29.9	4830	ND	ND	No
DYRK2	APEVILGAR	Yes	463.28	416.3	11.68	60.8	28.9	77747	ND	ND	No
DYRK2	APEVILGAR	Yes	463.28	529.3	11.68	60.8	25.9	87960	ND	ND	No
DYRK2	APEVILGAR	Yes	463.28	628.4	11.68	60.8	31.9	57507	ND	ND	No
DYRK2	APEVILGAR	Yes	463.28	757.5	11.68	60.8	31.9	57830	ND	ND	No
DYRK2	ASNAAAAAHTIGGSK	Yes	663.84	770.4	6.85	86.6	31.7	3171	ND	ND	No
DYRK2	ASNAAAAAHTIGGSK	Yes	663.84	841.5	6.85	86.6	34.7	6161	ND	ND	No
DYRK2	ASNAAAAAHTIGGSK	Yes	663.84	912.5	6.85	86.6	37.7	7032	ND	ND	No
DYRK2	ASNAAAAAHTIGGSK	Yes	663.84	983.5	6.85	86.6	40.7	3956	ND	ND	No
DYRK2	QLQASPGLGAGATR	Yes	663.86	528.3	9.48	86.6	31.7	15578	ND	ND	No
DYRK2	QLQASPGLGAGATR	Yes	663.86	799.4	9.48	86.6	34.7	75614	ND	ND	No
DYRK2	QLQASPGLGAGATR	Yes	663.86	886.5	9.48	86.6	37.7	24031	ND	ND	No
DYRK2	QLQASPGLGAGATR	Yes	663.86	957.5	9.48	86.6	40.7	17358	ND	ND	No
DYRK2	SGVGTGPPSPIALPPLR	Yes	808.46	402.2	17.86	105.3	38.1	23000	ND	ND	No
DYRK2	SGVGTGPPSPIALPPLR	Yes	808.46	482.3	17.86	105.3	38.1	268169	ND	ND	No
DYRK2	SGVGTGPPSPIALPPLR	Yes	808.46	595.4	17.86	105.3	41.1	24024	ND	ND	No
DYRK2	SGVGTGPPSPIALPPLR	Yes	808.46	876.6	17.86	105.3	47.1	46280	ND	ND	No
DYRK2	TGLPVVPER	Yes	484.28	304.2	11.77	63.5	32.8	1150	ND	ND	No

Table S5. MRM assay of individual proteins.												
Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
DYRK2	TGLPVVPER	Yes	484.28	401.2	11.77	63.5	32.8	87032	ND	ND	No
DYRK2	TGLPVVPER	Yes	484.28	599.4	11.77	63.5	32.8	21439	ND	ND	No
DYRK2	TGLPVVPER	Yes	484.28	696.4	11.77	63.5	23.8	77098	ND	ND	No
EDN2	GQAAATLEQPASSSHAQGTHLR	Yes	740.04	257.1	8.49	96.5	35.3	7803	ND	ND	No
EDN2	GQAAATLEQPASSSHAQGTHLR	Yes	740.04	328.2	8.49	96.5	35.3	3101	ND	ND	No
EDN2	GQAAATLEQPASSSHAQGTHLR	Yes	740.04	399.2	8.49	96.5	32.3	3119	ND	ND	No
EDN2	GQAAATLEQPASSSHAQGTHLR	Yes	740.04	583.3	8.49	96.5	41.3	1956	ND	ND	No
EDN2	TGATTGELLQR	Yes	573.81	416.3	10.56	75	30.7	17219	ND	ND	No
EDN2	TGATTGELLQR	Yes	573.81	715.4	10.56	75	36.7	48380	ND	ND	No
EDN2	TGATTGELLQR	Yes	573.81	816.5	10.56	75	27.7	40807	ND	ND	No
EDN2	TGATTGELLQR	Yes	573.81	917.5	10.56	75	36.7	12458	ND	ND	No
EF1A1	EHALLAYTLGVK	Yes	438.92	517.3	18.30	57.6	19.9	282452	ND	ND	No
EF1A1	EHALLAYTLGVK	Yes	438.92	564.3	18.30	57.6	19.9	467029	ND	ND	No
EF1A1	EHALLAYTLGVK	Yes	438.92	635.4	18.30	57.6	19.9	542339	ND	ND	No
EF1A1	EHALLAYTLGVK	Yes	438.92	680.4	18.30	57.6	19.9	469927	ND	ND	No
EF1A1	IGGIGTVPVGR	Yes	513.31	428.3	13.61	67.2	25.1	1279522	166904	126364	No
EF1A1	IGGIGTVPVGR	Yes	513.31	628.4	13.61	67.2	25.1	302840	110651	83854	No
EF1A1	IGGIGTVPVGR	Yes	513.31	685.4	13.61	67.2	25.1	1565234	48256	53207	No
EF1A1	IGGIGTVPVGR	Yes	513.31	912.5	13.61	67.2	34.1	309703	11997	5702	No
EF1A1	LPLQDVYK	Yes	488.28	524.3	15.00	64	33	307378	ND	ND	No
EF1A1	LPLQDVYK	Yes	488.28	652.3	15.00	64	33	513178	ND	ND	No
EF1A1	LPLQDVYK	Yes	488.28	765.4	15.00	64	27	911992	ND	ND	No
EF1A1	LPLQDVYK	Yes	488.28	862.5	15.00	64	24	789437	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
EF1A1	MDSTEPPYSQK	Yes	641.78	334.1	8.81	83.8	30.7	196746	ND	ND	No
EF1A1	MDSTEPPYSQK	Yes	641.78	362.2	8.81	83.8	39.7	193866	ND	ND	No
EF1A1	MDSTEPPYSQK	Yes	641.78	719.4	8.81	83.8	30.7	1652112	ND	ND	No
EF1A1	MDSTEPPYSQK	Yes	641.78	848.4	8.81	83.8	30.7	187924	ND	ND	No
EF1A1	QTVAVGVIK	Yes	457.79	416.3	12.59	60.1	22.6	1717888	ND	ND	No
EF1A1	QTVAVGVIK	Yes	457.79	515.4	12.59	60.1	25.6	628376	ND	ND	No
EF1A1	QTVAVGVIK	Yes	457.79	586.4	12.59	60.1	25.6	1088864	ND	ND	No
EF1A1	QTVAVGVIK	Yes	457.79	685.5	12.59	60.1	25.6	582848	ND	ND	No
EF1A1	STTTGHLIYK	Yes	560.8	310.2	10.10	73.3	36.2	1142965	ND	ND	No
EF1A1	STTTGHLIYK	Yes	560.8	730.4	10.10	73.3	36.2	406164	ND	ND	No
EF1A1	STTTGHLIYK	Yes	560.8	831.5	10.10	73.3	33.2	679393	ND	ND	No
EF1A1	STTTGHLIYK	Yes	560.8	932.5	10.10	73.3	30.2	592464	ND	ND	No
EF1A1	THINIVVIGHVDSGK	Yes	530.3	579.3	15.10	69.4	27.6	196084	ND	ND	No
EF1A1	THINIVVIGHVDSGK	Yes	530.3	678.4	15.10	69.4	27.6	86371	ND	ND	No
EF1A1	THINIVVIGHVDSGK	Yes	530.3	699.3	15.10	69.4	27.6	134502	ND	ND	No
EF1A1	THINIVVIGHVDSGK	Yes	530.3	812.4	15.10	69.4	24.6	86539	ND	ND	No
EF1A1	VETGVLKPGMVVTFAPVNVTTEVK	No									
EF1A1	YAWVLDK	Yes	447.74	375.2	17.35	58.8	31.2	479314	ND	ND	No
EF1A1	YAWVLDK	Yes	447.74	474.3	17.35	58.8	31.2	190801	ND	ND	No
EF1A1	YAWVLDK	Yes	447.74	660.4	17.35	58.8	22.2	885828	ND	ND	No
EF1A1	YAWVLDK	Yes	447.74	731.4	17.35	58.8	22.2	289406	ND	ND	No
EF1A1	YYVTIIDAPGHR	Yes	702.87	537.3	15.85	91.7	42.4	324122	ND	ND	No
EF1A1	YYVTIIDAPGHR	Yes	702.87	652.3	15.85	91.7	42.4	119764	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
EF1A1	YYVTIIDAPGHR	Yes	702.87	765.4	15.85	91.7	33.4	255891	ND	ND	No
EF1A1	YYVTIIDAPGHR	Yes	702.87	979.5	15.85	91.7	33.4	123113	ND	ND	No
EF1D	FEEHVQSVDIAAFNK	No									
EF1D	GVVQELQQAISK	Yes	650.37	513.3	19.83	84.9	34.1	14649	ND	ND	No
EF1D	GVVQELQQAISK	Yes	650.37	674.4	19.83	84.9	31.1	21091	ND	ND	No
EF1D	GVVQELQQAISK	Yes	650.37	787.5	19.83	84.9	31.1	28300	ND	ND	No
EF1D	GVVQELQQAISK	Yes	650.37	916.5	19.83	84.9	31.1	25870	ND	ND	No
EF1D	LNVLEK	Yes	358.22	276.2	10.10	47.2	24.3	410865	ND	ND	No
EF1D	LNVLEK	Yes	358.22	389.2	10.10	47.2	18.3	253465	ND	ND	No
EF1D	LNVLEK	Yes	358.22	488.3	10.10	47.2	18.3	420978	ND	ND	No
EF1D	LNVLEK	Yes	358.22	602.4	10.10	47.2	18.3	381046	ND	ND	No
EF1D	SIQLDGLVWGASK	Yes	687.38	362.2	19.99	89.7	41.7	78640	ND	ND	No
EF1D	SIQLDGLVWGASK	Yes	687.38	548.3	19.99	89.7	41.7	129921	ND	ND	No
EF1D	SIQLDGLVWGASK	Yes	687.38	647.4	19.99	89.7	32.7	32955	ND	ND	No
EF1D	SIQLDGLVWGASK	Yes	687.38	932.5	19.99	89.7	32.7	50509	ND	ND	No
EF1D	VGTDLLEEEITK	Yes	673.86	619.3	16.53	87.9	41.1	48089	ND	ND	No
EF1D	VGTDLLEEEITK	Yes	673.86	748.4	16.53	87.9	35.1	153287	ND	ND	No
EF1D	VGTDLLEEEITK	Yes	673.86	861.5	16.53	87.9	32.1	109510	ND	ND	No
EF1D	VGTDLLEEEITK	Yes	673.86	974.5	16.53	87.9	41.1	25033	ND	ND	No
EF2	DSVVAGFQWATK	Yes	654.83	401.2	17.58	85.5	28.3	32974	ND	ND	No
EF2	DSVVAGFQWATK	Yes	654.83	780.4	17.58	85.5	28.3	6934	ND	ND	No
EF2	DSVVAGFQWATK	Yes	654.83	837.4	17.58	85.5	31.3	32045	ND	ND	No
EF2	DSVVAGFQWATK	Yes	654.83	908.5	17.58	85.5	31.3	27154	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
EF2	EGIPALDNFLDK	Yes	444.57	468.2	21.45	58.3	20.2	ND	ND	ND	No
EF2	EGIPALDNFLDK	Yes	444.57	522.3	21.45	58.3	26.2	ND	ND	ND	No
EF2	EGIPALDNFLDK	Yes	444.57	636.3	21.45	58.3	20.2	ND	ND	ND	No
EF2	EGIPALDNFLDK	Yes	444.57	751.4	21.45	58.3	20.2	5705	ND	ND	No
EF2	FSVSPVVR	Yes	445.76	470.3	12.42	58.5	22.1	60775	ND	ND	No
EF2	FSVSPVVR	Yes	445.76	557.3	12.42	58.5	22.1	82628	ND	ND	No
EF2	FSVSPVVR	Yes	445.76	656.4	12.42	58.5	22.1	53597	ND	ND	No
EF2	FSVSPVVR	Yes	445.76	743.4	12.42	58.5	31.1	28009	ND	ND	No
EF2	GEGQLGPAER	No									
EF2	GVQYLNEIK	Yes	532.29	503.3	13.17	69.7	25.9	35864	ND	ND	No
EF2	GVQYLNEIK	Yes	532.29	616.4	13.17	69.7	25.9	30433	ND	ND	No
EF2	GVQYLNEIK	Yes	532.29	779.4	13.17	69.7	25.9	59020	ND	ND	No
EF2	GVQYLNEIK	Yes	532.29	907.5	13.17	69.7	25.9	16284	ND	ND	No
EGF	FIFWSSEVAGSLYR	Yes	831.42	408.2	23.25	108.3	36.1	13750	ND	ND	No
EGF	FIFWSSEVAGSLYR	Yes	831.42	666.4	23.25	108.3	42.1	12118	ND	ND	No
EGF	FIFWSSEVAGSLYR	Yes	831.42	765.4	23.25	108.3	39.1	8433	ND	ND	No
EGF	FIFWSSEVAGSLYR	Yes	831.42	981.5	23.25	108.3	48.1	8311	ND	ND	No
EGF	INLHSSFVPLGELK	Yes	777.44	478.3	18.33	101.3	36.7	22872	ND	ND	No
EGF	INLHSSFVPLGELK	Yes	777.44	656.4	18.33	101.3	45.7	73164	ND	ND	No
EGF	INLHSSFVPLGELK	Yes	777.44	898.5	18.33	101.3	39.7	17241	ND	ND	No
EGF	INLHSSFVPLGELK	Yes	777.44	989.6	18.33	101.3	45.7	10391	ND	ND	No
EGF	LVIASSDLIWPSGITIDFLTDK	No									
EGF	NQVTPLDILSK	Yes	614.35	342.2	18.53	80.3	29.5	827205	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
EGF	NQVTPLDILSK	Yes	614.35	785.5	18.53	80.3	29.5	585562	ND	ND	No
EGF	NQVTPLDILSK	Yes	614.35	886.5	18.53	80.3	29.5	371396	ND	ND	No
EGF	NQVTPLDILSK	Yes	614.35	985.6	18.53	80.3	29.5	313103	ND	ND	No
EGF	YPANVAVDPVER	Yes	665.34	500.3	11.58	86.8	37.8	82787	ND	ND	No
EGF	YPANVAVDPVER	Yes	665.34	714.4	11.58	86.8	40.8	20064	ND	ND	No
EGF	YPANVAVDPVER	Yes	665.34	785.4	11.58	86.8	40.8	38784	ND	ND	No
EGF	YPANVAVDPVER	Yes	665.34	884.5	11.58	86.8	34.8	5715	ND	ND	No
EGFL6	EDDFDWNPADR	Yes	690.28	458.2	15.22	90	32.9	41409	ND	ND	No
EGFL6	EDDFDWNPADR	Yes	690.28	572.3	15.22	90	29.9	24782	ND	ND	No
EGFL6	EDDFDWNPADR	Yes	690.28	758.4	15.22	90	41.9	19741	ND	ND	No
EGFL6	EDDFDWNPADR	Yes	690.28	873.4	15.22	90	41.9	10492	ND	ND	No
EGFL6	GDVFFPK	Yes	405.21	272.1	14.03	53.3	20.3	32940	ND	ND	No
EGFL6	GDVFFPK	Yes	405.21	538.3	14.03	53.3	20.3	63421	ND	ND	No
EGFL6	GDVFFPK	Yes	405.21	637.4	14.03	53.3	20.3	30089	ND	ND	No
EGFL6	GDVFFPK	Yes	405.21	752.4	14.03	53.3	17.3	ND	ND	ND	No
EGFL6	IQLYQGTDATK	Yes	619.33	355.2	10.66	80.9	29.8	85510	ND	ND	No
EGFL6	IQLYQGTDATK	Yes	619.33	592.3	10.66	80.9	29.8	49106	ND	ND	No
EGFL6	IQLYQGTDATK	Yes	619.33	883.4	10.66	80.9	29.8	35055	ND	ND	No
EGFL6	IQLYQGTDATK	Yes	619.33	996.5	10.66	80.9	29.8	57152	ND	ND	No
EGFL6	NSNNALAWEK	Yes	573.78	462.2	11.61	75	36.7	37910	ND	ND	No
EGFL6	NSNNALAWEK	Yes	573.78	533.3	11.61	75	27.7	44862	ND	ND	No
EGFL6	NSNNALAWEK	Yes	573.78	646.4	11.61	75	27.7	25476	ND	ND	No
EGFL6	NSNNALAWEK	Yes	573.78	717.4	11.61	75	27.7	14599	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
EGFL6	VNLQPFNYEEIVSR	Yes	854.44	262.2	19.33	111.2	37.1	25124	ND	ND	No
EGFL6	VNLQPFNYEEIVSR	Yes	854.44	327.2	19.33	111.2	37.1	114032	ND	ND	No
EGFL6	VNLQPFNYEEIVSR	Yes	854.44	455.3	19.33	111.2	37.1	107500	ND	ND	No
EGFL6	VNLQPFNYEEIVSR	Yes	854.44	895.5	19.33	111.2	49.1	12114	ND	ND	No
ENOA	AVEHINK	Yes	405.73	374.2	5.55	53.3	26.4	69683	ND	ND	No
ENOA	AVEHINK	Yes	405.73	437.2	5.55	53.3	26.4	30725	ND	ND	No
ENOA	AVEHINK	Yes	405.73	511.3	5.55	53.3	23.4	51910	ND	ND	No
ENOA	AVEHINK	Yes	405.73	640.3	5.55	53.3	20.4	114288	ND	ND	No
ENOA	GNPTVEVDLFTSK	Yes	703.86	335.2	18.48	91.8	42.5	11414	ND	ND	No
ENOA	GNPTVEVDLFTSK	Yes	703.86	595.3	18.48	91.8	36.5	5021	ND	ND	No
ENOA	GNPTVEVDLFTSK	Yes	703.86	809.4	18.48	91.8	36.5	3943	ND	ND	No
ENOA	GNPTVEVDLFTSK	Yes	703.86	938.5	18.48	91.8	39.5	4426	ND	ND	No
ENOA	IGAEVYHNLK	Yes	572.31	674.4	9.82	74.8	27.7	45359	ND	ND	No
ENOA	IGAEVYHNLK	Yes	572.31	773.4	9.82	74.8	30.7	37643	ND	ND	No
ENOA	IGAEVYHNLK	Yes	572.31	902.5	9.82	74.8	27.7	11652	ND	ND	No
ENOA	IGAEVYHNLK	Yes	572.31	973.5	9.82	74.8	27.7	5767	ND	ND	No
ENOA	YISPDQLADLYK	Yes	713.37	277.2	18.15	93	33.9	662293	21499	15828	No
ENOA	YISPDQLADLYK	Yes	713.37	364.2	18.15	93	33.9	366844	1249	7169	Yes (Based on Transition Ratios)
ENOA	YISPDQLADLYK	Yes	713.37	609.3	18.15	93	42.9	120477	3404	ND	No
ENOA	YISPDQLADLYK	Yes	713.37	965.5	18.15	93	42.9	48642	1723	ND	No
ENOA	YNQLLR	Yes	403.73	278.1	10.19	53.1	20.3	153241	ND	ND	No
ENOA	YNQLLR	Yes	403.73	288.2	10.19	53.1	29.3	222958	13878	23898	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
ENOA	YNQLLR	Yes	403.73	529.3	10.19	53.1	20.3	213830	7357	5631	No
ENOA	YNQLLR	Yes	403.73	643.4	10.19	53.1	20.3	123313	6065	5148	No
ENOG	DATNVGDEGGFAPNILENSEALELVK	No									
ENOG	GNPTVEVDLYTAK	Yes	703.86	482.3	13.91	91.8	42.5	14402	46090	31666	No
ENOG	GNPTVEVDLYTAK	Yes	703.86	598.3	13.91	91.8	42.5	ND	ND	ND	No
ENOG	IEEELGDEAR	Yes	580.78	547.2	9.04	75.9	28.1	43465	ND	ND	No
ENOG	IEEELGDEAR	Yes	580.78	660.3	9.04	75.9	37.1	18199	ND	ND	No
ENOG	IEEELGDEAR	Yes	580.78	789.4	9.04	75.9	37.1	14565	ND	ND	No
ENOG	IEEELGDEAR	Yes	580.78	918.4	9.04	75.9	28.1	23663	ND	ND	No
ENOG	LGAEVYHTLK	Yes	377.55	498.3	10.48	49.7	22.8	68660	ND	ND	No
ENOG	LGAEVYHTLK	Yes	377.55	661.4	10.48	49.7	25.8	65356	ND	ND	No
ENOG	LGAEVYHTLK	Yes	377.55	760.4	10.48	49.7	25.8	13284	ND	ND	No
ENOG	LGAEVYHTLK	Yes	377.55	889.5	10.48	49.7	25.8	ND	ND	ND	No
ENOG	YITGDQLGALYQDFVR	Yes	620.32	536.3	23.42	81	29.2	39286	ND	ND	No
ENOG	YITGDQLGALYQDFVR	Yes	620.32	664.3	23.42	81	26.2	46305	ND	ND	No
ENOG	YITGDQLGALYQDFVR	Yes	620.32	827.4	23.42	81	29.2	77152	ND	ND	No
ENOG	YITGDQLGALYQDFVR	Yes	620.32	940.5	23.42	81	32.2	12170	ND	ND	No
ENOX2	ALYLSGYR	No									
ENOX2	ETEESALVSQAEALK	Yes	535.61	647.3	16.55	70.1	24.9	19602	ND	ND	No
ENOX2	ETEESALVSQAEALK	Yes	535.61	746.4	16.55	70.1	24.9	50961	ND	ND	No
ENOX2	ETEESALVSQAEALK	Yes	535.61	760.3	16.55	70.1	24.9	18019	ND	ND	No
ENOX2	ETEESALVSQAEALK	Yes	535.61	845.5	16.55	70.1	24.9	12619	ND	ND	No
ENOX2	FSEAVQTLLTWIER	Yes	846.95	435.2	24.73	110.3	36.8	1948	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
ENOX2	FSEAVQTLLTWIER	Yes	846.95	704.4	24.73	110.3	39.8	2300	ND	ND	No
ENOX2	FSEAVQTLLTWIER	Yes	846.95	817.5	24.73	110.3	36.8	3734	ND	ND	No
ENOX2	FSEAVQTLLTWIER	Yes	846.95	930.5	24.73	110.3	36.8	2040	ND	ND	No
ENOX2	QALSGILIQFEQIVAVYHSASK	Yes	801.44	313.2	24.67	104.4	35.4	15951	ND	ND	No
ENOX2	QALSGILIQFEQIVAVYHSASK	Yes	801.44	692.3	24.67	104.4	41.4	12585	ND	ND	No
ENOX2	QALSGILIQFEQIVAVYHSASK	Yes	801.44	862.4	24.67	104.4	41.4	16454	ND	ND	No
ENOX2	QALSGILIQFEQIVAVYHSASK	Yes	801.44	961.5	24.67	104.4	38.4	11496	ND	ND	No
ENOX2	WLWVYEIGYAADNSR	Yes	921.94	300.2	24.40	119.9	46.1	6976	ND	ND	No
ENOX2	WLWVYEIGYAADNSR	Yes	921.94	633.3	24.40	119.9	43.1	2115	ND	ND	No
ENOX2	WLWVYEIGYAADNSR	Yes	921.94	853.4	24.40	119.9	43.1	7253	ND	ND	No
ENOX2	WLWVYEIGYAADNSR	Yes	921.94	966.5	24.40	119.9	46.1	3062	ND	ND	No
ENPL	EVEEDEYK	Yes	520.72	310.2	6.67	68.2	25.4	159859	ND	ND	No
ENPL	EVEEDEYK	Yes	520.72	554.2	6.67	68.2	25.4	138082	ND	ND	No
ENPL	EVEEDEYK	Yes	520.72	683.3	6.67	68.2	22.4	91890	ND	ND	No
ENPL	EVEEDEYK	Yes	520.72	812.3	6.67	68.2	22.4	122829	ND	ND	No
ENPL	LISLTDENALSGNEELTVK	No									
ENPL	SGTSEFLNK	Yes	491.75	521.3	9.98	64.4	27.1	153467	7020	9725	No
ENPL	SGTSEFLNK	Yes	491.75	650.4	9.98	64.4	27.1	115761	3255	3174	No
ENPL	SGTSEFLNK	Yes	491.75	737.4	9.98	64.4	24.1	162128	13512	9671	No
ENPL	SGTSEFLNK	Yes	491.75	838.4	9.98	64.4	24.1	53908	1878	1869	No
ENPL	SGYLLPDTK	Yes	497.27	460.2	12.37	65.1	24.4	700923	27388	28600	No
ENPL	SGYLLPDTK	Yes	497.27	573.3	12.37	65.1	24.4	522473	26652	15849	No
ENPL	SGYLLPDTK	Yes	497.27	686.4	12.37	65.1	24.4	430229	18227	12571	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
ENPL	SGYLLPDTK	Yes	497.27	849.5	12.37	65.1	24.4	40441	1030	1047	No
ENPL	TDDEVVQR	Yes	481.23	402.2	6.39	63.1	23.7	158185	ND	ND	No
ENPL	TDDEVVQR	Yes	481.23	501.3	6.39	63.1	23.7	86187	ND	ND	No
ENPL	TDDEVVQR	Yes	481.23	630.4	6.39	63.1	23.7	53938	ND	ND	No
ENPL	TDDEVVQR	Yes	481.23	745.4	6.39	63.1	23.7	185205	ND	ND	No
EPHB6	RPHFDQLVAAFDK	Yes	772.4	254.2	16.97	100.6	36.5	6478	23825	4931	No
EPHB6	RPHFDQLVAAFDK	Yes	772.4	480.2	16.97	100.6	42.5	6160	12516	ND	No
EPHB6	RPHFDQLVAAFDK	Yes	772.4	551.3	16.97	100.6	39.5	6601	19284	3474	No
EPHB6	RPHFDQLVAAFDK	Yes	772.4	653.3	16.97	100.6	45.5	8393	6547	ND	Yes (Based on Transition Ratios)
EPHB6	SFGPLTQR	Yes	453.25	404.2	11.72	59.5	25.4	34875	ND	ND	No
EPHB6	SFGPLTQR	Yes	453.25	517.3	11.72	59.5	28.4	30445	ND	ND	No
EPHB6	SFGPLTQR	Yes	453.25	614.4	11.72	59.5	22.4	31306	ND	ND	No
EPHB6	SFGPLTQR	Yes	453.25	671.4	11.72	59.5	22.4	111464	14453	15195	No
EPHB6	VDTIAADESFPSSSSSSSSSSSAAWAVGPHGAGQR	No									
EPHB6	VYFQTLPQGELSSQLPER	Yes	698.03	401.2	17.42	91	33.1	157460	ND	ND	No
EPHB6	VYFQTLPQGELSSQLPER	Yes	698.03	514.3	17.42	91	33.1	52989	ND	ND	No
EPHB6	VYFQTLPQGELSSQLPER	Yes	698.03	729.4	17.42	91	33.1	50535	ND	ND	No
EPHB6	VYFQTLPQGELSSQLPER	Yes	698.03	816.4	17.42	91	33.1	83906	ND	ND	No
EPHB6	WAAPEVIAHGK	Yes	393.55	341.2	12.29	51.8	23.6	189724	26283	ND	No
EPHB6	WAAPEVIAHGK	Yes	393.55	426.2	12.29	51.8	20.6	151412	74312	72181	Yes (Based on Transition Ratios)

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
EPHB6	WAAPEVIAHGK	Yes	393.55	525.3	12.29	51.8	20.6	205261	20303	16073	No
EPHB6	WAAPEVIAHGK	Yes	393.55	624.4	12.29	51.8	20.6	56079	ND	ND	No
EPOR	IWPGIPSPESEFEGLFTTHK	Yes	758.05	284.2	24.46	98.8	45.2	33116	ND	ND	No
EPOR	IWPGIPSPESEFEGLFTTHK	Yes	758.05	300.2	24.46	98.8	33.2	144234	ND	ND	No
EPOR	IWPGIPSPESEFEGLFTTHK	Yes	758.05	633.3	24.46	98.8	42.2	23782	ND	ND	No
EPOR	IWPGIPSPESEFEGLFTTHK	Yes	758.05	803.4	24.46	98.8	42.2	31798	ND	ND	No
EPOR	LADESGHVVLR	Yes	399.22	486.3	9.47	52.5	23.9	61944	ND	ND	No
EPOR	LADESGHVVLR	Yes	399.22	623.4	9.47	52.5	26.9	24880	ND	ND	No
EPOR	LADESGHVVLR	Yes	399.22	680.4	9.47	52.5	26.9	30395	ND	ND	No
EPOR	LADESGHVVLR	Yes	399.22	767.5	9.47	52.5	20.9	31603	ND	ND	No
EPOR	VIHINEVVLLDAPVGLVAR	Yes	676.41	711.5	22.76	88.3	29	117205	ND	ND	No
EPOR	VIHINEVVLLDAPVGLVAR	Yes	676.41	805.5	22.76	88.3	41	69973	ND	ND	No
EPOR	VIHINEVVLLDAPVGLVAR	Yes	676.41	897.5	22.76	88.3	29	48225	ND	ND	No
EPOR	VIHINEVVLLDAPVGLVAR	Yes	676.41	904.5	22.76	88.3	32	68395	ND	ND	No
EPOR	VTAASGAPR	Yes	415.23	629.3	5.61	54.6	20.8	229518	ND	ND	No
EPOR	VTAASGAPR	Yes	415.23	730.4	5.61	54.6	20.8	49616	ND	ND	No
EPOR	YEVDVSAGNGAGSVQR	Yes	536.93	293.1	10.18	70.3	27.9	31670	ND	ND	No
EPOR	YEVDVSAGNGAGSVQR	Yes	536.93	606.3	10.18	70.3	21.9	7098	ND	ND	No
EPOR	YEVDVSAGNGAGSVQR	Yes	536.93	617.3	10.18	70.3	24.9	5543	ND	ND	No
EPOR	YEVDVSAGNGAGSVQR	Yes	536.93	674.4	10.18	70.3	24.9	6936	ND	ND	No
ERBB3	GALGPQLLLNWGVQIAK	No									
ERBB3	GESIEPLDPSEK	Yes	650.82	460.2	11.37	85	40.1	293168	ND	ND	No
ERBB3	GESIEPLDPSEK	Yes	650.82	575.3	11.37	85	40.1	16213	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
ERBB3	GESIEPLDPSEK	Yes	650.82	785.4	11.37	85	31.1	202724	ND	ND	No
ERBB3	GESIEPLDPSEK	Yes	650.82	914.4	11.37	85	31.1	45628	ND	ND	No
ERBB3	LAEVPDLLEK	Yes	563.82	314.2	16.74	73.7	27.3	958105	ND	ND	No
ERBB3	LAEVPDLLEK	Yes	563.82	714.4	16.74	73.7	27.3	759834	ND	ND	No
ERBB3	LAEVPDLLEK	Yes	563.82	813.5	16.74	73.7	27.3	177956	ND	ND	No
ERBB3	LAEVPDLLEK	Yes	563.82	942.5	16.74	73.7	27.3	206519	ND	ND	No
ERBB3	SLEATDSAFDNPDYWHSR	Yes	704.31	399.2	15.86	91.9	39.5	16987	ND	ND	No
ERBB3	SLEATDSAFDNPDYWHSR	Yes	704.31	585.3	15.86	91.9	42.5	10383	ND	ND	No
ERBB3	SLEATDSAFDNPDYWHSR	Yes	704.31	748.4	15.86	91.9	42.5	12350	ND	ND	No
ERBB3	SLEATDSAFDNPDYWHSR	Yes	704.31	960.4	15.86	91.9	39.5	11282	ND	ND	No
ERBB3	SPSQVQVADFGVADLLPPDDK	Yes	733.37	262.1	21.26	95.6	44	7191	ND	45106	Yes (Based on Transition Ratios)
ERBB3	SPSQVQVADFGVADLLPPDDK	Yes	733.37	571.3	21.26	95.6	38	54317	ND	ND	No
ERBB3	SPSQVQVADFGVADLLPPDDK	Yes	733.37	627.3	21.26	95.6	35	5223	ND	3117	Yes (Based on Transition Ratios)
ERBB3	SPSQVQVADFGVADLLPPDDK	Yes	733.37	684.4	21.26	95.6	32	6658	ND	ND	No
EREG	VAQVSITK	Yes	423.26	448.3	8.24	55.6	30.1	63643	15149	26855	No
EREG	VAQVSITK	Yes	423.26	547.3	8.24	55.6	21.1	56975	11251	10492	No
EREG	VAQVSITK	Yes	423.26	675.4	8.24	55.6	21.1	105937	ND	ND	No
EREG	VAQVSITK	Yes	423.26	746.4	8.24	55.6	21.1	71973	ND	ND	No
EREG	VTSGDPELPQV	Yes	571.29	343.2	14.55	74.7	27.6	305277	ND	ND	No
EREG	VTSGDPELPQV	Yes	571.29	460.2	14.55	74.7	24.6	53166	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
EREG	VTSGDPELPQV	Yes	571.29	686.3	14.55	74.7	27.6	20165	ND	ND	No
EREG	VTSGDPELPQV	Yes	571.29	799.4	14.55	74.7	24.6	85149	ND	ND	No
ERO1A	AVLQWTK	Yes	423.25	562.3	12.94	55.6	21.1	45163	ND	ND	No
ERO1A	AVLQWTK	Yes	423.25	675.4	12.94	55.6	21.1	144756	ND	ND	No
ERO1A	AVLQWTK	Yes	423.25	699.4	12.94	55.6	21.1	2110	ND	ND	No
ERO1A	AVLQWTK	Yes	423.25	774.5	12.94	55.6	21.1	7725	ND	ND	No
ERO1A	LGAVDESLSEETQK	Yes	753.37	376.2	11.19	98.2	35.6	24992	ND	ND	No
ERO1A	LGAVDESLSEETQK	Yes	753.37	721.3	11.19	98.2	38.6	34456	ND	ND	No
ERO1A	LGAVDESLSEETQK	Yes	753.37	834.4	11.19	98.2	35.6	11287	ND	ND	No
ERO1A	LGAVDESLSEETQK	Yes	753.37	921.5	11.19	98.2	44.6	14954	ND	ND	No
ERO1A	LLESDYFR	Yes	521.76	485.3	14.82	68.3	34.5	48917	ND	4165	No
ERO1A	LLESDYFR	Yes	521.76	687.3	14.82	68.3	25.5	38479	ND	1818	No
ERO1A	LLESDYFR	Yes	521.76	816.4	14.82	68.3	25.5	110559	ND	8550	No
ERO1A	LLESDYFR	Yes	521.76	929.4	14.82	68.3	34.5	8952	ND	ND	No
ERO1A	NLLQNIH	Yes	426.24	383.2	13.42	56	21.3	35545	6471	ND	No
ERO1A	NLLQNIH	Yes	426.24	469.3	13.42	56	24.3	17521	1787	1459	No
ERO1A	NLLQNIH	Yes	426.24	511.3	13.42	56	21.3	52614	ND	ND	No
ERO1A	NLLQNIH	Yes	426.24	624.3	13.42	56	21.3	114838	5388	4068	No
ERO1A	VLPFFERPDFQLFTGNK	Yes	685.7	318.2	24.08	89.5	41.5	184511	ND	ND	No
ERO1A	VLPFFERPDFQLFTGNK	Yes	685.7	419.2	24.08	89.5	41.5	230266	ND	ND	No
ERO1A	VLPFFERPDFQLFTGNK	Yes	685.7	566.3	24.08	89.5	35.5	90886	ND	ND	No
ERO1A	VLPFFERPDFQLFTGNK	Yes	685.7	954.5	24.08	89.5	35.5	28868	ND	ND	No
ESM1	FPFFQYSVTK	Yes	632.32	392.2	20.18	82.6	33.3	134086	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
ESM1	FPFFQYSVTK	Yes	632.32	597.3	20.18	82.6	39.3	138780	ND	ND	No
ESM1	FPFFQYSVTK	Yes	632.32	725.4	20.18	82.6	33.3	118244	ND	ND	No
ESM1	FPFFQYSVTK	Yes	632.32	872.5	20.18	82.6	33.3	242120	ND	ND	No
EZRI	EAQDDLVK	Yes	459.23	359.3	7.74	60.2	22.7	290721	ND	ND	No
EZRI	EAQDDLVK	Yes	459.23	589.3	7.74	60.2	22.7	311887	ND	ND	No
EZRI	EAQDDLVK	Yes	459.23	717.4	7.74	60.2	22.7	94101	ND	ND	No
EZRI	ELSEQIQR	Yes	501.76	303.2	8.24	65.7	24.6	36442	5003	2466	No
EZRI	ELSEQIQR	Yes	501.76	416.3	8.24	65.7	21.6	16893	ND	2803	No
EZRI	ELSEQIQR	Yes	501.76	544.3	8.24	65.7	24.6	23090	1915	2814	No
EZRI	ELSEQIQR	Yes	501.76	760.4	8.24	65.7	27.6	42622	4757	6660	No
EZRI	IQVWHAEHR	Yes	392.54	312.2	8.88	51.6	26.6	10843	ND	ND	No
EZRI	IQVWHAEHR	Yes	392.54	512.3	8.88	51.6	26.6	9140	ND	ND	No
EZRI	IQVWHAEHR	Yes	392.54	649.3	8.88	51.6	23.6	6875	ND	ND	No
EZRI	IQVWHAEHR	Yes	392.54	835.4	8.88	51.6	26.6	ND	ND	ND	No
EZRI	LQDYEEK	Yes	462.72	276.2	6.59	60.7	31.9	121469	ND	ND	No
EZRI	LQDYEEK	Yes	462.72	568.3	6.59	60.7	25.9	49412	ND	ND	No
EZRI	LQDYEEK	Yes	462.72	683.3	6.59	60.7	22.9	184425	ND	ND	No
EZRI	LQDYEEK	Yes	462.72	811.3	6.59	60.7	22.9	73890	ND	ND	No
EZRI	SGYLSSER	Yes	449.72	308.1	7.81	59	22.3	56775	ND	ND	No
EZRI	SGYLSSER	Yes	449.72	478.2	7.81	59	22.3	61830	ND	ND	No
EZRI	SGYLSSER	Yes	449.72	591.3	7.81	59	22.3	42151	ND	ND	No
EZRI	SGYLSSER	Yes	449.72	754.4	7.81	59	25.3	7934	ND	ND	No
F10A1	ADEPSSEESDLEIDK	Yes	832.36	262.1	11.02	108.4	39.1	30732	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
F10A1	ADEPSSEESDLEIDK	Yes	832.36	375.2	11.02	108.4	48.1	28226	ND	ND	No
F10A1	ADEPSSEESDLEIDK	Yes	832.36	617.4	11.02	108.4	48.1	20461	ND	ND	No
F10A1	ADEPSSEESDLEIDK	Yes	832.36	948.5	11.02	108.4	39.1	11096	ND	ND	No
F10A1	AIDLFTDAIK	Yes	553.81	300.2	19.40	72.4	26.9	622894	ND	ND	No
F10A1	AIDLFTDAIK	Yes	553.81	694.4	19.40	72.4	26.9	360087	ND	ND	No
F10A1	AIDLFTDAIK	Yes	553.81	807.5	19.40	72.4	26.9	189782	ND	ND	No
F10A1	AIDLFTDAIK	Yes	553.81	922.5	19.40	72.4	26.9	572031	ND	ND	No
F10A1	AIEINPDSAQPYK	Yes	723.37	314.2	12.13	94.3	34.3	408722	ND	ND	No
F10A1	AIEINPDSAQPYK	Yes	723.37	407.2	12.13	94.3	34.3	192727	ND	ND	No
F10A1	AIEINPDSAQPYK	Yes	723.37	427.3	12.13	94.3	31.3	103245	ND	ND	No
F10A1	AIEINPDSAQPYK	Yes	723.37	905.4	12.13	94.3	34.3	220982	ND	ND	No
F10A1	LQKPNAAIR	Yes	337.54	359.2	7.34	44.5	23.8	6030	ND	ND	No
F10A1	LQKPNAAIR	Yes	337.54	430.3	7.34	44.5	23.8	6383	ND	ND	No
F10A1	LQKPNAAIR	Yes	337.54	544.3	7.34	44.5	23.8	5425	ND	ND	No
F10A1	LQKPNAAIR	Yes	337.54	641.4	7.34	44.5	20.8	26173	2385	2333	No
F10A1	YQSNPK	Yes	368.69	292.1	5.30	48.6	15.7	31677	ND	ND	No
F10A1	YQSNPK	Yes	368.69	445.2	5.30	48.6	18.7	93292	ND	ND	No
F10A1	YQSNPK	Yes	368.69	493.2	5.30	48.6	18.7	1929	ND	ND	No
F10A1	YQSNPK	Yes	368.69	573.3	5.30	48.6	18.7	40205	ND	ND	No
FAM3C	GINVALANGK	Yes	478.78	502.3	10.94	62.8	23.6	23538	ND	ND	No
FAM3C	GINVALANGK	Yes	478.78	573.3	10.94	62.8	23.6	57540	ND	ND	No
FAM3C	GINVALANGK	Yes	478.78	672.4	10.94	62.8	23.6	12670	ND	ND	No
FAM3C	GINVALANGK	Yes	478.78	786.4	10.94	62.8	23.6	26251	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
FAM3C	LVVAVAVFLLTFYVISQVFEIK	No									
FAM3C	SALDTAAR	Yes	402.71	317.2	6.77	52.9	17.2	8208	ND	ND	No
FAM3C	SALDTAAR	Yes	402.71	533.3	6.77	52.9	23.2	61136	ND	ND	No
FAM3C	SALDTAAR	Yes	402.71	646.4	6.77	52.9	20.2	45390	ND	ND	No
FAM3C	SALDTAAR	Yes	402.71	717.4	6.77	52.9	20.2	1620	ND	ND	No
FAM3C	SPFEQHIK	Yes	493.26	525.3	8.62	64.6	27.2	23202	ND	ND	No
FAM3C	SPFEQHIK	Yes	493.26	654.4	8.62	64.6	27.2	48767	ND	ND	No
FAM3C	SPFEQHIK	Yes	493.26	801.4	8.62	64.6	24.2	57377	ND	ND	No
FAM3C	SPFEQHIK	Yes	493.26	839.4	8.62	64.6	24.2	13692	ND	ND	No
FAM3C	TGEVLDTK	Yes	431.73	476.3	7.46	56.7	21.5	323199	ND	ND	No
FAM3C	TGEVLDTK	Yes	431.73	575.3	7.46	56.7	21.5	398328	ND	ND	No
FAM3C	TGEVLDTK	Yes	431.73	704.4	7.46	56.7	21.5	318410	ND	ND	No
FAM3C	TGEVLDTK	Yes	431.73	761.4	7.46	56.7	21.5	356025	ND	ND	No
FAS	GNAGQSNYGFANSAMER	Yes	887.4	1145.5	14.50	100	44.5	ND	ND	ND	No
FAS	GNAGQSNYGFANSAMER	Yes	887.4	707.3	14.50	100	44.5	ND	ND	ND	No
FAS	GNAGQSNYGFANSAMER	Yes	887.4	778.4	14.50	100	44.5	ND	ND	ND	No
FAS	GNAGQSNYGFANSAMER	Yes	887.4	982.4	14.50	100	44.5	ND	ND	ND	No
FAS	LPEDPLLSGLLDSPALK	Yes	889.5	1000.6	26.80	100	44.6	ND	ND	ND	No
FAS	LPEDPLLSGLLDSPALK	Yes	889.5	455.2	26.80	100	44.6	ND	ND	ND	No
FAS	LPEDPLLSGLLDSPALK	Yes	889.5	515.3	26.80	100	44.6	ND	ND	ND	No
FAS	LPEDPLLSGLLDSPALK	Yes	889.5	913.5	26.80	100	44.6	ND	ND	ND	No
FAS	LQVVDQPLPVR	Yes	632.4	1022.6	13.18	100	33.3	ND	ND	ND	No
FAS	LQVVDQPLPVR	Yes	632.4	242.2	13.18	100	33.3	ND	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
FAS	LQVVDQPLPVR	Yes	632.4	581.4	13.18	100	33.3	ND	ND	ND	No
FAS	LQVVDQPLPVR	Yes	632.4	923.5	13.18	100	33.3	ND	ND	ND	No
FAS	MVVPGLDGAQIPR	Yes	676.9	1023.6	19.20	100	35.3	ND	ND	ND	No
FAS	MVVPGLDGAQIPR	Yes	676.9	512.3	19.20	100	35.3	ND	ND	ND	No
FAS	MVVPGLDGAQIPR	Yes	676.9	561.8	19.20	100	35.3	ND	ND	ND	No
FAS	MVVPGLDGAQIPR	Yes	676.9	641.4	19.20	100	35.3	ND	ND	ND	No
FAS	SEGVVAVLLTK	Yes	558.3	373.2	19.80	100	30.1	ND	15703	18358	No
FAS	SEGVVAVLLTK	Yes	558.3	644.4	19.80	100	30.1	ND	13257	19030	No
FAS	SEGVVAVLLTK	Yes	558.3	743.5	19.80	100	30.1	ND	ND	ND	No
FAS	SEGVVAVLLTK	Yes	558.3	899.6	19.80	100	30.1	ND	ND	ND	No
FAS	VLEALLPLK	Yes	498.329	213.16	17.93	100	21.4	ND	28550	28826	No
FAS	VLEALLPLK	Yes	498.329	357.3	17.93	100	27.4	ND	6268	ND	No
FAS	VLEALLPLK	Yes	498.329	654.5	17.93	100	27.4	ND	ND	ND	No
FAS	VLEALLPLK	Yes	498.329	783.498	17.93	100	24.4	ND	6983	5103	No
FCGR1	GWLLLQVSSR	No									
FCGR1	HLEEELK	Yes	449.24	260.2	7.56	59	25.3	340537	2110	4383	No
FCGR1	HLEEELK	Yes	449.24	638.3	7.56	59	25.3	227886	2374	ND	No
FCGR1	HLEEELK	Yes	449.24	647.3	7.56	59	22.3	77002	ND	ND	No
FCGR1	HLEEELK	Yes	449.24	760.4	7.56	59	22.3	73769	ND	ND	No
FCGR1	LVYNVLYYR	Yes	601.83	501.2	17.52	78.6	29	58433	ND	ND	No
FCGR1	LVYNVLYYR	Yes	601.83	713.4	17.52	78.6	29	26965	ND	ND	No
FCGR1	LVYNVLYYR	Yes	601.83	827.4	17.52	78.6	38	59326	ND	ND	No
FCGR1	LVYNVLYYR	Yes	601.83	990.5	17.52	78.6	29	87290	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
FCGR1	VFTEGEPLALR	Yes	616.34	569.4	15.36	80.5	38.6	198000	ND	ND	No
FCGR1	VFTEGEPLALR	Yes	616.34	755.4	15.36	80.5	38.6	162685	ND	ND	No
FCGR1	VFTEGEPLALR	Yes	616.34	884.5	15.36	80.5	38.6	32375	ND	ND	No
FCGR1	VFTEGEPLALR	Yes	616.34	985.5	15.36	80.5	29.6	78184	ND	ND	No
FCGR1	YTSAGISVTVK	Yes	563.31	533.3	11.56	73.7	24.3	33544	ND	ND	No
FCGR1	YTSAGISVTVK	Yes	563.31	703.4	11.56	73.7	30.3	54360	ND	ND	No
FCGR1	YTSAGISVTVK	Yes	563.31	774.5	11.56	73.7	27.3	31140	ND	ND	No
FCGR1	YTSAGISVTVK	Yes	563.31	861.5	11.56	73.7	27.3	83725	ND	ND	No
FGF10	IEENGYNTYASFNWQHNGR	Yes	767.34	483.2	15.04	100	39.7	1893	ND	ND	No
FGF10	IEENGYNTYASFNWQHNGR	Yes	767.34	486.2	15.04	100	45.7	2705	ND	ND	No
FGF10	IEENGYNTYASFNWQHNGR	Yes	767.34	543.2	15.04	100	45.7	1841	ND	ND	No
FGF10	IEENGYNTYASFNWQHNGR	Yes	767.34	797.4	15.04	100	36.7	3547	ND	ND	No
FGF10	SYNHLQGDVR	Yes	396.86	274.2	7.64	52.2	26.8	109849	ND	ND	No
FGF10	SYNHLQGDVR	Yes	396.86	446.2	7.64	52.2	20.8	14466	ND	ND	No
FGF10	SYNHLQGDVR	Yes	396.86	574.3	7.64	52.2	26.8	15544	ND	ND	No
FGF10	SYNHLQGDVR	Yes	396.86	687.4	7.64	52.2	23.8	10073	ND	ND	No
FGF2	LESNNYNTYR	Yes	637.29	553.3	8.13	83.2	30.5	14632	ND	ND	No
FGF2	LESNNYNTYR	Yes	637.29	716.3	8.13	83.2	39.5	6892	ND	ND	No
FGF2	LESNNYNTYR	Yes	637.29	830.4	8.13	83.2	30.5	5414	ND	ND	No
FGF2	LESNNYNTYR	Yes	637.29	944.4	8.13	83.2	33.5	3719	ND	ND	No
FGF2	LQLQAEER	Yes	493.77	355.2	9.15	64.7	24.2	15664	ND	ND	No
FGF2	LQLQAEER	Yes	493.77	433.2	9.15	64.7	27.2	10139	ND	ND	No
FGF2	LQLQAEER	Yes	493.77	632.3	9.15	64.7	24.2	27638	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
FGF2	LQLQAEER	Yes	493.77	745.4	9.15	64.7	24.2	82344	ND	ND	No
FGF2	NGGFFLR	Yes	405.72	288.2	15.25	53.3	26.4	236086	ND	ND	No
FGF2	NGGFFLR	Yes	405.72	435.3	15.25	53.3	20.4	180822	ND	ND	No
FGF2	NGGFFLR	Yes	405.72	639.4	15.25	53.3	20.4	79566	ND	ND	No
FGF2	NGGFFLR	Yes	405.72	696.4	15.25	53.3	20.4	72112	ND	ND	No
FGF7	ELILENHYNTYASAK	Yes	589.3	305.2	13.21	77	36.6	183207	ND	ND	No
FGF7	ELILENHYNTYASAK	Yes	589.3	376.2	13.21	77	36.6	43676	ND	ND	No
FGF7	ELILENHYNTYASAK	Yes	589.3	640.3	13.21	77	27.6	85427	ND	ND	No
FGF7	ELILENHYNTYASAK	Yes	589.3	754.4	13.21	77	36.6	28332	ND	ND	No
FGF7	TQWYLR	No									
FGF7	TVAVGIVAIK	No									
FGF7	WILTWILPTLLYR	Yes	844.5	514.3	25.06	109.9	36.7	ND	ND	ND	No
FGF7	WILTWILPTLLYR	Yes	844.5	762.5	25.06	109.9	39.7	1996	ND	ND	No
FGF7	WILTWILPTLLYR	Yes	844.5	875.5	25.06	109.9	39.7	1701	ND	ND	No
FGF7	WILTWILPTLLYR	Yes	844.5	988.6	25.06	109.9	39.7	1352	ND	ND	No
FGF9	EQFEENWYNTYSSNLYK	Yes	1107.98	537.3	18.62	143.9	60.3	3614	ND	ND	No
FGF9	EQFEENWYNTYSSNLYK	Yes	1107.98	711.4	18.62	143.9	51.3	12390	ND	ND	No
FGF9	EQFEENWYNTYSSNLYK	Yes	1107.98	874.4	18.62	143.9	48.3	6068	ND	ND	No
FGF9	EQFEENWYNTYSSNLYK	Yes	1107.98	975.5	18.62	143.9	51.3	6444	ND	ND	No
FGF9	FGILEFISIAVGLVSIR	No									
FGF9	FTHFLPRPVDPDK	Yes	523.61	359.2	12.77	68.5	27.3	1196128	ND	ND	No
FGF9	FTHFLPRPVDPDK	Yes	523.61	386.2	12.77	68.5	27.3	145839	ND	ND	No
FGF9	FTHFLPRPVDPDK	Yes	523.61	474.2	12.77	68.5	27.3	35138	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
FGF9	FTHFLPRPVDPDK	Yes	523.61	646.3	12.77	68.5	24.3	25476	ND	ND	No
FGF9	GELYGSEK	Yes	441.71	300.2	7.34	58	18.9	257454	ND	ND	No
FGF9	GELYGSEK	Yes	441.71	420.2	7.34	58	24.9	430201	ND	5894	No
FGF9	GELYGSEK	Yes	441.71	583.3	7.34	58	21.9	546511	ND	ND	No
FGF9	GELYGSEK	Yes	441.71	696.4	7.34	58	21.9	449118	ND	ND	No
FGF9	GPAVTDLDHLK	Yes	389.21	512.3	11.97	51.2	20.4	153580	1230	4907	No
FGF9	GPAVTDLDHLK	Yes	389.21	625.4	11.97	51.2	26.4	125532	2891	6598	No
FGF9	GPAVTDLDHLK	Yes	389.21	740.4	11.97	51.2	17.4	85383	ND	1198	No
FGF9	GPAVTDLDHLK	Yes	389.21	841.4	11.97	51.2	26.4	1218	ND	ND	No
FGFR2	EIEVLYIR	Yes	517.8	451.3	17.23	67.8	25.3	51145	21240	22725	No
FGFR2	EIEVLYIR	Yes	517.8	564.4	17.23	67.8	25.3	ND	ND	ND	Yes (Based on Manual Review)
FGFR2	EIEVLYIR	Yes	517.8	663.4	17.23	67.8	34.3	20438	16510	16602	No
FGFR2	EIEVLYIR	Yes	517.8	792.5	17.23	67.8	25.3	34827	6047	11105	No
FGFR2	QLVEDLDR	Yes	494.26	518.3	11.25	64.8	24.2	14993	ND	ND	No
FGFR2	QLVEDLDR	Yes	494.26	647.3	11.25	64.8	24.2	20398	ND	ND	No
FGFR2	QLVEDLDR	Yes	494.26	746.4	11.25	64.8	33.2	20939	ND	ND	No
FGFR2	QLVEDLDR	Yes	494.26	859.5	11.25	64.8	33.2	2040	ND	ND	No
FGFR2	TVLIGEYLQIK	Yes	638.88	314.2	20.32	83.4	30.6	26171	ND	ND	No
FGFR2	TVLIGEYLQIK	Yes	638.88	793.4	20.32	83.4	30.6	3361	ND	ND	No
FGFR2	TVLIGEYLQIK	Yes	638.88	850.5	20.32	83.4	30.6	20889	ND	3356	No
FGFR2	TVLIGEYLQIK	Yes	638.88	963.6	20.32	83.4	30.6	6521	ND	ND	No
FGFR2	YGPDGLPYLK	Yes	561.8	520.3	15.81	73.5	33.2	233341	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
FGFR2	YGPDGLPYLK	Yes	561.8	690.4	15.81	73.5	27.2	88367	ND	ND	No
FGFR2	YGPDGLPYLK	Yes	561.8	805.4	15.81	73.5	30.2	101872	ND	ND	No
FGFR2	YGPDGLPYLK	Yes	561.8	959.5	15.81	73.5	36.2	22783	ND	ND	No
FGFR2	YQISQPEVYVAAPGESLEVR	Yes	745.71	274.2	17.21	97.2	35.6	3807	ND	ND	No
FGFR2	YQISQPEVYVAAPGESLEVR	Yes	745.71	292.1	17.21	97.2	35.6	8138	ND	ND	No
FGFR2	YQISQPEVYVAAPGESLEVR	Yes	745.71	789.4	17.21	97.2	41.6	3718	ND	ND	No
FGFR2	YQISQPEVYVAAPGESLEVR	Yes	745.71	886.5	17.21	97.2	32.6	13817	ND	ND	No
FGFR3	DGTGLVPSER	Yes	515.76	488.2	9.53	67.5	25.2	279428	ND	ND	No
FGFR3	DGTGLVPSER	Yes	515.76	587.3	9.53	67.5	25.2	116643	ND	ND	No
FGFR3	DGTGLVPSER	Yes	515.76	700.4	9.53	67.5	34.2	20119	ND	ND	No
FGFR3	DGTGLVPSER	Yes	515.76	757.4	9.53	67.5	34.2	55073	ND	ND	No
FGFR3	LSSGEGPTLANVSELELPADPK	Yes	742.05	527.3	18.67	96.7	35.4	16898	ND	ND	No
FGFR3	LSSGEGPTLANVSELELPADPK	Yes	742.05	640.4	18.67	96.7	35.4	9393	ND	ND	No
FGFR3	LSSGEGPTLANVSELELPADPK	Yes	742.05	769.4	18.67	96.7	35.4	7431	ND	ND	No
FGFR3	LSSGEGPTLANVSELELPADPK	Yes	742.05	882.5	18.67	96.7	35.4	3841	ND	ND	No
FGFR3	QLVEDLDR	Yes	494.26	518.3	11.25	64.8	24.2	14993	ND	ND	No
FGFR3	QLVEDLDR	Yes	494.26	647.3	11.25	64.8	24.2	20398	ND	ND	No
FGFR3	QLVEDLDR	Yes	494.26	746.4	11.25	64.8	33.2	20939	ND	ND	No
FGFR3	QLVEDLDR	Yes	494.26	859.5	11.25	64.8	33.2	2040	ND	ND	No
FGFR3	TAGANTTDK	Yes	439.71	578.3	5.22	57.7	24.8	34724	ND	ND	No
FGFR3	TAGANTTDK	Yes	439.71	649.3	5.22	57.7	24.8	21721	ND	ND	No
FGFR3	TAGANTTDK	Yes	439.71	706.3	5.22	57.7	21.8	326122	ND	ND	No
FGFR3	TAGANTTDK	Yes	439.71	777.4	5.22	57.7	21.8	44560	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
FGFR3	VGPDGTPYVTVLK	Yes	673.37	527.2	14.85	87.9	32.1	109094	ND	ND	No
FGFR3	VGPDGTPYVTVLK	Yes	673.37	624.3	14.85	87.9	32.1	123855	ND	ND	No
FGFR3	VGPDGTPYVTVLK	Yes	673.37	819.5	14.85	87.9	32.1	435767	ND	ND	No
FGFR3	VGPDGTPYVTVLK	Yes	673.37	977.6	14.85	87.9	41.1	59252	ND	ND	No
FGL2	ELESEVNK	Yes	474.24	261.2	6.85	62.2	32.4	385689	ND	ND	No
FGL2	ELESEVNK	Yes	474.24	576.3	6.85	62.2	23.4	439142	ND	ND	No
FGL2	ELESEVNK	Yes	474.24	687.3	6.85	62.2	26.4	102265	ND	ND	No
FGL2	ELESEVNK	Yes	474.24	705.3	6.85	62.2	23.4	207094	ND	ND	No
FGL2	LHVGNYNGTAGDALR	Yes	779.39	251.2	11.37	101.5	42.8	77385	ND	ND	No
FGL2	LHVGNYNGTAGDALR	Yes	779.39	350.2	11.37	101.5	42.8	23924	ND	ND	No
FGL2	LHVGNYNGTAGDALR	Yes	779.39	359.2	11.37	101.5	45.8	17649	ND	ND	No
FGL2	LHVGNYNGTAGDALR	Yes	779.39	874.4	11.37	101.5	39.8	2787	ND	ND	No
FGL2	LQADDNGDPGR	Yes	579.26	313.2	5.87	75.7	28	9746	ND	ND	No
FGL2	LQADDNGDPGR	Yes	579.26	329.2	5.87	75.7	34	110167	ND	ND	No
FGL2	LQADDNGDPGR	Yes	579.26	845.3	5.87	75.7	34	9261	ND	ND	No
FGL2	LQADDNGDPGR	Yes	579.26	916.4	5.87	75.7	28	34730	ND	ND	No
FGL2	NGLLLPSTGAPGEVGDNR	Yes	883.96	285.2	15.26	115	47.4	178497	ND	ND	No
FGL2	NGLLLPSTGAPGEVGDNR	Yes	883.96	398.2	15.26	115	41.4	79881	ND	ND	No
FGL2	NGLLLPSTGAPGEVGDNR	Yes	883.96	511.3	15.26	115	38.4	54188	ND	ND	No
FGL2	NGLLLPSTGAPGEVGDNR	Yes	883.96	843.4	15.26	115	47.4	18873	ND	ND	No
FGL2	VANLTFVVNSLDGK	Yes	738.91	285.2	20.54	96.3	38	21300	ND	ND	No
FGL2	VANLTFVVNSLDGK	Yes	738.91	499.3	20.54	96.3	32	5166	ND	ND	No
FGL2	VANLTFVVNSLDGK	Yes	738.91	831.5	20.54	96.3	35	9259	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
FGL2	VANLTFVVNSLDGK	Yes	738.91	978.5	20.54	96.3	38	8010	ND	ND	No
FHIT	EDFPASWR	No									
FHIT	FGQHLIKPSVVFLK	Yes	538.32	583.3	16.39	70.4	31	33627	ND	ND	No
FHIT	FGQHLIKPSVVFLK	Yes	538.32	692.4	16.39	70.4	28	6722	ND	ND	No
FHIT	FGQHLIKPSVVFLK	Yes	538.32	696.4	16.39	70.4	28	20202	ND	ND	No
FHIT	FGQHLIKPSVVFLK	Yes	538.32	789.5	16.39	70.4	25	18357	ND	ND	No
FHIT	FHDLRPDEVADLFQTTQR	Yes	730.03	285.1	18.90	95.2	40.8	55166	ND	ND	No
FHIT	FHDLRPDEVADLFQTTQR	Yes	730.03	505.3	18.90	95.2	37.8	31304	ND	ND	No
FHIT	FHDLRPDEVADLFQTTQR	Yes	730.03	633.3	18.90	95.2	37.8	25649	ND	ND	No
FHIT	FHDLRPDEVADLFQTTQR	Yes	730.03	780.4	18.90	95.2	37.8	34383	ND	ND	No
FHIT	NDSIYEELQK	Yes	619.8	317.1	13.54	81	29.8	123167	ND	ND	No
FHIT	NDSIYEELQK	Yes	619.8	646.3	13.54	81	29.8	47158	ND	ND	No
FHIT	NDSIYEELQK	Yes	619.8	809.4	13.54	81	29.8	203022	ND	ND	No
FHIT	NDSIYEELQK	Yes	619.8	922.5	13.54	81	29.8	34240	ND	ND	No
FHIT	VGTVVEK	Yes	366.22	258.1	6.17	48.2	27.6	322881	124324	82128	No
FHIT	VGTVVEK	Yes	366.22	474.3	6.17	48.2	18.6	43761	ND	ND	No
FHIT	VGTVVEK	Yes	366.22	575.3	6.17	48.2	18.6	152201	ND	ND	No
FHIT	VGTVVEK	Yes	366.22	632.4	6.17	48.2	15.6	315975	122374	86772	No
FIBA	GGSTSYGTGSETESPR	Yes	786.84	359.2	6.60	102.5	34.1	10536	251042	128435	No
FIBA	GGSTSYGTGSETESPR	Yes	786.84	589.3	6.60	102.5	34.1	4729	85096	52250	No
FIBA	GGSTSYGTGSETESPR	Yes	786.84	862.4	6.60	102.5	43.1	13782	258324	191387	No
FIBA	GGSTSYGTGSETESPR	Yes	786.84	963.4	6.60	102.5	37.1	4944	92896	80685	No
FIBA	GLIDEVNQDFTNR	No									

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
FIBA	NSLFEYQK	Yes	514.76	315.2	12.75	67.4	25.1	280129	335170	271272	No
FIBA	NSLFEYQK	Yes	514.76	567.3	12.75	67.4	25.1	145176	176963	154518	No
FIBA	NSLFEYQK	Yes	514.76	714.3	12.75	67.4	25.1	306108	445913	309747	No
FIBA	NSLFEYQK	Yes	514.76	827.4	12.75	67.4	25.1	139234	207608	149704	No
FIBA	TVIGPDGHK	Yes	308.5	341.2	6.20	40.8	22.3	52939	60633	38900	No
FIBA	TVIGPDGHK	Yes	308.5	456.2	6.20	40.8	22.3	43078	46803	25976	No
FIBA	TVIGPDGHK	Yes	308.5	553.3	6.20	40.8	16.3	58799	68942	41070	No
FIBA	TVIGPDGHK	Yes	308.5	610.3	6.20	40.8	13.3	115226	141698	66202	No
FIBA	VQHIQLLQK	Yes	369.56	501.3	11.15	48.7	19.4	41693	37127	15096	No
FIBA	VQHIQLLQK	Yes	369.56	606.3	11.15	48.7	25.4	12694	13190	1629	No
FIBA	VQHIQLLQK	Yes	369.56	629.4	11.15	48.7	19.4	15393	16804	4338	No
FIBA	VQHIQLLQK	Yes	369.56	742.5	11.15	48.7	16.4	10161	7888	3283	No
FINC	HTSVQTTSSGSGPFTDVR	Yes	621.97	274.2	10.99	81.2	38.3	ND	ND	ND	No
FINC	HTSVQTTSSGSGPFTDVR	Yes	621.97	734.4	10.99	81.2	29.3	ND	ND	ND	No
FINC	HTSVQTTSSGSGPFTDVR	Yes	621.97	878.4	10.99	81.2	29.3	15533	ND	ND	No
FINC	HTSVQTTSSGSGPFTDVR	Yes	621.97	935.5	10.99	81.2	35.3	ND	ND	ND	No
FINC	SSPVVIDASTAIDAPSNLR	No									
FINC	SYTITGLQPGTDYK	Yes	772.39	352.2	13.93	100.6	36.5	106423	ND	ND	No
FINC	SYTITGLQPGTDYK	Yes	772.39	680.3	13.93	100.6	36.5	120465	ND	ND	No
FINC	SYTITGLQPGTDYK	Yes	772.39	808.4	13.93	100.6	33.5	21020	ND	ND	No
FINC	SYTITGLQPGTDYK	Yes	772.39	978.5	13.93	100.6	36.5	38438	ND	ND	No
FINC	VPGTSTSATLTGLTR	Yes	487.94	446.3	13.14	63.9	22.4	54973	ND	ND	No
FINC	VPGTSTSATLTGLTR	Yes	487.94	547.3	13.14	63.9	22.4	43942	ND	ND	No

Table S5. MRM assay of individual proteins.											
Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
FINC	VPGTSTSATLTGLTR	Yes	487.94	660.4	13.14	63.9	25.4	8324	ND	ND	No
FINC	VPGTSTSATLTGLTR	Yes	487.94	701.3	13.14	63.9	22.4	5016	ND	ND	No
FINC	VVTPLSPPTNLHLEANPDTGVLTVSWER	Yes	1014.87	300.2	21.70	131.9	46.3	ND	ND	ND	No
FINC	VVTPLSPPTNLHLEANPDTGVLTVSWER	Yes	1014.87	577.3	21.70	131.9	46.3	ND	ND	ND	No
FINC	VVTPLSPPTNLHLEANPDTGVLTVSWER	Yes	1014.87	777.4	21.70	131.9	49.3	ND	ND	ND	No
FINC	VVTPLSPPTNLHLEANPDTGVLTVSWER	Yes	1014.87	890.5	21.70	131.9	46.3	ND	ND	ND	No
FKB11	AEAGLETESPVR	Yes	629.82	371.2	10.11	82.2	30.2	35197	ND	ND	No
FKB11	AEAGLETESPVR	Yes	629.82	688.4	10.11	82.2	33.2	44723	ND	ND	No
FKB11	AEAGLETESPVR	Yes	629.82	817.4	10.11	82.2	33.2	45902	ND	ND	No
FKB11	AEAGLETESPVR	Yes	629.82	987.5	10.11	82.2	39.2	13030	ND	ND	No
FKB11	ANYWLK	Yes	397.71	260.2	13.24	52.3	29	153600	ND	ND	No
FKB11	ANYWLK	Yes	397.71	446.3	13.24	52.3	20	54095	ND	ND	No
FKB11	ANYWLK	Yes	397.71	609.3	13.24	52.3	20	145690	ND	ND	No
FKB11	ANYWLK	Yes	397.71	723.4	13.24	52.3	20	32858	ND	ND	No
FKB11	DPLVIELGQK	Yes	556.32	326.2	16.11	72.8	27	960171	ND	ND	No
FKB11	DPLVIELGQK	Yes	556.32	445.3	16.11	72.8	36	222987	ND	ND	No
FKB11	DPLVIELGQK	Yes	556.32	687.4	16.11	72.8	27	591374	ND	ND	No
FKB11	DPLVIELGQK	Yes	556.32	786.5	16.11	72.8	27	355708	ND	ND	No
FKB11	IIDTSLTR	Yes	459.77	342.2	10.42	60.3	22.7	14359	ND	ND	No
FKB11	IIDTSLTR	Yes	459.77	577.3	10.42	60.3	31.7	31213	ND	ND	No
FKB11	IIDTSLTR	Yes	459.77	692.4	10.42	60.3	22.7	93052	ND	ND	No
FKB11	IIDTSLTR	Yes	459.77	805.4	10.42	60.3	22.7	12380	ND	ND	No
FOLH1	DSWVFGGIDPQSGAAVVHEIVR	Yes	780.4	387.3	22.74	101.7	46.4	4920	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
FOLH1	DSWVFGGIDPQSGAAVVHEIVR	Yes	780.4	389.1	22.74	101.7	37.4	44712	ND	ND	No
FOLH1	DSWVFGGIDPQSGAAVVHEIVR	Yes	780.4	488.2	22.74	101.7	34.4	15888	ND	ND	No
FOLH1	DSWVFGGIDPQSGAAVVHEIVR	Yes	780.4	752.4	22.74	101.7	43.4	6717	ND	ND	No
FOLH1	GVILYSDPADYFAPGVK	Yes	906.46	270.2	20.76	117.9	42.4	621589	ND	ND	No
FOLH1	GVILYSDPADYFAPGVK	Yes	906.46	383.3	20.76	117.9	39.4	319322	ND	ND	No
FOLH1	GVILYSDPADYFAPGVK	Yes	906.46	400.3	20.76	117.9	51.4	571945	ND	ND	No
FOLH1	GVILYSDPADYFAPGVK	Yes	906.46	471.3	20.76	117.9	51.4	131760	ND	ND	No
FOLH1	LGSGNDFEVFFQR	Yes	758.37	450.2	21.06	98.8	35.9	95476	66837	87446	Yes (Based on Transition Ratios)
FOLH1	LGSGNDFEVFFQR	Yes	758.37	597.3	21.06	98.8	35.9	180812	45786	53409	No
FOLH1	LGSGNDFEVFFQR	Yes	758.37	696.4	21.06	98.8	44.9	99088	42721	51820	No
FOLH1	LGSGNDFEVFFQR	Yes	758.37	825.4	21.06	98.8	38.9	137502	51353	50481	No
FOLH1	SYPDGWNLPGGGVQR	Yes	534.93	459.3	15.52	70	30.8	ND	ND	ND	No
FOLH1	SYPDGWNLPGGGVQR	Yes	534.93	573.3	15.52	70	27.8	26690	ND	ND	No
FOLH1	SYPDGWNLPGGGVQR	Yes	534.93	670.4	15.52	70	24.8	65126	ND	ND	No
FOLH1	SYPDGWNLPGGGVQR	Yes	534.93	783.4	15.52	70	24.8	ND	ND	ND	No
FOLH1	TYSVSFDSLFSAVK	Yes	775.89	352.2	23.30	101.1	36.6	36780	ND	ND	No
FOLH1	TYSVSFDSLFSAVK	Yes	775.89	404.3	23.30	101.1	42.6	16594	ND	ND	No
FOLH1	TYSVSFDSLFSAVK	Yes	775.89	751.4	23.30	101.1	45.6	10770	ND	ND	No
FOLH1	TYSVSFDSLFSAVK	Yes	775.89	866.5	23.30	101.1	33.6	17893	ND	ND	No
FOLR1	DVSYLYR	Yes	458.23	302.1	11.97	60.1	19.7	20349	ND	ND	No
FOLR1	DVSYLYR	Yes	458.23	338.2	11.97	60.1	25.7	22175	ND	ND	No
FOLR1	DVSYLYR	Yes	458.23	614.3	11.97	60.1	25.7	18355	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
FOLR1	DVSYLYR	Yes	458.23	701.4	11.97	60.1	22.7	141112	ND	ND	No
FOLR1	EKPGPEDK	Yes	450.23	262.1	5.29	59.1	31.3	57632	ND	ND	No
FOLR1	EKPGPEDK	Yes	450.23	488.2	5.29	59.1	31.3	55564	ND	ND	No
FOLR1	EKPGPEDK	Yes	450.23	545.3	5.29	59.1	31.3	79863	ND	ND	No
FOLR1	EKPGPEDK	Yes	450.23	642.3	5.29	59.1	22.3	232514	ND	ND	No
FOLR1	GWNWTSGFNK	Yes	598.78	552.3	18.11	78.2	37.8	47714	ND	ND	No
FOLR1	GWNWTSGFNK	Yes	598.78	653.3	18.11	78.2	28.8	53968	ND	ND	No
FOLR1	GWNWTSGFNK	Yes	598.78	839.4	18.11	78.2	28.8	44300	ND	ND	No
FOLR1	GWNWTSGFNK	Yes	598.78	953.4	18.11	78.2	28.8	38690	ND	ND	No
FOLR1	VSNYSR	Yes	363.18	262.2	5.49	47.9	27.5	7736	ND	ND	No
FOLR1	VSNYSR	Yes	363.18	425.2	5.49	47.9	24.5	4258	ND	ND	No
FOLR1	VSNYSR	Yes	363.18	539.3	5.49	47.9	18.5	17561	ND	ND	No
FOLR1	VSNYSR	Yes	363.18	626.3	5.49	47.9	18.5	20804	ND	ND	No
FOXA2	AYEQVMHYPGYGSPMPGSLAMGPVTNK	Yes	961.45	558.3	17.74	125	46.6	24850	ND	ND	No
FOXA2	AYEQVMHYPGYGSPMPGSLAMGPVTNK	Yes	961.45	615.3	17.74	125	52.6	8781	ND	ND	No
FOXA2	AYEQVMHYPGYGSPMPGSLAMGPVTNK	Yes	961.45	817.4	17.74	125	46.6	ND	ND	ND	No
FOXA2	AYEQVMHYPGYGSPMPGSLAMGPVTNK	Yes	961.45	930.5	17.74	125	46.6	ND	ND	ND	No
FOXA2	EAAGAAGSGK	Yes	409.7	348.2	5.76	53.9	20.5	192883	ND	ND	No
FOXA2	EAAGAAGSGK	Yes	409.7	490.3	5.76	53.9	20.5	105898	ND	ND	No
FOXA2	EAAGAAGSGK	Yes	409.7	547.3	5.76	53.9	20.5	235811	ND	ND	No
FOXA2	EAAGAAGSGK	Yes	409.7	618.3	5.76	53.9	23.5	150181	ND	ND	No
FOXA2	MHSASSMLGAVK	Yes	406.87	374.2	13.15	53.5	18.3	1840859	ND	ND	No
FOXA2	MHSASSMLGAVK	Yes	406.87	487.3	13.15	53.5	18.3	1116955	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
FOXA2	MHSASSMLGAVK	Yes	406.87	601.2	13.15	53.5	15.3	392109	ND	ND	No
FOXA2	MHSASSMLGAVK	Yes	406.87	732.3	13.15	53.5	18.3	480754	ND	ND	No
FOXA2	MLTLSEIYQWIMDLFPFYR	No									
FOXA2	SYTHAKPPYSYISLITMAIQQSPNK	No									
FOXA2	TGLDASPLAADTSYYQGVYSRPIMNSS	Yes	955.45	387.2	20.08	124.3	52.3	12986	ND	ND	No
FOXA2	TGLDASPLAADTSYYQGVYSRPIMNSS	Yes	955.45	545.3	20.08	124.3	52.3	9178	ND	ND	No
FOXA2	TGLDASPLAADTSYYQGVYSRPIMNSS	Yes	955.45	648.3	20.08	124.3	43.3	21099	ND	ND	No
FOXA2	TGLDASPLAADTSYYQGVYSRPIMNSS	Yes	955.45	826.4	20.08	124.3	49.3	6470	ND	ND	No
FOXA2	WQNSIR	No									
FP100	AEYLPPSVASIK	Yes	637.85	364.2	17.16	83.3	30.6	ND	ND	ND	No
FP100	AEYLPPSVASIK	Yes	637.85	477.2	17.16	83.3	27.6	ND	ND	ND	No
FP100	AEYLPPSVASIK	Yes	637.85	701.4	17.16	83.3	39.6	ND	ND	ND	No
FP100	AEYLPPSVASIK	Yes	637.85	798.5	17.16	83.3	30.6	ND	ND	ND	No
FP100	APSPLGPTR	Yes	448.25	256.1	8.32	58.8	22.2	25923	ND	ND	No
FP100	APSPLGPTR	Yes	448.25	543.3	8.32	58.8	31.2	17147	ND	ND	No
FP100	APSPLGPTR	Yes	448.25	640.4	8.32	58.8	25.2	35916	ND	ND	No
FP100	APSPLGPTR	Yes	448.25	727.4	8.32	58.8	22.2	16442	ND	ND	No
FP100	ELLSGIGNISER	Yes	644.35	675.3	16.18	84.1	30.9	41926	ND	ND	No
FP100	ELLSGIGNISER	Yes	644.35	788.4	16.18	84.1	30.9	9248	ND	ND	No
FP100	ELLSGIGNISER	Yes	644.35	845.4	16.18	84.1	30.9	21635	ND	ND	No
FP100	ELLSGIGNISER	Yes	644.35	932.5	16.18	84.1	30.9	22228	ND	ND	No
FP100	EPGSQPAGPASLR	Yes	633.83	499.2	8.74	82.8	30.4	16923	ND	ND	No
FP100	EPGSQPAGPASLR	Yes	633.83	543.3	8.74	82.8	39.4	25039	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
FP100	EPGSQPAGPASLR	Yes	633.83	600.3	8.74	82.8	39.4	46345	ND	ND	No
FP100	EPGSQPAGPASLR	Yes	633.83	768.4	8.74	82.8	30.4	202001	ND	ND	No
FP100	SAPGDPNALVK	Yes	534.79	428.2	9.29	70	23	49117	ND	ND	No
FP100	SAPGDPNALVK	Yes	534.79	641.4	9.29	70	32	513839	ND	ND	No
FP100	SAPGDPNALVK	Yes	534.79	813.4	9.29	70	29	301921	ND	ND	No
FP100	SAPGDPNALVK	Yes	534.79	910.5	9.29	70	26	186353	ND	ND	No
FRIH	HTLGDSDNES	No									
FRIH	NVNQSLLELHK	Yes	432.24	397.3	12.80	56.8	28.6	110216	188672	198440	No
FRIH	NVNQSLLELHK	Yes	432.24	526.3	12.80	56.8	22.6	59293	179028	170681	No
FRIH	NVNQSLLELHK	Yes	432.24	639.4	12.80	56.8	22.6	42222	92092	125788	No
FRIH	NVNQSLLELHK	Yes	432.24	839.5	12.80	56.8	19.6	23532	74505	73009	No
FRIH	QNYHQDSEAAINR	No									
FRIH	YFLHQSHEER	Yes	449.21	311.1	7.82	58.9	23.5	12003	ND	ND	No
FRIH	YFLHQSHEER	Yes	449.21	570.3	7.82	58.9	29.5	3782	ND	ND	No
FRIH	YFLHQSHEER	Yes	449.21	657.3	7.82	58.9	29.5	7495	ND	ND	No
FRIH	YFLHQSHEER	Yes	449.21	785.4	7.82	58.9	29.5	11764	ND	ND	No
FRIL	ALFQDIK	Yes	417.74	260.2	16.18	54.9	29.9	3810242	23807	39385	No
FRIL	ALFQDIK	Yes	417.74	503.3	16.18	54.9	20.9	1658809	21084	10678	No
FRIL	ALFQDIK	Yes	417.74	650.4	16.18	54.9	20.9	13108685	108507	108354	No
FRIL	ALFQDIK	Yes	417.74	763.4	16.18	54.9	20.9	594854	5486	8152	No
FRIL	DDVALEGVSHFFR	Yes	497.91	469.3	21.28	65.2	31.9	227599	ND	ND	No
FRIL	DDVALEGVSHFFR	Yes	497.91	693.3	21.28	65.2	28.9	386963	ND	ND	No
FRIL	DDVALEGVSHFFR	Yes	497.91	849.4	21.28	65.2	31.9	365420	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
FRIL	DDVALEGVSHFFR	Yes	497.91	978.5	21.28	65.2	28.9	190128	ND	ND	No
FRIL	KPAEDEWGK	Yes	353.84	297.2	8.64	46.6	24.6	29602	ND	ND	No
FRIL	KPAEDEWGK	Yes	353.84	390.2	8.64	46.6	18.6	108976	ND	ND	No
FRIL	KPAEDEWGK	Yes	353.84	541.3	8.64	46.6	15.6	50904	ND	ND	No
FRIL	KPAEDEWGK	Yes	353.84	634.3	8.64	46.6	12.6	15648	ND	ND	No
FRIL	LGGPEAGLGEYLFER	Yes	804.41	451.2	22.04	104.8	46.9	39822	30769	20834	No
FRIL	LGGPEAGLGEYLFER	Yes	804.41	525.3	22.04	104.8	37.9	66747	53070	46944	No
FRIL	LGGPEAGLGEYLFER	Yes	804.41	564.3	22.04	104.8	46.9	36082	37791	21762	No
FRIL	LGGPEAGLGEYLFER	Yes	804.41	913.4	22.04	104.8	46.9	88924	73407	54708	No
FRIL	LNQALLDLHALGSAR	Yes	531.3	356.2	19.29	69.5	33.6	194342	ND	ND	No
FRIL	LNQALLDLHALGSAR	Yes	531.3	427.2	19.29	69.5	24.6	63877	ND	ND	No
FRIL	LNQALLDLHALGSAR	Yes	531.3	574.3	19.29	69.5	27.6	157532	ND	ND	No
FRIL	LNQALLDLHALGSAR	Yes	531.3	711.4	19.29	69.5	33.6	127649	ND	ND	No
FRIL	MGDHLTNLHR	Yes	398.53	312.2	9.46	52.4	26.9	220056	11477	7008	No
FRIL	MGDHLTNLHR	Yes	398.53	539.3	9.46	52.4	26.9	118206	5587	4786	No
FRIL	MGDHLTNLHR	Yes	398.53	640.4	9.46	52.4	23.9	266343	12654	10610	No
FRIL	MGDHLTNLHR	Yes	398.53	753.4	9.46	52.4	26.9	102197	3213	1675	No
G3P	GALQNIIPASTGAAK	Yes	706.399	1042.6	13.97	100	36.6	ND	11890	13713	No
G3P	GALQNIIPASTGAAK	Yes	706.399	597.336	13.97	100	30.6	ND	17514	20777	No
G3P	GALQNIIPASTGAAK	Yes	706.399	815.463	13.97	100	30.6	ND	85112	81049	No
G3P	GALQNIIPASTGAAK	Yes	706.399	928.5	13.97	100	36.6	ND	11299	18298	No
G3P	LISWYDNEFGYSNR	Yes	882.405	1101.5	17.92	100	44.3	ND	3801	4720	No
G3P	LISWYDNEFGYSNR	Yes	882.405	596.279	17.92	100	38.3	ND	10800	8992	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
G3P	LISWYDNEFGYSNR	Yes	882.405	743.348	17.92	100	50.3	ND	10181	10233	No
G3P	LVINGNPITIFQER	Yes	807.5	1003.6	23.00	100	41	ND	ND	ND	No
G3P	LVINGNPITIFQER	Yes	807.5	579.3	23.00	100	41	ND	ND	ND	No
G3P	LVINGNPITIFQER	Yes	807.5	692.4	23.00	100	41	ND	ND	ND	No
G3P	LVINGNPITIFQER	Yes	807.5	793.4	23.00	100	41	ND	ND	ND	No
G3P	VVDLMAHMASK	Yes	401.2	315.2	14.50	100	21	ND	ND	ND	No
G3P	VVDLMAHMASK	Yes	401.2	388.2	14.50	100	21	ND	ND	ND	No
G3P	VVDLMAHMASK	Yes	401.2	444.7	14.50	100	21	ND	ND	ND	No
G3P	VVDLMAHMASK	Yes	401.2	775.4	14.50	100	21	ND	ND	ND	No
G3P	VVDLMAHMASK	Yes	601.3	1003.5	14.50	100	32	ND	ND	ND	No
G3P	VVDLMAHMASK	Yes	601.3	314.2	14.50	100	32	ND	ND	ND	No
G3P	VVDLMAHMASK	Yes	601.3	644.3	14.50	100	32	ND	ND	ND	No
G3P	VVDLMAHMASK	Yes	601.3	775.4	14.50	100	32	ND	ND	ND	No
G6PD	DGLLPENTFIVGYAR	Yes	832.94	286.1	20.81	108.4	36.1	428263	ND	ND	No
G6PD	DGLLPENTFIVGYAR	Yes	832.94	399.2	20.81	108.4	36.1	112758	ND	ND	No
G6PD	DGLLPENTFIVGYAR	Yes	832.94	466.2	20.81	108.4	48.1	43955	ND	ND	No
G6PD	DGLLPENTFIVGYAR	Yes	832.94	565.3	20.81	108.4	48.1	48322	ND	ND	No
G6PD	GGYFDEFGIIR	Yes	637.31	605.4	20.57	83.2	36.5	69714	10686	12201	No
G6PD	GGYFDEFGIIR	Yes	637.31	734.4	20.57	83.2	39.5	ND	16302	9970	Yes (Based on Manual Review)
G6PD	GGYFDEFGIIR	Yes	637.31	849.4	20.57	83.2	30.5	102889	17417	26108	No
G6PD	GGYFDEFGIIR	Yes	637.31	996.5	20.57	83.2	39.5	30773	1913	ND	No
G6PD	IFTPLLHQIELEKPKPIPYIYGSR	No									

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
G6PD	LPDAYER	Yes	432.22	467.2	8.41	56.8	30.5	12163	ND	ND	No
G6PD	LPDAYER	Yes	432.22	538.3	8.41	56.8	30.5	81157	ND	ND	No
G6PD	LPDAYER	Yes	432.22	653.3	8.41	56.8	24.5	74697	ND	ND	No
G6PD	LPDAYER	Yes	432.22	750.3	8.41	56.8	21.5	33761	ND	ND	No
G6PD	NSYVAGQYDDAASYQR	Yes	904.4	365.1	10.77	117.7	42.3	74299	ND	ND	No
G6PD	NSYVAGQYDDAASYQR	Yes	904.4	464.2	10.77	117.7	42.3	15219	ND	ND	No
G6PD	NSYVAGQYDDAASYQR	Yes	904.4	553.3	10.77	117.7	39.3	11328	ND	ND	No
G6PD	NSYVAGQYDDAASYQR	Yes	904.4	695.3	10.77	117.7	51.3	11108	ND	ND	No
G6PI	AVLHVALR	Yes	293.52	359.2	11.56	38.9	18.5	36350	ND	ND	No
G6PI	AVLHVALR	Yes	293.52	421.3	11.56	38.9	18.5	1669	ND	ND	No
G6PI	AVLHVALR	Yes	293.52	458.3	11.56	38.9	18.5	2941	ND	ND	No
G6PI	AVLHVALR	Yes	293.52	595.4	11.56	38.9	15.5	7750	ND	ND	No
G6PI	FNHFSLTLNTNHGHILVDYSK	No									
G6PI	TLAQLNPESSLFIIASK	Yes	611.34	418.3	22.58	79.9	34.7	5901	ND	ND	No
G6PI	TLAQLNPESSLFIIASK	Yes	611.34	641.4	22.58	79.9	25.7	5970	ND	ND	No
G6PI	TLAQLNPESSLFIIASK	Yes	611.34	678.4	22.58	79.9	25.7	9215	ND	ND	No
G6PI	TLAQLNPESSLFIIASK	Yes	611.34	965.6	22.58	79.9	25.7	3963	ND	ND	No
G6PI	VDHQTGPIVWGEPGTNGQHAFYQLIHQGTK	No									
G6PI	VFEGNRPTNSIVFTK	No									
GA2L1	AAPPAPNAPAAGEDTTETAPAPGTPAR	Yes	833.74	408.2	9.38	108.6	40.1	9438	ND	ND	No
GA2L1	AAPPAPNAPAAGEDTTETAPAPGTPAR	Yes	833.74	598.3	9.38	108.6	43.1	8577	ND	ND	No
GA2L1	AAPPAPNAPAAGEDTTETAPAPGTPAR	Yes	833.74	690.4	9.38	108.6	37.1	5333	ND	ND	No
GA2L1	AAPPAPNAPAAGEDTTETAPAPGTPAR	Yes	833.74	766.4	9.38	108.6	40.1	33081	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
GA2L1	ALEAVASVTPTGPVPDPAR	Yes	616.67	343.2	15.33	80.6	38	80156	150208	161856	No
GA2L1	ALEAVASVTPTGPVPDPAR	Yes	616.67	484.3	15.33	80.6	29	7613	ND	ND	No
GA2L1	ALEAVASVTPTGPVPDPAR	Yes	616.67	751.4	15.33	80.6	29	5008	ND	ND	No
GA2L1	ALEAVASVTPTGPVPDPAR	Yes	616.67	808.4	15.33	80.6	26	ND	4252	ND	No
GA2L1	LVQFEQEIER	Yes	645.84	341.2	14.37	84.3	27.9	15577	ND	ND	No
GA2L1	LVQFEQEIER	Yes	645.84	674.3	14.37	84.3	39.9	9018	ND	ND	No
GA2L1	LVQFEQEIER	Yes	645.84	803.4	14.37	84.3	39.9	7909	ND	ND	No
GA2L1	LVQFEQEIER	Yes	645.84	950.5	14.37	84.3	30.9	9723	ND	ND	No
GA2L1	VGDSSLLIFVR	Yes	603.35	421.3	21.09	78.8	26	28472	ND	ND	No
GA2L1	VGDSSLLIFVR	Yes	603.35	534.3	21.09	78.8	26	19137	ND	ND	No
GA2L1	VGDSSLLIFVR	Yes	603.35	647.4	21.09	78.8	29	21420	ND	ND	No
GA2L1	VGDSSLLIFVR	Yes	603.35	847.5	21.09	78.8	26	10368	ND	ND	No
GA2L1	VSSPSPELGTTPASIFR	Yes	873.46	322.2	17.73	113.7	40.9	20263	ND	ND	No
GA2L1	VSSPSPELGTTPASIFR	Yes	873.46	458.2	17.73	113.7	37.9	20641	ND	ND	No
GA2L1	VSSPSPELGTTPASIFR	Yes	873.46	690.4	17.73	113.7	49.9	46546	ND	ND	No
GA2L1	VSSPSPELGTTPASIFR	Yes	873.46	949.5	17.73	113.7	46.9	54866	ND	ND	No
GALT2	EIILVDDYSNDPEDGALLGK	Yes	1088.54	356.2	19.01	141.4	56.4	37389	ND	ND	No
GALT2	EIILVDDYSNDPEDGALLGK	Yes	1088.54	469.3	19.01	141.4	47.4	15038	ND	ND	No
GALT2	EIILVDDYSNDPEDGALLGK	Yes	1088.54	558.4	19.01	141.4	59.4	12550	ND	ND	No
GALT2	EIILVDDYSNDPEDGALLGK	Yes	1088.54	899.5	19.01	141.4	56.4	19712	ND	ND	No
GALT2	GGFDWNLVFK	Yes	591.8	294.2	23.12	77.3	28.5	99298	ND	ND	No
GALT2	GGFDWNLVFK	Yes	591.8	620.4	23.12	77.3	25.5	36850	ND	ND	No
GALT2	GGFDWNLVFK	Yes	591.8	806.5	23.12	77.3	28.5	69687	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
GALT2	GGFDWNLVFK	Yes	591.8	921.5	23.12	77.3	28.5	54662	ND	ND	No
GALT2	NFYYAAVPSAR	Yes	629.81	425.2	13.67	82.2	30.2	159543	ND	ND	No
GALT2	NFYYAAVPSAR	Yes	629.81	671.4	13.67	82.2	30.2	109544	ND	ND	No
GALT2	NFYYAAVPSAR	Yes	629.81	834.4	13.67	82.2	39.2	75865	ND	ND	No
GALT2	NFYYAAVPSAR	Yes	629.81	997.5	13.67	82.2	30.2	41053	ND	ND	No
GALT2	VDLPATSVVITFHNEAR	Yes	623.67	489.2	18.09	81.5	38.4	17673	ND	ND	No
GALT2	VDLPATSVVITFHNEAR	Yes	623.67	773.4	18.09	81.5	35.4	24800	ND	ND	No
GALT2	VDLPATSVVITFHNEAR	Yes	623.67	874.4	18.09	81.5	35.4	34995	ND	ND	No
GALT2	VDLPATSVVITFHNEAR	Yes	623.67	987.5	18.09	81.5	38.4	27583	ND	ND	No
GALT2	WYLENVYPELR	Yes	741.38	350.2	20.56	96.6	32.1	19591	ND	ND	No
GALT2	WYLENVYPELR	Yes	741.38	514.3	20.56	96.6	32.1	16651	ND	ND	No
GALT2	WYLENVYPELR	Yes	741.38	677.4	20.56	96.6	35.1	19105	ND	ND	No
GALT2	WYLENVYPELR	Yes	741.38	890.5	20.56	96.6	38.1	9228	ND	ND	No
GAS6	DGEATLEVDGTR	Yes	631.8	676.3	9.97	82.5	30.3	85491	ND	ND	No
GAS6	DGEATLEVDGTR	Yes	631.8	789.4	9.97	82.5	27.3	71226	ND	ND	No
GAS6	DGEATLEVDGTR	Yes	631.8	890.5	9.97	82.5	30.3	50653	ND	ND	No
GAS6	DGEATLEVDGTR	Yes	631.8	961.5	9.97	82.5	30.3	29416	ND	ND	No
GAS6	EVFENDPETDYFYPR	Yes	960.92	272.2	17.39	125	41.8	77744	ND	ND	No
GAS6	EVFENDPETDYFYPR	Yes	960.92	435.2	17.39	125	41.8	27734	ND	ND	No
GAS6	EVFENDPETDYFYPR	Yes	960.92	582.3	17.39	125	47.8	8184	ND	ND	No
GAS6	EVFENDPETDYFYPR	Yes	960.92	734.3	17.39	125	41.8	10789	ND	ND	No
GAS6	GQSEVSAAQLQER	Yes	701.85	432.2	9.28	91.5	39.4	2813	ND	ND	No
GAS6	GQSEVSAAQLQER	Yes	701.85	744.4	9.28	91.5	33.4	4991	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
GAS6	GQSEVSAAQLQER	Yes	701.85	815.4	9.28	91.5	39.4	4077	ND	ND	No
GAS6	GQSEVSAAQLQER	Yes	701.85	902.5	9.28	91.5	33.4	7031	ND	ND	No
GAS6	IAVAGDLFQPER	Yes	658.35	401.2	16.82	85.9	31.5	44520	ND	ND	No
GAS6	IAVAGDLFQPER	Yes	658.35	529.3	16.82	85.9	31.5	18485	ND	ND	No
GAS6	IAVAGDLFQPER	Yes	658.35	789.4	16.82	85.9	37.5	11136	ND	ND	No
GAS6	IAVAGDLFQPER	Yes	658.35	961.5	16.82	85.9	31.5	14751	ND	ND	No
GAS6	SWNWLNGEDTTIQETVK	Yes	1010.98	274.1	20.29	131.4	53	4193	ND	ND	No
GAS6	SWNWLNGEDTTIQETVK	Yes	1010.98	574.2	20.29	131.4	47	2379	ND	ND	No
GAS6	SWNWLNGEDTTIQETVK	Yes	1010.98	604.3	20.29	131.4	47	2341	ND	ND	No
GAS6	SWNWLNGEDTTIQETVK	Yes	1010.98	919.5	20.29	131.4	56	794	ND	ND	No
GDIR2	APEPHVEEDDDDELDSK	Yes	647.3	560.2	12.00	100	33.5	ND	ND	ND	No
GDIR2	APEPHVEEDDDDELDSK	Yes	647.3	631.3	12.00	100	33.5	ND	ND	ND	No
GDIR2	APEPHVEEDDDDELDSK	Yes	647.3	706.3	12.00	100	33.5	ND	ND	ND	No
GDIR2	APEPHVEEDDDDELDSK	Yes	647.3	821.4	12.00	100	33.5	ND	ND	ND	No
GDIR2	APEPHVEEDDDDELDSK	Yes	970.4	591.3	12.00	100	48.2	ND	ND	ND	No
GDIR2	APEPHVEEDDDDELDSK	Yes	970.4	706.3	12.00	100	48.2	ND	ND	ND	No
GDIR2	APEPHVEEDDDDELDSK	Yes	970.4	821.4	12.00	100	48.2	ND	ND	ND	No
GDIR2	APEPHVEEDDDDELDSK	Yes	970.4	936.4	12.00	100	48.2	ND	ND	ND	No
GDIR2	DIVSGLK	Yes	366.219	229.119	10.44	100	15.6	ND	53721	58451	No
GDIR2	DIVSGLK	Yes	366.219	317.2	10.44	100	21.6	ND	ND	2271	No
GDIR2	DIVSGLK	Yes	366.219	404.3	10.44	100	21.6	ND	ND	ND	No
GDIR2	DIVSGLK	Yes	366.219	503.319	10.44	100	18.6	ND	121539	108244	No
GDIR2	LNYKPPPQK	Yes	362.21	228.1	6.82	100	19	ND	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
GDIR2	LNYKPPPQK	Yes	362.21	283.669	6.82	100	19	ND	18358	5165	No
GDIR2	LNYKPPPQK	Yes	362.21	372.2	6.82	100	19	ND	ND	ND	No
GDIR2	LNYKPPPQK	Yes	362.21	566.33	6.82	100	22	ND	42222	12654	No
GDIR2	LNYKPPPQK	Yes	542.8	228.1	6.82	100	29.4	ND	ND	ND	No
GDIR2	LNYKPPPQK	Yes	542.8	372.2	6.82	100	29.4	ND	ND	ND	No
GDIR2	LNYKPPPQK	Yes	542.8	391.2	6.82	100	29.4	ND	ND	ND	No
GDIR2	LNYKPPPQK	Yes	542.8	566.3	6.82	100	29.4	ND	ND	ND	No
GDIR2	QDHLSWEWNLSIK	Yes	552.6	244.1	21.30	100	28.7	ND	ND	ND	No
GDIR2	QDHLSWEWNLSIK	Yes	552.6	381.2	21.30	100	28.7	ND	ND	ND	No
GDIR2	QDHLSWEWNLSIK	Yes	552.6	574.4	21.30	100	28.7	ND	ND	ND	No
GDIR2	QDHLSWEWNLSIK	Yes	552.6	760.4	21.30	100	28.7	ND	ND	ND	No
GDIR2	SFFTDDDK	Yes	487.7	235.1	13.90	100	27	ND	ND	ND	No
GDIR2	SFFTDDDK	Yes	487.7	262.1	13.90	100	27	ND	ND	ND	No
GDIR2	SFFTDDDK	Yes	487.7	593.2	13.90	100	27	ND	ND	ND	No
GDIR2	SFFTDDDK	Yes	487.7	740.3	13.90	100	27	ND	ND	ND	No
GDIR2	TLLGDGPVVTDPK	Yes	656.4	1097.6	15.90	100	34.4	ND	ND	ND	No
GDIR2	TLLGDGPVVTDPK	Yes	656.4	244.2	15.90	100	34.4	ND	ND	ND	No
GDIR2	TLLGDGPVVTDPK	Yes	656.4	812.5	15.90	100	34.4	ND	ND	ND	No
GDIR2	TLLGDGPVVTDPK	Yes	656.4	984.5	15.90	100	34.4	ND	ND	ND	No
GELS	AQPVQVAEGSEPDGFWEALGGK	Yes	758.03	374.2	21.06	98.8	42.2	15183	736000	786148	No
GELS	AQPVQVAEGSEPDGFWEALGGK	Yes	758.03	396.2	21.06	98.8	42.2	8515	551349	580613	No
GELS	AQPVQVAEGSEPDGFWEALGGK	Yes	758.03	623.4	21.06	98.8	33.2	6798	1117023	1289572	Yes (Based on Transition Ratios)

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
GELS	AQPVQVAEGSEPDGFWEALGGK	Yes	758.03	964.5	21.06	98.8	36.2	ND	435840	483999	No
GELS	EPGLQIWR	Yes	499.77	361.2	16.37	65.5	24.5	38296	145881	189051	No
GELS	EPGLQIWR	Yes	499.77	474.3	16.37	65.5	24.5	29025	112499	119758	No
GELS	EPGLQIWR	Yes	499.77	602.3	16.37	65.5	24.5	29313	98531	131620	No
GELS	EPGLQIWR	Yes	499.77	772.4	16.37	65.5	33.5	10154	35833	46838	No
GELS	FDLVPVPTNLYGDFFTGDAYVILK	No									
GELS	TASDFITK	Yes	441.73	508.3	9.72	58	24.9	96930	1110983	983434	No
GELS	TASDFITK	Yes	441.73	623.3	9.72	58	21.9	48373	377884	403974	No
GELS	TASDFITK	Yes	441.73	710.4	9.72	58	21.9	823945	6477637	6712576	No
GELS	TASDFITK	Yes	441.73	781.4	9.72	58	21.9	124084	1053469	1135052	No
GELS	TPSAAYLWVGTGASEAEK	Yes	919.45	428.2	17.09	119.6	49	7386	84966	111772	No
GELS	TPSAAYLWVGTGASEAEK	Yes	919.45	591.3	17.09	119.6	46	6289	68514	105592	No
GELS	TPSAAYLWVGTGASEAEK	Yes	919.45	704.4	17.09	119.6	43	5668	70031	70186	No
GELS	TPSAAYLWVGTGASEAEK	Yes	919.45	849.4	17.09	119.6	43	10488	143036	193849	No
GGH	DYEILFK	Yes	464.25	294.2	17.32	60.9	31.9	684607	ND	ND	No
GGH	DYEILFK	Yes	464.25	407.3	17.32	60.9	19.9	167814	ND	ND	No
GGH	DYEILFK	Yes	464.25	520.3	17.32	60.9	22.9	222792	ND	ND	No
GGH	DYEILFK	Yes	464.25	649.4	17.32	60.9	22.9	434097	ND	ND	No
GGH	NLDGISHAPNAVK	Yes	445.91	528.3	9.69	58.5	29.3	189251	21130	14582	No
GGH	NLDGISHAPNAVK	Yes	445.91	599.4	9.69	58.5	26.3	138915	18079	15936	No
GGH	NLDGISHAPNAVK	Yes	445.91	736.4	9.69	58.5	23.3	31746	5487	5799	No
GGH	NLDGISHAPNAVK	Yes	445.91	823.4	9.69	58.5	20.3	32039	3979	5855	No
GGH	YLESAGAR	No									

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
GGH	YPVYGVQWHPEK	Yes	501.59	360.2	13.92	65.7	23.1	31686	ND	ND	No
GGH	YPVYGVQWHPEK	Yes	501.59	373.2	13.92	65.7	29.1	185190	ND	ND	No
GGH	YPVYGVQWHPEK	Yes	501.59	696.3	13.92	65.7	23.1	16067	ND	ND	No
GGH	YPVYGVQWHPEK	Yes	501.59	980.5	13.92	65.7	32.1	6030	ND	ND	No
GGH	YYIAASYVK	Yes	539.28	567.3	12.97	70.6	26.2	ND	19751	5473	Yes (Based on Manual Review)
GGH	YYIAASYVK	Yes	539.28	638.4	12.97	70.6	26.2	184756	35965	33185	No
GGH	YYIAASYVK	Yes	539.28	751.4	12.97	70.6	26.2	261730	46876	38678	No
GGH	YYIAASYVK	Yes	539.28	914.5	12.97	70.6	35.2	7158	3258	2454	No
GPC3	FLAELAYDLDVDDAPGNSQQATPK	Yes	860.08	345.2	20.88	112	41.4	4492	ND	ND	No
GPC3	FLAELAYDLDVDDAPGNSQQATPK	Yes	860.08	574.3	20.88	112	50.4	3137	ND	ND	No
GPC3	FLAELAYDLDVDDAPGNSQQATPK	Yes	860.08	645.4	20.88	112	38.4	4501	ND	ND	No
GPC3	FLAELAYDLDVDDAPGNSQQATPK	Yes	860.08	930.5	20.88	112	41.4	3101	ND	ND	No
GPC3	FLIIQNAAVFQEAFEIVVR	No									
GPC3	GPEPVVSQIIDK	No									
GPC3	IFLQALNLGIEVINTTDHLK	No									
GPC3	NQFNLHELK	Yes	381.54	260.2	12.20	50.2	20	93058	ND	6427	No
GPC3	NQFNLHELK	Yes	381.54	526.3	12.20	50.2	23	83200	ND	2627	No
GPC3	NQFNLHELK	Yes	381.54	639.4	12.20	50.2	23	17834	ND	ND	No
GPC3	NQFNLHELK	Yes	381.54	753.4	12.20	50.2	17	6821	ND	2107	Yes (Based on Transition Ratios)
GRAN	ELWAALNAWK	Yes	601.32	631.4	21.98	78.6	29	46323	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
GRAN	ELWAALNAWK	Yes	601.32	702.4	21.98	78.6	29	60006	ND	ND	No
GRAN	ELWAALNAWK	Yes	601.32	773.4	21.98	78.6	29	81207	ND	ND	No
GRAN	ELWAALNAWK	Yes	601.32	959.5	21.98	78.6	29	35984	ND	ND	No
GREB1	ASQGPPSAISR	No									
GREB1	EVNYELVTGK	Yes	576.3	305.2	12.42	75.3	27.9	497980	ND	ND	No
GREB1	EVNYELVTGK	Yes	576.3	517.3	12.42	75.3	27.9	192099	ND	ND	No
GREB1	EVNYELVTGK	Yes	576.3	646.4	12.42	75.3	27.9	219258	ND	ND	No
GREB1	EVNYELVTGK	Yes	576.3	923.5	12.42	75.3	27.9	111936	ND	ND	No
GREB1	ILSESLLTPAEYQK	Yes	531.29	638.3	16.75	69.5	24.6	15373	ND	ND	No
GREB1	ILSESLLTPAEYQK	Yes	531.29	643.4	16.75	69.5	24.6	28528	ND	ND	No
GREB1	ILSESLLTPAEYQK	Yes	531.29	735.4	16.75	69.5	21.6	79610	ND	ND	No
GREB1	ILSESLLTPAEYQK	Yes	531.29	836.4	16.75	69.5	27.6	16529	ND	ND	No
GREB1	TALEQELGLAAYFVSNEVPLEK	Yes	807.76	486.3	24.62	105.2	41.7	53638	80513	58012	No
GREB1	TALEQELGLAAYFVSNEVPLEK	Yes	807.76	714.4	24.62	105.2	35.7	ND	ND	ND	Yes (Based on Manual Review)
GREB1	TALEQELGLAAYFVSNEVPLEK	Yes	807.76	828.4	24.62	105.2	35.7	7463	17458	10822	No
GREB1	TALEQELGLAAYFVSNEVPLEK	Yes	807.76	915.5	24.62	105.2	35.7	14455	16090	13541	No
GREB1	TGAYLQFLSVLSR	Yes	727.9	561.3	24.43	94.9	37.5	21162	ND	ND	No
GREB1	TGAYLQFLSVLSR	Yes	727.9	674.4	24.43	94.9	34.5	13033	ND	ND	No
GREB1	TGAYLQFLSVLSR	Yes	727.9	821.5	24.43	94.9	34.5	30127	ND	ND	No
GREB1	TGAYLQFLSVLSR	Yes	727.9	949.5	24.43	94.9	31.5	16085	ND	ND	No
GREM1	AQHNDSEQTQSPQQPGSR	No									
GRP	ALGNQQPSWDSEDSSNFK	Yes	1005.45	484.3	12.96	130.7	46.7	5561	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
GRP	ALGNQQPSWDSEDSSNFK	Yes	1005.45	582.3	12.96	130.7	52.7	5673	ND	ND	No
GRP	ALGNQQPSWDSEDSSNFK	Yes	1005.45	612.3	12.96	130.7	46.7	7849	ND	ND	No
GRP	ALGNQQPSWDSEDSSNFK	Yes	1005.45	913.4	12.96	130.7	46.7	3338	ND	ND	No
GRP	AVPLPAGGGTVLTK	Yes	640.88	268.2	13.33	83.7	30.7	312921	ND	ND	No
GRP	AVPLPAGGGTVLTK	Yes	640.88	732.4	13.33	83.7	36.7	166500	ND	ND	No
GRP	AVPLPAGGGTVLTK	Yes	640.88	803.5	13.33	83.7	39.7	122645	ND	ND	No
GRP	AVPLPAGGGTVLTK	Yes	640.88	900.5	13.33	83.7	30.7	383936	ND	ND	No
GRP	LSAPGSQR	Yes	408.22	272.2	6.34	53.7	20.5	45181	ND	ND	No
GRP	LSAPGSQR	Yes	408.22	544.3	6.34	53.7	20.5	101248	ND	ND	No
GRP	LSAPGSQR	Yes	408.22	615.3	6.34	53.7	20.5	28471	ND	ND	No
GRP	LSAPGSQR	Yes	408.22	702.4	6.34	53.7	20.5	19402	ND	ND	No
GRP	NLLGLIEAK	Yes	485.8	341.2	20.30	63.7	20.9	289061	ND	ND	No
GRP	NLLGLIEAK	Yes	485.8	460.3	20.30	63.7	26.9	52915	ND	ND	No
GRP	NLLGLIEAK	Yes	485.8	630.4	20.30	63.7	20.9	392202	ND	ND	No
GRP	NLLGLIEAK	Yes	485.8	743.5	20.30	63.7	23.9	527924	ND	ND	No
GRP	NPQLNQQ	No									
GRP78	GVPQIEVTFEIDVNGILR	No									
GRP78	LTPEEIER	No									
GRP78	LYGSAGPPPTGEEDTAEK	Yes	909.92	334.2	9.16	118.4	51.5	14470	ND	ND	No
GRP78	LYGSAGPPPTGEEDTAEK	Yes	909.92	492.2	9.16	118.4	42.5	9477	ND	ND	No
GRP78	LYGSAGPPPTGEEDTAEK	Yes	909.92	549.3	9.16	118.4	39.5	12433	ND	ND	No
GRP78	LYGSAGPPPTGEEDTAEK	Yes	909.92	878.4	9.16	118.4	51.5	7011	ND	ND	No
GRP78	TWNDPSVQQDIK	Yes	715.85	260.2	12.10	93.3	43	117575	38607	37974	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
GRP78	TWNDPSVQQDIK	Yes	715.85	288.1	12.10	93.3	34	149601	37952	37875	No
GRP78	TWNDPSVQQDIK	Yes	715.85	517.2	12.10	93.3	31	31831	8135	15704	No
GRP78	TWNDPSVQQDIK	Yes	715.85	914.5	12.10	93.3	34	27711	12458	15129	No
GRP78	VYEGERPLTK	Yes	397.88	458.3	7.57	52.3	26.8	30025	5025	4180	No
GRP78	VYEGERPLTK	Yes	397.88	614.4	7.57	52.3	26.8	18067	3699	ND	No
GRP78	VYEGERPLTK	Yes	397.88	800.5	7.57	52.3	20.8	89615	4277	4630	No
GRP78	VYEGERPLTK	Yes	397.88	929.5	7.57	52.3	26.8	ND	ND	ND	No
GSLG1	IIIQESALDYR	Yes	660.86	338.2	15.11	86.3	40.6	33005	69985	79200	No
GSLG1	IIIQESALDYR	Yes	660.86	724.4	15.11	86.3	40.6	7033	ND	ND	No
GSLG1	IIIQESALDYR	Yes	660.86	853.4	15.11	86.3	34.6	5813	ND	ND	No
GSLG1	IIIQESALDYR	Yes	660.86	981.5	15.11	86.3	40.6	3419	ND	ND	No
GSLG1	LDPALQDK	Yes	450.25	503.3	8.31	59.1	31.3	153201	ND	ND	No
GSLG1	LDPALQDK	Yes	450.25	574.3	8.31	59.1	31.3	260964	ND	ND	No
GSLG1	LDPALQDK	Yes	450.25	671.4	8.31	59.1	22.3	499839	ND	ND	No
GSLG1	LDPALQDK	Yes	450.25	786.4	8.31	59.1	22.3	48377	ND	ND	No
GSLG1	LIAQDYK	Yes	425.74	310.2	8.28	55.9	30.2	352025	ND	ND	No
GSLG1	LIAQDYK	Yes	425.74	553.3	8.28	55.9	21.2	39457	ND	ND	No
GSLG1	LIAQDYK	Yes	425.74	624.3	8.28	55.9	21.2	707457	ND	ND	No
GSLG1	LIAQDYK	Yes	425.74	737.4	8.28	55.9	21.2	92099	ND	ND	No
GSLG1	NDINILK	Yes	415.24	260.2	12.27	54.6	26.8	3113670	30155	ND	Yes (Based on Transition Ratios)
GSLG1	NDINILK	Yes	415.24	487.3	12.27	54.6	20.8	118856	ND	ND	No
GSLG1	NDINILK	Yes	415.24	600.4	12.27	54.6	20.8	109536	12160	5682	Yes (Based on

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
											Transition Ratios)
GSLG1	NDINILK	Yes	415.24	715.4	12.27	54.6	20.8	41568	ND	ND	No
GSLG1	VAELSSDDFHLDR	Yes	501.91	403.2	14.18	65.7	32.1	39562	ND	ND	No
GSLG1	VAELSSDDFHLDR	Yes	501.91	540.3	14.18	65.7	29.1	21425	ND	ND	No
GSLG1	VAELSSDDFHLDR	Yes	501.91	687.4	14.18	65.7	29.1	13431	ND	ND	No
GSLG1	VAELSSDDFHLDR	Yes	501.91	702.3	14.18	65.7	23.1	7013	ND	ND	No
GSTP1	AFLASPEYVNLPINGNGK	Yes	952.5	332.2	18.87	123.9	41.4	23819	ND	ND	No
GSTP1	AFLASPEYVNLPINGNGK	Yes	952.5	489.2	18.87	123.9	53.4	12541	ND	ND	No
GSTP1	AFLASPEYVNLPINGNGK	Yes	952.5	699.4	18.87	123.9	50.4	30955	ND	ND	No
GSTP1	AFLASPEYVNLPINGNGK	Yes	952.5	926.5	18.87	123.9	53.4	7734	ND	ND	No
GSTP1	ALPGQLKPFETLLSQNQGGK	Yes	709.39	261.2	19.96	92.5	42.7	71103	ND	ND	No
GSTP1	ALPGQLKPFETLLSQNQGGK	Yes	709.39	503.3	19.96	92.5	42.7	55795	ND	ND	No
GSTP1	ALPGQLKPFETLLSQNQGGK	Yes	709.39	631.3	19.96	92.5	33.7	45630	ND	ND	No
GSTP1	ALPGQLKPFETLLSQNQGGK	Yes	709.39	831.4	19.96	92.5	30.7	151412	ND	ND	No
GSTP1	EEVVTVETWQEGSLK	No									
GSTP1	FQDGDLTLYQSNTILR	No									
GSTP1	YISLIYTNYEAGK	Yes	767.89	277.2	17.39	100.1	33.3	34906	ND	ND	No
GSTP1	YISLIYTNYEAGK	Yes	767.89	364.2	17.39	100.1	39.3	28066	ND	ND	No
GSTP1	YISLIYTNYEAGK	Yes	767.89	477.3	17.39	100.1	33.3	14079	ND	ND	No
GSTP1	YISLIYTNYEAGK	Yes	767.89	945.4	17.39	100.1	36.3	23839	ND	ND	No
GTR1	AGVQQPVYATIGSGIVNTAFTVVSLFVVER	No									
GTR1	QPILIAVVLQLSQQLSGINAVFYYSTSIFEK	No									

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
GTR1	TFDEIASGFR	Yes	571.78	466.2	15.92	74.8	27.7	109067	ND	ND	No
GTR1	TFDEIASGFR	Yes	571.78	537.3	15.92	74.8	27.7	352766	ND	ND	No
GTR1	TFDEIASGFR	Yes	571.78	650.4	15.92	74.8	36.7	103882	ND	ND	No
GTR1	TFDEIASGFR	Yes	571.78	894.4	15.92	74.8	27.7	241044	ND	ND	No
GTR1	TPEELFHPLGADSQV	Yes	820.4	457.2	18.24	106.8	41.6	20663	ND	ND	No
GTR1	TPEELFHPLGADSQV	Yes	820.4	717.3	18.24	106.8	38.6	9811	ND	ND	No
GTR1	TPEELFHPLGADSQV	Yes	820.4	786.4	18.24	106.8	38.6	30658	ND	ND	No
GTR1	TPEELFHPLGADSQV	Yes	820.4	854.4	18.24	106.8	38.6	21689	ND	ND	No
GTR1	VIEEFYNQTWVHR	Yes	574.29	312.2	16.13	75.1	32.8	27635	20284	10172	No
GTR1	VIEEFYNQTWVHR	Yes	574.29	411.2	16.13	75.1	32.8	15033	3047	ND	No
GTR1	VIEEFYNQTWVHR	Yes	574.29	597.3	16.13	75.1	32.8	11958	2870	3085	No
GTR1	VIEEFYNQTWVHR	Yes	574.29	698.4	16.13	75.1	35.8	8496	6444	ND	No
GTR3	AFEGQAHGADR	Yes	579.77	418.2	6.62	75.8	37	202946	ND	ND	No
GTR3	AFEGQAHGADR	Yes	579.77	555.3	6.62	75.8	31	162420	ND	ND	No
GTR3	AFEGQAHGADR	Yes	579.77	626.3	6.62	75.8	37	163316	ND	ND	No
GTR3	AFEGQAHGADR	Yes	579.77	940.4	6.62	75.8	31	85746	ND	ND	No
GTR3	DAGVQEPIYATIGAGVVNTIFTVVSLFLVER	No									
GTR3	DGVMEMNSIEPAK	Yes	710.83	315.2	15.01	92.7	42.8	651156	ND	ND	No
GTR3	DGVMEMNSIEPAK	Yes	710.83	444.2	15.01	92.7	42.8	131000	ND	ND	No
GTR3	DGVMEMNSIEPAK	Yes	710.83	758.4	15.01	92.7	33.8	126153	ND	ND	No
GTR3	DGVMEMNSIEPAK	Yes	710.83	889.4	15.01	92.7	33.8	165465	ND	ND	No
GTR3	FLLINR	Yes	388.25	261.2	17.40	51.1	19.6	38683431	ND	ND	No
GTR3	FLLINR	Yes	388.25	289.2	17.40	51.1	28.6	6071848	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
GTR3	FLLINR	Yes	388.25	515.3	17.40	51.1	19.6	49971898	ND	ND	No
GTR3	FLLINR	Yes	388.25	628.4	17.40	51.1	19.6	8139252	ND	ND	No
GTR3	LWGTQDVSQDIQEMK	No									
GTR3	QPIIISIVLQLSQQLSGINAVFYYSTGIFK	No									
GTR3	QVTVLELFR	Yes	552.82	435.3	23.99	72.3	35.8	377428	ND	ND	No
GTR3	QVTVLELFR	Yes	552.82	677.4	23.99	72.3	26.8	949411	ND	ND	No
GTR3	QVTVLELFR	Yes	552.82	776.5	23.99	72.3	29.8	325275	ND	ND	No
GTR3	QVTVLELFR	Yes	552.82	877.5	23.99	72.3	26.8	951549	ND	ND	No
GTR3	SVEMLILGR	Yes	509.29	458.3	20.26	66.7	33.9	2020205	ND	ND	No
GTR3	SVEMLILGR	Yes	509.29	571.4	20.26	66.7	33.9	2117179	ND	ND	No
GTR3	SVEMLILGR	Yes	509.29	702.4	20.26	66.7	24.9	1909577	ND	ND	No
GTR3	SVEMLILGR	Yes	509.29	831.5	20.26	66.7	24.9	5305893	ND	ND	No
GTR3	TFEDITR	Yes	441.22	276.2	11.87	57.9	30.9	373896	ND	ND	No
GTR3	TFEDITR	Yes	441.22	389.3	11.87	57.9	30.9	1351614	ND	ND	No
GTR3	TFEDITR	Yes	441.22	504.3	11.87	57.9	24.9	1422622	ND	ND	No
GTR3	TFEDITR	Yes	441.22	633.3	11.87	57.9	21.9	4958845	ND	ND	No
GTR3	VTPALIFAITVATIGSFQFGYNTGVINAPEK	No									
H2A1	AGLQFPVGR	No									
H2A1	HLQLAIR	No									
H2A1	NDEELNK	Yes	431.2	261.2	5.76	56.6	30.5	358680	ND	ND	No
H2A1	NDEELNK	Yes	431.2	503.3	5.76	56.6	21.5	148320	ND	ND	No
H2A1	NDEELNK	Yes	431.2	632.3	5.76	56.6	18.5	219226	ND	ND	No
H2A1	NDEELNK	Yes	431.2	747.4	5.76	56.6	18.5	103303	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
H2A1	VGAGAPVYLAAVLEYLTAEILELAGNAAR	Yes	972.53	488.3	24.83	126.5	53.1	ND	ND	ND	
H2A1	VGAGAPVYLAAVLEYLTAEILELAGNAAR	Yes	972.53	559.3	24.83	126.5	50.1	ND	ND	ND	
H2A1	VGAGAPVYLAAVLEYLTAEILELAGNAAR	Yes	972.53	672.4	24.83	126.5	53.1	ND	ND	ND	
H2A1	VGAGAPVYLAAVLEYLTAEILELAGNAAR	Yes	972.53	914.5	24.83	126.5	44.1	ND	ND	ND	
H2A1B	AGLQFPVGR	No									
H2A1B	HLQLAIR	No									
H2A1B	NDEELNK	Yes	431.2	261.2	5.76	56.6	30.5	358680	ND	ND	No
H2A1B	NDEELNK	Yes	431.2	503.3	5.76	56.6	21.5	148320	ND	ND	No
H2A1B	NDEELNK	Yes	431.2	632.3	5.76	56.6	18.5	219226	ND	ND	No
H2A1B	NDEELNK	Yes	431.2	747.4	5.76	56.6	18.5	103303	ND	ND	No
H2A1B	VGAGAPVYLAAVLEYLTAEILELAGNAAR	Yes	972.53	488.3	24.83	126.5	53.1	ND	ND	ND	
H2A1B	VGAGAPVYLAAVLEYLTAEILELAGNAAR	Yes	972.53	559.3	24.83	126.5	50.1	ND	ND	ND	
H2A1B	VGAGAPVYLAAVLEYLTAEILELAGNAAR	Yes	972.53	672.4	24.83	126.5	53.1	ND	ND	ND	
H2A1B	VGAGAPVYLAAVLEYLTAEILELAGNAAR	Yes	972.53	914.5	24.83	126.5	44.1	ND	ND	ND	
H2A1C	AGLQFPVGR	No									
H2A1C	HLQLAIR	No									
H2A1C	NDEELNK	Yes	431.2	261.2	5.76	56.6	30.5	358680	ND	ND	No
H2A1C	NDEELNK	Yes	431.2	503.3	5.76	56.6	21.5	148320	ND	ND	No
H2A1C	NDEELNK	Yes	431.2	632.3	5.76	56.6	18.5	219226	ND	ND	No
H2A1C	NDEELNK	Yes	431.2	747.4	5.76	56.6	18.5	103303	ND	ND	No
H2A1C	VGAGAPVYLAAVLEYLTAEILELAGNAAR	Yes	972.53	488.3	24.83	126.5	53.1	ND	ND	ND	
H2A1C	VGAGAPVYLAAVLEYLTAEILELAGNAAR	Yes	972.53	559.3	24.83	126.5	50.1	ND	ND	ND	
H2A1C	VGAGAPVYLAAVLEYLTAEILELAGNAAR	Yes	972.53	672.4	24.83	126.5	53.1	ND	ND	ND	

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
H2A1C	VGAGAPVYLAAVLEYLTAEILELAGNAAR	Yes	972.53	914.5	24.83	126.5	44.1	ND	ND	ND	
H2A1D	AGLQFPVGR	No									
H2A1D	HLQLAIR	No									
H2A1D	NDEELNK	Yes	431.2	261.2	5.76	56.6	30.5	358680	ND	ND	No
H2A1D	NDEELNK	Yes	431.2	503.3	5.76	56.6	21.5	148320	ND	ND	No
H2A1D	NDEELNK	Yes	431.2	632.3	5.76	56.6	18.5	219226	ND	ND	No
H2A1D	NDEELNK	Yes	431.2	747.4	5.76	56.6	18.5	103303	ND	ND	No
H2A1D	VGAGAPVYLAAVLEYLTAEILELAGNAAR	Yes	972.53	488.3	24.83	126.5	53.1	ND	ND	ND	
H2A1D	VGAGAPVYLAAVLEYLTAEILELAGNAAR	Yes	972.53	559.3	24.83	126.5	50.1	ND	ND	ND	
H2A1D	VGAGAPVYLAAVLEYLTAEILELAGNAAR	Yes	972.53	672.4	24.83	126.5	53.1	ND	ND	ND	
H2A1D	VGAGAPVYLAAVLEYLTAEILELAGNAAR	Yes	972.53	914.5	24.83	126.5	44.1	ND	ND	ND	
HG2A	GALYTGFSILVTLLLAGQATTAYFLYQQQGR	No									
HG2A	GSFPENLR	No									
HG2A	HSLEQKPTDAPPK	Yes	483.26	341.2	5.90	63.3	31.2	284567	14745	9016	No
HG2A	HSLEQKPTDAPPK	Yes	483.26	412.3	5.90	63.3	25.2	130149	5586	4053	No
HG2A	HSLEQKPTDAPPK	Yes	483.26	595.3	5.90	63.3	25.2	84823	ND	ND	No
HG2A	HSLEQKPTDAPPK	Yes	483.26	725.4	5.90	63.3	22.2	72450	ND	ND	No
HG2A	LPKPPKPVSK	Yes	545.85	339.2	7.55	71.4	29.5	27425	ND	ND	No
HG2A	LPKPPKPVSK	Yes	545.85	655.4	7.55	71.4	35.5	11314	ND	ND	No
HG2A	LPKPPKPVSK	Yes	545.85	752.5	7.55	71.4	32.5	91445	ND	ND	No
HG2A	LPKPPKPVSK	Yes	545.85	880.6	7.55	71.4	29.5	6838	ND	ND	No
HG2A	LTVTSQNLQLENLR	Yes	814.95	999.6	15.91	106.1	38.4	3011	ND	ND	No
HG2A	LTVTSQNLQLENLR	Yes	814.95	415.3	15.91	106.1	35.4	3189	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
HG2A	LTVTSQNLQLENLR	Yes	814.95	644.4	15.91	106.1	47.4	3400	ND	ND	No
HG2A	LTVTSQNLQLENLR	Yes	814.95	772.4	15.91	106.1	44.4	5691	ND	ND	No
HGF	DYEAWLGIHDVHGR	Yes	556.6	369.2	15.95	72.8	34.9	36842	ND	ND	No
HGF	DYEAWLGIHDVHGR	Yes	556.6	479.2	15.95	72.8	22.9	18086	ND	ND	No
HGF	DYEAWLGIHDVHGR	Yes	556.6	720.4	15.95	72.8	28.9	29052	ND	ND	No
HGF	DYEAWLGIHDVHGR	Yes	556.6	890.5	15.95	72.8	34.9	24754	ND	ND	No
HGF	ESWVLTAR	Yes	481.26	347.2	14.31	63.1	23.7	108816	14807	6858	No
HGF	ESWVLTAR	Yes	481.26	460.3	14.31	63.1	23.7	148806	20539	27008	No
HGF	ESWVLTAR	Yes	481.26	559.4	14.31	63.1	32.7	77786	23800	19406	No
HGF	ESWVLTAR	Yes	481.26	745.4	14.31	63.1	23.7	16615	ND	ND	No
HGF	HIFWEPDASK	Yes	615.3	251.2	14.07	80.4	29.6	169205	ND	ND	No
HGF	HIFWEPDASK	Yes	615.3	517.3	14.07	80.4	38.6	75524	ND	ND	No
HGF	HIFWEPDASK	Yes	615.3	832.4	14.07	80.4	38.6	5449	ND	ND	No
HGF	HIFWEPDASK	Yes	615.3	979.5	14.07	80.4	29.6	34372	ND	ND	No
HGF	VVNGIPTR	Yes	428.26	373.2	8.35	56.2	21.3	171382	ND	ND	No
HGF	VVNGIPTR	Yes	428.26	543.3	8.35	56.2	30.3	61338	ND	ND	No
HGF	VVNGIPTR	Yes	428.26	657.4	8.35	56.2	21.3	227036	ND	ND	No
HGF	VVNGIPTR	Yes	428.26	756.4	8.35	56.2	30.3	12988	ND	ND	No
HGF	WDHQTPHR	Yes	359.51	312.2	5.82	47.4	21.9	10795	5240	1870	No
HGF	WDHQTPHR	Yes	359.51	409.2	5.82	47.4	24.9	14498	18187	10563	No
HGF	WDHQTPHR	Yes	359.51	510.3	5.82	47.4	21.9	3774	2846	1852	No
HGF	WDHQTPHR	Yes	359.51	638.3	5.82	47.4	24.9	3466	9889	17840	Yes (Based on Transition Ratios)

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
HMGA1	EEEEGISQESSEEEQ	No									
HMGA1	SSQPLASK	Yes	409.22	305.2	5.84	53.8	29.5	121228	ND	ND	No
HMGA1	SSQPLASK	Yes	409.22	515.3	5.84	53.8	17.5	204593	ND	ND	No
HMGA1	SSQPLASK	Yes	409.22	584.3	5.84	53.8	17.5	7491	ND	ND	No
HMGA1	SSQPLASK	Yes	409.22	643.4	5.84	53.8	17.5	66697	ND	ND	No
HPRT	FFADLLDYIK	Yes	622.83	295.1	24.59	81.3	26.9	ND	ND	ND	Yes (Based on Manual Review)
HPRT	FFADLLDYIK	Yes	622.83	764.5	24.59	81.3	26.9	123982	12683	7919	No
HPRT	FFADLLDYIK	Yes	622.83	879.5	24.59	81.3	29.9	ND	ND	5780	Yes (Based on Manual Review)
HPRT	FFADLLDYIK	Yes	622.83	950.5	24.59	81.3	26.9	ND	6648	ND	No
HPRT	FVVGYALDYNEYFR	Yes	878.42	322.2	21.85	114.3	44.2	2966	ND	ND	No
HPRT	FVVGYALDYNEYFR	Yes	878.42	403.2	21.85	114.3	38.2	4633	ND	ND	No
HPRT	FVVGYALDYNEYFR	Yes	878.42	485.3	21.85	114.3	41.2	3352	ND	ND	No
HPRT	FVVGYALDYNEYFR	Yes	878.42	728.3	21.85	114.3	44.2	3399	ND	ND	No
HPRT	NVLIVEDIIDTGK	Yes	714.9	327.2	21.47	93.2	34	73763	ND	ND	No
HPRT	NVLIVEDIIDTGK	Yes	714.9	761.4	21.47	93.2	43	7195	ND	ND	No
HPRT	NVLIVEDIIDTGK	Yes	714.9	890.4	21.47	93.2	34	14608	ND	ND	No
HPRT	NVLIVEDIIDTGK	Yes	714.9	989.5	21.47	93.2	31	33260	ND	ND	No
HPRT	SVGYKPDFVGFEIPDK	Yes	599.97	359.2	18.43	78.4	34.1	1617303	ND	ND	No
HPRT	SVGYKPDFVGFEIPDK	Yes	599.97	748.4	18.43	78.4	25.1	179212	ND	ND	No
HPRT	SVGYKPDFVGFEIPDK	Yes	599.97	805.4	18.43	78.4	28.1	560936	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
HPRT	SVGYKPDFVGFEIPDK	Yes	599.97	894.4	18.43	78.4	28.1	250225	ND	ND	No
HPRT	VIGGDDLSTLTGK	Yes	638.34	305.2	14.52	83.3	39.6	260470	22697	22738	No
HPRT	VIGGDDLSTLTGK	Yes	638.34	519.3	14.52	83.3	36.6	68556	6820	4600	No
HPRT	VIGGDDLSTLTGK	Yes	638.34	606.3	14.52	83.3	36.6	169979	22690	12254	No
HPRT	VIGGDDLSTLTGK	Yes	638.34	834.5	14.52	83.3	39.6	43930	ND	ND	No
HPSE	EDFLNPDVLDIFISSVQK	No									
HPSE	FLILLGSPK	Yes	494.32	261.2	20.09	64.8	21.2	338489	ND	ND	No
HPSE	FLILLGSPK	Yes	494.32	614.4	20.09	64.8	24.2	146451	ND	ND	No
HPSE	FLILLGSPK	Yes	494.32	727.5	20.09	64.8	24.2	207347	ND	ND	No
HPSE	FLILLGSPK	Yes	494.32	840.6	20.09	64.8	24.2	19142	ND	ND	No
HPSE	LPYPFSNK	Yes	483.26	261.2	15.34	63.3	29.8	1011806	ND	ND	No
HPSE	LPYPFSNK	Yes	483.26	592.3	15.34	63.3	26.8	1487499	ND	ND	No
HPSE	LPYPFSNK	Yes	483.26	755.4	15.34	63.3	23.8	446849	ND	ND	No
HPSE	LPYPFSNK	Yes	483.26	852.4	15.34	63.3	23.8	240499	ND	ND	No
HPSE	SVQLNGLTLK	Yes	536.82	315.2	15.13	70.2	26.1	327247	ND	ND	No
HPSE	SVQLNGLTLK	Yes	536.82	645.4	15.13	70.2	26.1	201502	ND	ND	No
HPSE	SVQLNGLTLK	Yes	536.82	758.5	15.13	70.2	26.1	290963	ND	ND	No
HPSE	SVQLNGLTLK	Yes	536.82	886.5	15.13	70.2	26.1	198064	ND	ND	No
HPSE	YLLRPLGPHGLLSK	Yes	521.98	347.2	16.37	68.3	30.2	23423	ND	ND	No
HPSE	YLLRPLGPHGLLSK	Yes	521.98	654.4	16.37	68.3	30.2	17391	ND	ND	No
HPSE	YLLRPLGPHGLLSK	Yes	521.98	756.5	16.37	68.3	30.2	9021	ND	ND	No
HPSE	YLLRPLGPHGLLSK	Yes	521.98	813.5	16.37	68.3	30.2	62938	ND	ND	No
HPT	DYAEVGR	No									

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
HPT	TEGDGVYTLNNEK	Yes	720.34	276.2	10.14	93.9	43.2	17841	13045	20290	No
HPT	TEGDGVYTLNNEK	Yes	720.34	504.2	10.14	93.9	43.2	91844	37862	54054	No
HPT	TEGDGVYTLNNEK	Yes	720.34	559.2	10.14	93.9	31.2	83609	42050	58976	No
HPT	TEGDGVYTLNNEK	Yes	720.34	881.4	10.14	93.9	34.2	134179	59901	92959	No
HPT	VGYVSGWGR	Yes	490.75	320.2	12.67	64.3	24.1	52113	1517194	2582783	No
HPT	VGYVSGWGR	Yes	490.75	562.3	12.67	64.3	24.1	61353	2002672	3753143	No
HPT	VGYVSGWGR	Yes	490.75	661.3	12.67	64.3	24.1	20325	491848	956761	No
HPT	VGYVSGWGR	Yes	490.75	881.4	12.67	64.3	24.1	10877	352213	587428	No
HPT	VTSIQDWVQK	Yes	602.32	560.3	14.77	78.7	38	23492	232078	399588	No
HPT	VTSIQDWVQK	Yes	602.32	675.3	14.77	78.7	29	16142	228972	311938	No
HPT	VTSIQDWVQK	Yes	602.32	803.4	14.77	78.7	29	28954	397427	714863	No
HPT	VTSIQDWVQK	Yes	602.32	916.5	14.77	78.7	29	5465	59084	119399	No
HPT	VVLHPNYSQVDIGLIK	Yes	599.01	658.4	18.11	78.3	37.1	35523	ND	ND	No
HPT	VVLHPNYSQVDIGLIK	Yes	599.01	660.4	18.11	78.3	28.1	17215	ND	ND	No
HPT	VVLHPNYSQVDIGLIK	Yes	599.01	757.5	18.11	78.3	25.1	74634	ND	ND	No
HPT	VVLHPNYSQVDIGLIK	Yes	599.01	823.4	18.11	78.3	25.1	25221	ND	ND	No
HS90A	DNSTMGYMAAK	Yes	594.8	230.1	12.70	100	31.7	ND	ND	ND	No
HS90A	DNSTMGYMAAK	Yes	594.8	640.3	12.70	100	31.7	ND	ND	ND	No
HS90A	DNSTMGYMAAK	Yes	594.8	771.4	12.70	100	31.7	ND	ND	ND	No
HS90A	DNSTMGYMAAK	Yes	594.8	872.4	12.70	100	31.7	ND	ND	ND	No
HS90A	HLEINPDHSIIETLR	Yes	596.3	522.2	17.40	100	30.9	ND	5206	ND	No
HS90A	HLEINPDHSIIETLR	Yes	596.3	631.4	17.40	100	30.9	ND	ND	ND	No
HS90A	HLEINPDHSIIETLR	Yes	596.3	819.4	17.40	100	30.9	ND	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
HS90A	HLEINPDHSIIETLR	Yes	596.3	831.5	17.40	100	30.9	ND	ND	ND	No
HS90A	HLEINPDHSIIETLR	Yes	894	1180.6	17.40	100	44.8	ND	ND	ND	No
HS90A	HLEINPDHSIIETLR	Yes	894	831.5	17.40	100	44.8	ND	ND	ND	No
HS90A	HLEINPDHSIIETLR	Yes	894	968.6	17.40	100	44.8	ND	ND	ND	No
HS90A	SLTNDWEDHLAVK	Yes	764.4	664.3	14.52	100	39.1	ND	ND	ND	No
HS90A	SLTNDWEDHLAVK	Yes	764.4	682.4	14.52	100	45.1	ND	ND	ND	No
HS90A	SLTNDWEDHLAVK	Yes	764.4	811.4	14.52	100	39.1	ND	ND	ND	No
HS90A	SLTNDWEDHLAVK	Yes	764.4	997.5	14.52	100	39.1	ND	ND	ND	No
HS90A	TLTIVDTGIGMTK	Yes	675.4	1034.6	18.80	100	35.2	ND	ND	ND	No
HS90A	TLTIVDTGIGMTK	Yes	675.4	1135.6	18.80	100	35.2	ND	ND	ND	No
HS90A	TLTIVDTGIGMTK	Yes	675.4	822.4	18.80	100	35.2	ND	ND	ND	No
HS90A	TLTIVDTGIGMTK	Yes	675.4	921.5	18.80	100	35.2	ND	ND	ND	No
HS90B	ADHGEPIGR	Yes	476.24	324.1	5.85	62.4	26.5	24850	ND	ND	No
HS90B	ADHGEPIGR	Yes	476.24	442.3	5.85	62.4	32.5	57462	ND	ND	No
HS90B	ADHGEPIGR	Yes	476.24	510.2	5.85	62.4	23.5	7185	ND	ND	No
HS90B	ADHGEPIGR	Yes	476.24	628.3	5.85	62.4	32.5	61511	ND	ND	No
HS90B	DLVVLLFETALLSSGFSLEDPQTHSNR	No									
HS90B	IDIIPNPQER	Yes	597.83	342.2	14.13	78.1	28.8	418149	ND	ND	No
HS90B	IDIIPNPQER	Yes	597.83	529.3	14.13	78.1	37.8	53632	ND	ND	No
HS90B	IDIIPNPQER	Yes	597.83	740.4	14.13	78.1	28.8	360933	ND	ND	No
HS90B	IDIIPNPQER	Yes	597.83	853.5	14.13	78.1	37.8	22546	ND	ND	No
HS90B	LGLGIDEDEVAAEEPNAAVPDEIPPLEGDEDASR	No									
HS90B	NPDDITQEEYGEFYK	Yes	924.4	310.2	14.90	120.2	49.2	16155	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
HS90B	NPDDITQEEYGEFYK	Yes	924.4	442.2	14.90	120.2	46.2	23643	ND	ND	No
HS90B	NPDDITQEEYGEFYK	Yes	924.4	555.2	14.90	120.2	40.2	14334	ND	ND	No
HS90B	NPDDITQEEYGEFYK	Yes	924.4	643.3	14.90	120.2	52.2	9715	ND	ND	No
HSPB1	AQLGGPEAAK	Yes	471.26	313.2	7.89	61.8	20.2	851057	ND	ND	No
HSPB1	AQLGGPEAAK	Yes	471.26	427.2	7.89	61.8	23.2	141244	ND	ND	No
HSPB1	AQLGGPEAAK	Yes	471.26	629.3	7.89	61.8	23.2	1584458	ND	ND	No
HSPB1	AQLGGPEAAK	Yes	471.26	742.4	7.89	61.8	23.2	2223895	ND	ND	No
HSPB1	DGVVEITGK	Yes	459.25	305.2	11.35	60.2	31.7	1394788	ND	ND	No
HSPB1	DGVVEITGK	Yes	459.25	418.3	11.35	60.2	31.7	626394	ND	ND	No
HSPB1	DGVVEITGK	Yes	459.25	547.3	11.35	60.2	22.7	1350464	ND	ND	No
HSPB1	DGVVEITGK	Yes	459.25	646.4	11.35	60.2	22.7	3456399	ND	ND	No
HSPB1	GPSWDPFR	Yes	481.23	419.2	19.53	63.1	32.7	23035290	ND	ND	No
HSPB1	GPSWDPFR	Yes	481.23	534.3	19.53	63.1	23.7	6742572	ND	ND	No
HSPB1	GPSWDPFR	Yes	481.23	720.3	19.53	63.1	26.7	4111401	ND	ND	No
HSPB1	GPSWDPFR	Yes	481.23	807.4	19.53	63.1	26.7	8859724	ND	ND	No
HSPB1	LATQSNEITIPVTFESR	Yes	953.5	639.3	19.20	124	50.5	9087	ND	ND	No
HSPB1	LATQSNEITIPVTFESR	Yes	953.5	744.4	19.20	124	41.5	5242	ND	ND	No
HSPB1	LATQSNEITIPVTFESR	Yes	953.5	835.4	19.20	124	44.5	77710	ND	ND	No
HSPB1	LATQSNEITIPVTFESR	Yes	953.5	857.4	19.20	124	50.5	ND	ND	ND	No
HSPB1	LFDQAFGLPR	Yes	582.31	272.2	20.10	76.1	28.1	628928	ND	ND	No
HSPB1	LFDQAFGLPR	Yes	582.31	442.3	20.10	76.1	34.1	440470	ND	ND	No
HSPB1	LFDQAFGLPR	Yes	582.31	660.4	20.10	76.1	37.1	354601	ND	ND	No
HSPB1	LFDQAFGLPR	Yes	582.31	903.5	20.10	76.1	25.1	602661	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
HSPB1	QDEHGYISR	Yes	368.84	262.2	7.57	48.6	25.4	400624	ND	ND	No
HSPB1	QDEHGYISR	Yes	368.84	538.3	7.57	48.6	22.4	95424	ND	ND	No
HSPB1	QDEHGYISR	Yes	368.84	595.3	7.57	48.6	19.4	161121	ND	ND	No
HSPB1	QDEHGYISR	Yes	368.84	730.3	7.57	48.6	19.4	2964	ND	ND	No
HSPB1	QLSSGVSEIR	Yes	538.29	504.3	11.50	70.4	35.2	367364	ND	ND	No
HSPB1	QLSSGVSEIR	Yes	538.29	660.4	11.50	70.4	29.2	270601	ND	ND	No
HSPB1	QLSSGVSEIR	Yes	538.29	747.4	11.50	70.4	32.2	194070	ND	ND	No
HSPB1	QLSSGVSEIR	Yes	538.29	834.4	11.50	70.4	29.2	523539	ND	ND	No
HSPB1	VPFSLLR	Yes	416.26	288.2	19.21	54.7	29.8	96172	ND	ND	No
HSPB1	VPFSLLR	Yes	416.26	488.3	19.21	54.7	29.8	3827893	ND	ND	No
HSPB1	VPFSLLR	Yes	416.26	635.4	19.21	54.7	29.8	4012191	ND	ND	No
HSPB1	VPFSLLR	Yes	416.26	732.4	19.21	54.7	20.8	1358917	ND	ND	No
HSPB1	VSLDVNHFAPDELTVK	Yes	595.31	347.2	18.53	77.8	36.9	134368	ND	ND	No
HSPB1	VSLDVNHFAPDELTVK	Yes	595.31	460.3	18.53	77.8	36.9	60865	ND	ND	No
HSPB1	VSLDVNHFAPDELTVK	Yes	595.31	801.4	18.53	77.8	27.9	157605	ND	ND	No
HSPB1	VSLDVNHFAPDELTVK	Yes	595.31	872.5	18.53	77.8	30.9	130188	ND	ND	No
HSPB1	YTLPPGVDPTQVSSSLSPEGTLTVEAPMPK	No									
HTRA1	LHRPPVIVLQR	Yes	443.28	416.3	11.57	58.2	23.2	52408	ND	ND	No
HTRA1	LHRPPVIVLQR	Yes	443.28	515.3	11.57	58.2	26.2	86522	ND	7666	No
HTRA1	LHRPPVIVLQR	Yes	443.28	628.4	11.57	58.2	29.2	75304	ND	1467	Yes (Based on Transition Ratios)
HTRA1	LHRPPVIVLQR	Yes	443.28	700.4	11.57	58.2	29.2	25796	5752	6861	Yes (Based on Transition

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
											Ratios)
HTRA1	LPVLLLGR	Yes	440.8	345.2	19.04	57.9	27.9	71563	1414	ND	No
HTRA1	LPVLLLGR	Yes	440.8	571.4	19.04	57.9	27.9	282890	3857	5462	No
HTRA1	LPVLLLGR	Yes	440.8	670.5	19.04	57.9	24.9	ND	5516	11063	Yes (Based on Manual Review)
HTRA1	LPVLLLGR	Yes	440.8	767.5	19.04	57.9	30.9	39379	ND	ND	No
HTRA1	SSELRPGEFVVAIGSPFSLQNTVTTGIVSTTQR	No									
HTRA1	VTAGISFAIPSDK	Yes	653.36	446.2	16.54	85.3	37.2	1023574	ND	ND	No
HTRA1	VTAGISFAIPSDK	Yes	653.36	630.3	16.54	85.3	31.2	94417	ND	ND	No
HTRA1	VTAGISFAIPSDK	Yes	653.36	777.4	16.54	85.3	31.2	75984	ND	ND	No
HTRA1	VTAGISFAIPSDK	Yes	653.36	864.4	16.54	85.3	31.2	173460	ND	ND	No
HTRA1	YNFIADVVEK	Yes	599.31	278.1	18.07	78.3	25.9	640990	ND	ND	No
HTRA1	YNFIADVVEK	Yes	599.31	660.4	18.07	78.3	28.9	345816	ND	ND	No
HTRA1	YNFIADVVEK	Yes	599.31	773.4	18.07	78.3	28.9	186541	ND	ND	No
HTRA1	YNFIADVVEK	Yes	599.31	920.5	18.07	78.3	28.9	153701	ND	ND	No
HXK1	DFNPTATVK	No									
HXK1	FLLSESGSGK	Yes	512.77	435.2	12.19	67.1	34.1	485056	ND	ND	No
HXK1	FLLSESGSGK	Yes	512.77	651.3	12.19	67.1	25.1	811751	ND	ND	No
HXK1	FLLSESGSGK	Yes	512.77	764.4	12.19	67.1	25.1	1431663	ND	ND	No
HXK1	FLLSESGSGK	Yes	512.77	877.5	12.19	67.1	25.1	71555	ND	ND	No
HXK1	HIDLVEGDEGR	Yes	620.3	251.2	9.91	81	32.8	22343	ND	ND	No
HXK1	HIDLVEGDEGR	Yes	620.3	361.2	9.91	81	35.8	6728	ND	ND	No
HXK1	HIDLVEGDEGR	Yes	620.3	874.4	9.91	81	38.8	2808	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
HXK1	HIDLVEGDEGR	Yes	620.3	989.5	9.91	81	38.8	5739	ND	ND	No
HXK1	LVDEYSLNAGK	Yes	604.81	389.2	11.43	79	38.1	419168	ND	ND	No
HXK1	LVDEYSLNAGK	Yes	604.81	752.4	11.43	79	29.1	335361	ND	ND	No
HXK1	LVDEYSLNAGK	Yes	604.81	881.4	11.43	79	29.1	116547	ND	ND	No
HXK1	LVDEYSLNAGK	Yes	604.81	996.5	11.43	79	29.1	643321	ND	ND	No
HXK1	SANLVAATLGAILNR	Yes	742.43	999.6	24.68	96.8	35.2	40068	7036	7200	No
HXK1	SANLVAATLGAILNR	Yes	742.43	386.2	24.68	96.8	35.2	ND	ND	ND	Yes (Based on Manual Review)
HXK1	SANLVAATLGAILNR	Yes	742.43	643.4	24.68	96.8	32.2	52419	12428	ND	No
HXK1	SANLVAATLGAILNR	Yes	742.43	928.6	24.68	96.8	38.2	17977	ND	7200	No
HYAL2	HPDWPPDR	No									
HYAL2	NDQLAWLWAESTALFPSVYLDETLASSR	No									
HYAL2	QAAGGASEAWAGSHLTSLLALAALAFTWTL	No									
HYAL2	TQESAGLAVIDWEDWRPVWVR	Yes	838.42	359.2	24.54	109.2	37.3	3367	ND	ND	No
HYAL2	TQESAGLAVIDWEDWRPVWVR	Yes	838.42	687.3	24.54	109.2	43.3	1445	ND	ND	No
HYAL2	TQESAGLAVIDWEDWRPVWVR	Yes	838.42	970.5	24.54	109.2	37.3	1254	ND	ND	No
HYAL2	TQESAGLAVIDWEDWRPVWVR	Yes	838.42	998.6	24.54	109.2	37.3	1489	ND	ND	No
HYAL2	VPLDLNAFDVQASPNEGFVNQNITIFYR	No									
HYOU1	FFGDSAASMAIK	Yes	622.8	295.1	17.80	100	32.9	ND	ND	ND	No
HYOU1	FFGDSAASMAIK	Yes	622.8	691.4	17.80	100	32.9	ND	ND	ND	No
HYOU1	FFGDSAASMAIK	Yes	622.8	778.4	17.80	100	32.9	ND	ND	ND	No
HYOU1	FFGDSAASMAIK	Yes	622.8	950.5	17.80	100	32.9	ND	ND	ND	No
HYOU1	FPEHELTFDPQR	Yes	758.366	1005.5	12.96	100	38.9	ND	4664	3388	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
HYOU1	FPEHELTFDPQR	Yes	758.366	1116.5	12.96	100	38.9	ND	ND	ND	No
HYOU1	FPEHELTFDPQR	Yes	758.366	400.231	12.96	100	44.9	ND	11727	9505	No
HYOU1	FPEHELTFDPQR	Yes	758.366	876.458	12.96	100	44.9	ND	31845	41805	No
HYOU1	LAGLFNEQR	Yes	524.3	242.2	15.40	100	28.6	ND	ND	ND	No
HYOU1	LAGLFNEQR	Yes	524.3	546.3	15.40	100	28.6	ND	6119	ND	No
HYOU1	LAGLFNEQR	Yes	524.3	693.3	15.40	100	28.6	ND	12434	9339	No
HYOU1	LAGLFNEQR	Yes	524.3	863.4	15.40	100	28.6	ND	7844	11404	No
HYOU1	LGNTISSLFGGGTTPDAK	Yes	868.4	1237.6	20.30	100	43.7	ND	ND	ND	No
HYOU1	LGNTISSLFGGGTTPDAK	Yes	868.4	430.2	20.30	100	43.7	ND	ND	ND	No
HYOU1	LGNTISSLFGGGTTPDAK	Yes	868.4	803.4	20.30	100	43.7	ND	ND	ND	No
HYOU1	LGNTISSLFGGGTTPDAK	Yes	868.4	950.5	20.30	100	43.7	ND	ND	ND	No
HYOU1	LPATEKPVLLSK	Yes	432.603	211.1	10.74	100	22.6	ND	21741	21799	No
HYOU1	LPATEKPVLLSK	Yes	432.603	328.721	10.74	100	25.6	ND	20364	26663	No
HYOU1	LPATEKPVLLSK	Yes	432.603	543.332	10.74	100	25.6	ND	55273	51963	No
HYOU1	LPATEKPVLLSK	Yes	432.603	656.4	10.74	100	22.6	ND	19753	18732	No
HYOU1	LPATEKPVLLSK	Yes	648.4	1014.6	10.74	100	34	ND	ND	2008	No
HYOU1	LPATEKPVLLSK	Yes	648.4	1085.7	10.74	100	34	ND	1442	1125	No
HYOU1	LPATEKPVLLSK	Yes	648.4	591.9	10.74	100	34	ND	24852	24170	No
HYOU1	LPATEKPVLLSK	Yes	648.4	784.5	10.74	100	34	ND	5217	3591	No
HYOU1	VAIVKPGVPMEIVLNK	Yes	569.7	472.3	19.60	100	29.6	ND	ND	ND	No
HYOU1	VAIVKPGVPMEIVLNK	Yes	569.7	715.4	19.60	100	29.6	ND	ND	ND	No
HYOU1	VAIVKPGVPMEIVLNK	Yes	569.7	764.5	19.60	100	29.6	ND	ND	ND	No
HYOU1	VAIVKPGVPMEIVLNK	Yes	569.7	943.5	19.60	100	29.6	ND	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
HYOU1	VAIVKPGVPMEIVLNK	Yes	854	1196.7	19.60	100	43.1	ND	ND	ND	No
HYOU1	VAIVKPGVPMEIVLNK	Yes	854	284.2	19.60	100	43.1	ND	ND	ND	No
HYOU1	VAIVKPGVPMEIVLNK	Yes	854	383.3	19.60	100	43.1	ND	ND	ND	No
HYOU1	VAIVKPGVPMEIVLNK	Yes	854	943.5	19.60	100	43.1	ND	ND	ND	No
IBP2	AEVLFR	Yes	367.71	300.2	12.35	48.4	18.7	36030	ND	8094	No
IBP2	AEVLFR	Yes	367.71	435.3	12.35	48.4	18.7	81964	18545	40338	Yes (Based on Transition Ratios)
IBP2	AEVLFR	Yes	367.71	534.3	12.35	48.4	18.7	180797	10535	34372	No
IBP2	AEVLFR	Yes	367.71	663.4	12.35	48.4	18.7	10171	ND	2060	No
IBP2	ELAVFR	Yes	367.71	322.2	13.54	48.4	18.7	240327	229090	232464	No
IBP2	ELAVFR	Yes	367.71	421.3	13.54	48.4	18.7	52641	64258	64032	No
IBP2	ELAVFR	Yes	367.71	492.3	13.54	48.4	18.7	92548	94822	88956	No
IBP2	ELAVFR	Yes	367.71	605.4	13.54	48.4	15.7	8547	3100	1819	Yes (Based on Transition Ratios)
IBP2	HGLYNLK	Yes	422.74	537.3	9.26	55.5	27.1	36579	1552	ND	Yes (Based on Transition Ratios)
IBP2	HGLYNLK	Yes	422.74	585.3	9.26	55.5	24.1	222934	82402	49990	Yes (Based on Transition Ratios)
IBP2	HGLYNLK	Yes	422.74	698.4	9.26	55.5	24.1	60740	54596	28761	Yes (Based on Transition Ratios)
IBP2	HGLYNLK	Yes	422.74	707.4	9.26	55.5	21.1	106888	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
IBP2	LIQGAPTIR	Yes	484.8	389.3	10.85	63.5	32.8	ND	ND	ND	Yes (Based on Manual Review)
IBP2	LIQGAPTIR	Yes	484.8	557.3	10.85	63.5	23.8	18408	19983	14786	Yes (Based on Transition Ratios)
IBP2	LIQGAPTIR	Yes	484.8	614.4	10.85	63.5	23.8	136752	27031	34798	No
IBP2	LIQGAPTIR	Yes	484.8	742.4	10.85	63.5	23.8	200739	40944	35262	No
IBP2	VTEQHR	Yes	385.2	312.2	5.15	50.7	22.4	1845	ND	ND	No
IBP2	VTEQHR	Yes	385.2	440.2	5.15	50.7	25.4	2993	ND	ND	No
IBP2	VTEQHR	Yes	385.2	569.3	5.15	50.7	25.4	6944	ND	ND	No
IBP2	VTEQHR	Yes	385.2	670.3	5.15	50.7	22.4	4980	ND	ND	No
IBP3	AYLLPAPPAPGNASESEEDR	Yes	1042.5	348.2	14.91	135.5	48.4	50974	ND	ND	No
IBP3	AYLLPAPPAPGNASESEEDR	Yes	1042.5	461.3	14.91	135.5	45.4	11402	ND	ND	No
IBP3	AYLLPAPPAPGNASESEEDR	Yes	1042.5	558.3	14.91	135.5	48.4	2882	ND	ND	No
IBP3	AYLLPAPPAPGNASESEEDR	Yes	1042.5	629.4	14.91	135.5	45.4	8711	ND	ND	No
IBP3	FHPLHSK	Yes	433.24	285.1	6.14	56.9	24.6	495951	786225	692186	No
IBP3	FHPLHSK	Yes	433.24	371.2	6.14	56.9	27.6	106771	146682	135383	No
IBP3	FHPLHSK	Yes	433.24	581.3	6.14	56.9	21.6	362070	628985	637117	No
IBP3	FHPLHSK	Yes	433.24	632.3	6.14	56.9	21.6	5694	8284	8298	No
IBP3	FLNVLSPR	Yes	473.28	359.2	16.13	62.1	23.3	125520	1463013	1493907	No
IBP3	FLNVLSPR	Yes	473.28	571.4	16.13	62.1	23.3	69335	860695	845768	No
IBP3	FLNVLSPR	Yes	473.28	685.4	16.13	62.1	23.3	215753	2816423	2864718	No
IBP3	FLNVLSPR	Yes	473.28	798.5	16.13	62.1	32.3	17114	211946	223165	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
IBP3	SAGSVESPSVSSTHR	Yes	496.57	587.3	6.68	65.1	28.9	41821	9736	9127	No
IBP3	SAGSVESPSVSSTHR	Yes	496.57	773.4	6.68	65.1	28.9	13089	5706	2783	No
IBP3	SAGSVESPSVSSTHR	Yes	496.57	870.4	6.68	65.1	22.9	14425	1291	3536	No
IBP3	SAGSVESPSVSSTHR	Yes	496.57	957.5	6.68	65.1	22.9	6281	690	967	No
IBP3	YGQPLPGYTTK	Yes	612.82	559.3	10.71	80.1	29.5	46737	ND	ND	No
IBP3	YGQPLPGYTTK	Yes	612.82	569.3	10.71	80.1	38.5	37702	ND	ND	No
IBP3	YGQPLPGYTTK	Yes	612.82	666.3	10.71	80.1	35.5	269245	12957	15387	No
IBP3	YGQPLPGYTTK	Yes	612.82	779.4	10.71	80.1	38.5	28847	ND	ND	No
ICAM1	ASVSVTAEDEGTQR	Yes	725.34	461.2	8.04	94.6	31.4	6729	6395	4871	No
ICAM1	ASVSVTAEDEGTQR	Yes	725.34	705.3	8.04	94.6	43.4	7368	3373	3383	No
ICAM1	ASVSVTAEDEGTQR	Yes	725.34	834.4	8.04	94.6	34.4	13149	4130	3749	No
ICAM1	ASVSVTAEDEGTQR	Yes	725.34	905.4	8.04	94.6	37.4	15718	9377	5632	No
ICAM1	DGTFPLPIGESVTVTR	Yes	844.95	274.1	19.24	110	39.7	71670	ND	ND	No
ICAM1	DGTFPLPIGESVTVTR	Yes	844.95	421.2	19.24	110	36.7	25208	ND	ND	No
ICAM1	DGTFPLPIGESVTVTR	Yes	844.95	518.2	19.24	110	42.7	15789	ND	ND	No
ICAM1	DGTFPLPIGESVTVTR	Yes	844.95	631.3	19.24	110	36.7	31289	ND	ND	No
ICAM1	LNPTVTYGNDSFSAK	Yes	807.39	305.2	12.64	105.2	47	27406	ND	ND	No
ICAM1	LNPTVTYGNDSFSAK	Yes	807.39	426.2	12.64	105.2	35	5718	ND	ND	No
ICAM1	LNPTVTYGNDSFSAK	Yes	807.39	525.3	12.64	105.2	35	13220	ND	ND	No
ICAM1	LNPTVTYGNDSFSAK	Yes	807.39	988.4	12.64	105.2	38	18083	ND	ND	No
ICAM1	TFLTVYWTPER	Yes	471.58	362.2	20.79	61.8	24.6	1505	ND	ND	No
ICAM1	TFLTVYWTPER	Yes	471.58	401.2	20.79	61.8	21.6	25316	ND	ND	No
ICAM1	TFLTVYWTPER	Yes	471.58	502.3	20.79	61.8	21.6	10728	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
ICAM1	TFLTVYWTPER	Yes	471.58	688.3	20.79	61.8	21.6	4616	ND	ND	No
ICAM1	VELAPLPSWQPVGK	Yes	760.93	342.2	18.83	99.2	36	721731	ND	ND	No
ICAM1	VELAPLPSWQPVGK	Yes	760.93	400.3	18.83	99.2	45	299178	ND	ND	No
ICAM1	VELAPLPSWQPVGK	Yes	760.93	413.2	18.83	99.2	33	447767	ND	ND	No
ICAM1	VELAPLPSWQPVGK	Yes	760.93	898.5	18.83	99.2	36	205105	ND	ND	No
ICAM3	ADQEGAR	Yes	373.68	303.2	5.73	49.2	27.9	108216	ND	ND	No
ICAM3	ADQEGAR	Yes	373.68	432.2	5.73	49.2	21.9	106786	ND	ND	No
ICAM3	ADQEGAR	Yes	373.68	560.3	5.73	49.2	18.9	101171	ND	ND	No
ICAM3	ADQEGAR	Yes	373.68	675.3	5.73	49.2	21.9	19645	ND	ND	No
ICAM3	EESTYLPLTSMQPTEAMGEEPSR	Yes	861.72	359.2	19.59	112.2	50.5	52874	ND	ND	No
ICAM3	EESTYLPLTSMQPTEAMGEEPSR	Yes	861.72	610.2	19.59	112.2	47.5	12608	ND	ND	No
ICAM3	EESTYLPLTSMQPTEAMGEEPSR	Yes	861.72	674.3	19.59	112.2	50.5	37788	ND	ND	No
ICAM3	EESTYLPLTSMQPTEAMGEEPSR	Yes	861.72	723.3	19.59	112.2	47.5	13122	ND	ND	No
ICAM3	GNPYPELR	Yes	473.24	288.2	12.41	62	32.3	1467218	ND	ND	No
ICAM3	GNPYPELR	Yes	473.24	514.3	12.41	62	32.3	4781808	ND	ND	No
ICAM3	GNPYPELR	Yes	473.24	677.4	12.41	62	26.3	697296	ND	ND	No
ICAM3	GNPYPELR	Yes	473.24	774.4	12.41	62	23.3	2128386	ND	ND	No
ICAM3	IALETSLSK	Yes	481.28	535.3	13.78	63.1	32.7	775665	ND	ND	No
ICAM3	IALETSLSK	Yes	481.28	664.4	13.78	63.1	23.7	956656	ND	ND	No
ICAM3	IALETSLSK	Yes	481.28	777.4	13.78	63.1	23.7	2532858	ND	ND	No
ICAM3	IALETSLSK	Yes	481.28	848.5	13.78	63.1	23.7	1264298	ND	ND	No
ICAM3	QPAVEEPAEVTATVLASR	No									
ICAM3	TELDMQPQGLGLFVNTSAPR	No									

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
ICAM3	TFVLPVTPPR	Yes	563.83	348.2	18.56	73.7	27.3	5766033	197276	164252	No
ICAM3	TFVLPVTPPR	Yes	563.83	666.4	18.56	73.7	27.3	6265233	212884	160190	No
ICAM3	TFVLPVTPPR	Yes	563.83	779.5	18.56	73.7	27.3	1250287	46024	27547	No
ICAM3	TFVLPVTPPR	Yes	563.83	878.5	18.56	73.7	27.3	856345	30444	19967	No
ICAM3	VELAPLPPWQPVGQNFTLR	No									
ICAM3	VQVTLDGVPAAAPGQPAQLQLNATESDDGR	No									
IDHP	ATDFVADR	Yes	447.72	361.2	8.80	58.8	31.2	16069	ND	ND	No
IDHP	ATDFVADR	Yes	447.72	607.3	8.80	58.8	25.2	18446	ND	ND	No
IDHP	ATDFVADR	Yes	447.72	722.3	8.80	58.8	22.2	19957	ND	ND	No
IDHP	ATDFVADR	Yes	447.72	823.4	8.80	58.8	22.2	2670	ND	ND	No
IDHP	DIFQEIFDK	Yes	577.79	409.2	23.80	75.5	33.9	78291	ND	ND	No
IDHP	DIFQEIFDK	Yes	577.79	651.3	23.80	75.5	27.9	56424	ND	ND	No
IDHP	DIFQEIFDK	Yes	577.79	779.4	23.80	75.5	27.9	70925	ND	ND	No
IDHP	DIFQEIFDK	Yes	577.79	926.5	23.80	75.5	24.9	142564	ND	ND	No
IDHP	IIWQFIK	Yes	474.29	407.3	20.38	62.2	32.4	69184	ND	ND	No
IDHP	IIWQFIK	Yes	474.29	535.3	20.38	62.2	26.4	19326	ND	ND	No
IDHP	IIWQFIK	Yes	474.29	721.4	20.38	62.2	20.4	186832	ND	ND	No
IDHP	IIWQFIK	Yes	474.29	834.5	20.38	62.2	23.4	43703	ND	ND	No
IDHP	LILPHVDIQLK	Yes	644.9	616.4	19.02	84.2	39.9	20564	ND	ND	No
IDHP	LILPHVDIQLK	Yes	644.9	715.4	19.02	84.2	39.9	30639	ND	ND	No
IDHP	LILPHVDIQLK	Yes	644.9	852.5	19.02	84.2	39.9	14591	ND	ND	No
IDHP	LILPHVDIQLK	Yes	644.9	949.5	19.02	84.2	30.9	35764	ND	ND	No
IDHP	YFDLGLPNR	Yes	547.79	386.2	17.29	71.7	23.6	104243	7523	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
IDHP	YFDLGLPNR	Yes	547.79	426.2	17.29	71.7	26.6	101387	7140	ND	No
IDHP	YFDLGLPNR	Yes	547.79	669.4	17.29	71.7	35.6	55234	2292	2439	No
IDHP	YFDLGLPNR	Yes	547.79	784.4	17.29	71.7	26.6	101178	3156	8001	No
IF4A1	GIYAYGFEKPSAIQQR	Yes	914.5	1056.6	16.10	100	45.7	ND	ND	ND	No
IF4A1	GIYAYGFEKPSAIQQR	Yes	914.5	799.4	16.10	100	45.7	ND	ND	ND	No
IF4A1	GIYAYGFEKPSAIQQR	Yes	914.5	927.5	16.10	100	45.7	ND	ND	ND	No
IF4A1	GYDVIAQAQSGTGK	Yes	697.8	648.3	10.56	100	36.2	ND	ND	ND	No
IF4A1	GYDVIAQAQSGTGK	Yes	697.8	776.4	10.56	100	36.2	ND	ND	ND	No
IF4A1	GYDVIAQAQSGTGK	Yes	697.8	847.4	10.56	100	33.2	ND	ND	ND	No
IF4A1	GYDVIAQAQSGTGK	Yes	697.8	960.5	10.56	100	33.2	ND	ND	ND	No
IF4A1	LQMEAPHIIVGTPGR	Yes	540.3	242.2	17.00	100	28.1	ND	40371	30464	No
IF4A1	LQMEAPHIIVGTPGR	Yes	540.3	487.3	17.00	100	28.1	ND	24452	28716	No
IF4A1	LQMEAPHIIVGTPGR	Yes	540.3	586.3	17.00	100	28.1	ND	19872	18717	No
IF4A1	LQMEAPHIIVGTPGR	Yes	540.3	699.4	17.00	100	28.1	ND	44184	38411	No
IF4A1	LQMEAPHIIVGTPGR	Yes	809.9	1046.6	17.00	100	41.1	ND	ND	ND	No
IF4A1	LQMEAPHIIVGTPGR	Yes	809.9	1117.7	17.00	100	41.1	ND	ND	ND	No
IF4A1	LQMEAPHIIVGTPGR	Yes	809.9	586.3	17.00	100	41.1	ND	ND	ND	No
IF4A1	LQMEAPHIIVGTPGR	Yes	809.9	699.4	17.00	100	41.1	ND	ND	ND	No
IF4A1	MFVLDEADEMLSR	Yes	778.4	1065.5	23.80	100	39.7	ND	ND	ND	No
IF4A1	MFVLDEADEMLSR	Yes	778.4	1178.5	23.80	100	39.7	ND	ND	ND	No
IF4A1	MFVLDEADEMLSR	Yes	778.4	378.2	23.80	100	39.7	ND	ND	ND	No
IF4A1	MFVLDEADEMLSR	Yes	778.4	821.4	23.80	100	39.7	ND	ND	ND	No
IF4A1	VFDMLNR	Yes	447.7	247.1	16.00	100	25.2	ND	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
IF4A1	VFDMLNR	Yes	447.7	533.3	16.00	100	25.2	ND	ND	ND	No
IF4A1	VFDMLNR	Yes	447.7	648.3	16.00	100	25.2	ND	ND	ND	No
IF4A1	VFDMLNR	Yes	447.7	795.4	16.00	100	25.2	ND	ND	ND	No
IF4A1	VLITTDLLAR	Yes	557.8	213.2	16.96	100	27	ND	ND	ND	No
IF4A1	VLITTDLLAR	Yes	557.8	688.4	16.96	100	30	ND	ND	ND	No
IF4A1	VLITTDLLAR	Yes	557.8	789.4	16.96	100	30	ND	ND	ND	No
IF4A1	VLITTDLLAR	Yes	557.8	902.5	16.96	100	30	ND	ND	ND	No
IGF1	EGTEASLQIR	Yes	552.29	416.3	10.46	72.2	26.8	65483	ND	ND	No
IGF1	EGTEASLQIR	Yes	552.29	529.3	10.46	72.2	29.8	51553	ND	ND	No
IGF1	EGTEASLQIR	Yes	552.29	616.4	10.46	72.2	26.8	132844	ND	ND	No
IGF1	EGTEASLQIR	Yes	552.29	687.4	10.46	72.2	35.8	102699	ND	ND	No
IGF1	ISSLPTQLFK	Yes	567.33	636.4	17.77	74.2	36.5	71599	ND	ND	No
IGF1	ISSLPTQLFK	Yes	567.33	733.4	17.77	74.2	27.5	649084	ND	ND	No
IGF1	ISSLPTQLFK	Yes	567.33	846.5	17.77	74.2	27.5	50601	ND	ND	No
IGF1	ISSLPTQLFK	Yes	567.33	933.5	17.77	74.2	27.5	163909	ND	ND	No
IGF1	THPGGEQK	Yes	427.21	275.2	5.09	56.1	24.3	3888	ND	ND	No
IGF1	THPGGEQK	Yes	427.21	518.3	5.09	56.1	27.3	3859	ND	ND	No
IGF1	THPGGEQK	Yes	427.21	579.3	5.09	56.1	21.3	2110	ND	ND	No
IGF1	THPGGEQK	Yes	427.21	615.3	5.09	56.1	21.3	70252	ND	ND	No
IGF1	YQPPSTNK	No									
IKIP	LEPLVNDLTLR	Yes	641.87	502.3	19.11	83.8	39.7	33929	ND	ND	No
IKIP	LEPLVNDLTLR	Yes	641.87	731.4	19.11	83.8	39.7	66460	ND	ND	No
IKIP	LEPLVNDLTLR	Yes	641.87	830.5	19.11	83.8	36.7	81801	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
IKIP	LEPLVNDLTLR	Yes	641.87	943.6	19.11	83.8	39.7	20955	ND	ND	No
IKIP	LETNEFQQLQSK	Yes	732.87	475.3	13.09	95.5	43.7	85426	ND	ND	No
IKIP	LETNEFQQLQSK	Yes	732.87	587.3	13.09	95.5	34.7	31106	ND	ND	No
IKIP	LETNEFQQLQSK	Yes	732.87	603.3	13.09	95.5	34.7	68366	ND	ND	No
IKIP	LETNEFQQLQSK	Yes	732.87	878.5	13.09	95.5	34.7	60798	ND	ND	No
IKIP	NIGDLLSSSIDR	Yes	430.56	403.2	18.29	56.5	19.5	12940	ND	ND	No
IKIP	NIGDLLSSSIDR	Yes	430.56	490.3	18.29	56.5	28.5	25929	ND	ND	No
IKIP	NIGDLLSSSIDR	Yes	430.56	577.3	18.29	56.5	16.5	18767	ND	ND	No
IKIP	NIGDLLSSSIDR	Yes	430.56	664.3	18.29	56.5	19.5	26106	ND	ND	No
IKIP	SSGGGGWADPR	Yes	523.74	272.2	8.88	68.6	34.5	134688	ND	ND	No
IKIP	SSGGGGWADPR	Yes	523.74	458.2	8.88	68.6	25.5	9738	ND	ND	No
IKIP	SSGGGGWADPR	Yes	523.74	660.3	8.88	68.6	25.5	2650	ND	ND	No
IKIP	SSGGGGWADPR	Yes	523.74	758.4	8.88	68.6	25.5	4224	ND	ND	No
IKIP	TVTFANDLKPK	Yes	617.35	302.2	11.83	80.6	32.7	111694	ND	ND	No
IKIP	TVTFANDLKPK	Yes	617.35	714.4	11.83	80.6	38.7	21890	ND	ND	No
IKIP	TVTFANDLKPK	Yes	617.35	785.5	11.83	80.6	32.7	90940	ND	ND	No
IKIP	TVTFANDLKPK	Yes	617.35	932.5	11.83	80.6	29.7	22988	ND	ND	No
IL18	FIDNTLYFIAEDDENLESDYFGK	No									
IL18	SDIIFFQR	Yes	513.27	450.2	17.84	67.2	25.1	10191	ND	ND	No
IL18	SDIIFFQR	Yes	513.27	597.3	17.84	67.2	25.1	21196	ND	ND	No
IL18	SDIIFFQR	Yes	513.27	710.4	17.84	67.2	25.1	11432	ND	ND	No
IL18	SDIIFFQR	Yes	513.27	823.5	17.84	67.2	34.1	2324	ND	ND	No
IL18	SVPGHDNK	Yes	427.21	261.2	5.25	56.1	30.3	26278	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
IL18	SVPGHDNK	Yes	427.21	513.2	5.25	56.1	27.3	7998	ND	ND	No
IL18	SVPGHDNK	Yes	427.21	570.3	5.25	56.1	30.3	14346	ND	ND	No
IL18	SVPGHDNK	Yes	427.21	667.3	5.25	56.1	21.3	55214	ND	ND	No
IL19	DHQEPNPK	Yes	482.73	253.1	5.32	63.3	26.7	240863	ND	ND	No
IL19	DHQEPNPK	Yes	482.73	455.3	5.32	63.3	26.7	62495	ND	ND	No
IL19	DHQEPNPK	Yes	482.73	510.2	5.32	63.3	29.7	57267	ND	ND	No
IL19	DHQEPNPK	Yes	482.73	712.4	5.32	63.3	23.7	55067	ND	ND	No
IL19	NLLAFYVDR	Yes	555.8	341.2	19.75	72.7	24	50437	ND	ND	No
IL19	NLLAFYVDR	Yes	555.8	699.3	19.75	72.7	27	23856	ND	ND	No
IL19	NLLAFYVDR	Yes	555.8	770.4	19.75	72.7	27	55749	ND	ND	No
IL19	NLLAFYVDR	Yes	555.8	883.5	19.75	72.7	27	35675	ND	ND	No
IL19	QEATNATR	No									
IL19	SLGELDVFLAWINK	No									
IL19	VIHDNYDQLEVHAAAIK	Yes	646	610.4	12.76	84.3	33.5	28760	ND	ND	No
IL19	VIHDNYDQLEVHAAAIK	Yes	646	709.4	12.76	84.3	30.5	12364	ND	ND	No
IL19	VIHDNYDQLEVHAAAIK	Yes	646	838.5	12.76	84.3	30.5	17805	3124	3288	No
IL19	VIHDNYDQLEVHAAAIK	Yes	646	985.4	12.76	84.3	33.5	9482	5436	4135	No
IL22	EASLADNNTDVR	Yes	652.81	274.2	7.93	85.2	40.2	48202	ND	ND	No
IL22	EASLADNNTDVR	Yes	652.81	718.3	7.93	85.2	37.2	13462	ND	ND	No
IL22	EASLADNNTDVR	Yes	652.81	833.4	7.93	85.2	31.2	28926	ND	ND	No
IL22	EASLADNNTDVR	Yes	652.81	904.4	7.93	85.2	31.2	30259	ND	ND	No
IL22	QVLNFTLEEVLFPQSDR	No									
IL22	SNFQQPYITNR	Yes	684.34	349.2	11.29	89.3	38.6	29835	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
IL22	SNFQQPYITNR	Yes	684.34	390.2	11.29	89.3	32.6	36713	ND	ND	No
IL22	SNFQQPYITNR	Yes	684.34	763.4	11.29	89.3	32.6	78192	ND	ND	No
IL22	SNFQQPYITNR	Yes	684.34	891.5	11.29	89.3	32.6	18713	ND	ND	No
IL32	EELTPQK	Yes	422.72	259.1	6.47	55.5	21.1	53852	9777	4635	No
IL32	EELTPQK	Yes	422.72	275.2	6.47	55.5	30.1	65749	10979	ND	No
IL32	EELTPQK	Yes	422.72	586.4	6.47	55.5	21.1	95079	3864	ND	No
IL32	EELTPQK	Yes	422.72	715.4	6.47	55.5	24.1	6986	5575	ND	Yes (Based on Transition Ratios)
IL32	EGYLETVAAYYEEQHPELTPLLEK	No									
IL32	LQTWWHGVLAWVK	Yes	541.97	432.3	24.08	70.9	31.2	6056	ND	ND	No
IL32	LQTWWHGVLAWVK	Yes	541.97	503.3	24.08	70.9	31.2	4786	ND	ND	No
IL32	LQTWWHGVLAWVK	Yes	541.97	616.4	24.08	70.9	28.2	5085	ND	ND	No
IL32	LQTWWHGVLAWVK	Yes	541.97	772.5	24.08	70.9	28.2	8790	ND	ND	No
IL32	VVALVHAVQALWK	Yes	478.63	333.2	22.60	62.7	31	31150	ND	ND	No
IL32	VVALVHAVQALWK	Yes	478.63	744.4	22.60	62.7	25	6826	ND	ND	No
IL32	VVALVHAVQALWK	Yes	478.63	815.5	22.60	62.7	25	7354	ND	ND	No
IL32	VVALVHAVQALWK	Yes	478.63	952.5	22.60	62.7	22	4926	ND	ND	No
IL7	SLEENK	Yes	360.18	261.2	5.56	47.5	24.3	319825	ND	ND	No
IL7	SLEENK	Yes	360.18	390.2	5.56	47.5	15.3	74146	ND	ND	No
IL7	SLEENK	Yes	360.18	519.2	5.56	47.5	15.3	784703	ND	ND	No
IL7	SLEENK	Yes	360.18	632.3	5.56	47.5	18.3	40588	ND	ND	No
IL8	ENWVQR	Yes	416.21	303.2	8.90	54.7	20.8	166904	4966	4072	No
IL8	ENWVQR	Yes	416.21	529.2	8.90	54.7	17.8	3097	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
IL8	ENWVQR	Yes	416.21	588.3	8.90	54.7	20.8	32075	3121	1423	No
IL8	ENWVQR	Yes	416.21	702.4	8.90	54.7	20.8	3214	ND	ND	No
IL8	TYSKPFHPK	Yes	368.87	265.1	6.31	48.6	16.4	46204	ND	ND	No
IL8	TYSKPFHPK	Yes	368.87	528.3	6.31	48.6	19.4	5064	ND	ND	No
IL8	TYSKPFHPK	Yes	368.87	625.3	6.31	48.6	19.4	82744	ND	ND	No
IL8	TYSKPFHPK	Yes	368.87	753.4	6.31	48.6	22.4	2148	ND	ND	No
ILEU	EATTNAPFR	Yes	503.75	419.2	8.65	66	21.7	128614	ND	ND	No
ILEU	EATTNAPFR	Yes	503.75	604.3	8.65	66	24.7	74564	ND	ND	No
ILEU	EATTNAPFR	Yes	503.75	705.4	8.65	66	24.7	32665	ND	ND	No
ILEU	EATTNAPFR	Yes	503.75	806.4	8.65	66	33.7	31803	ND	ND	No
ILEU	LEESYTLNSDLAR	Yes	755.87	561.3	13.61	98.5	35.8	25325	ND	ND	No
ILEU	LEESYTLNSDLAR	Yes	755.87	675.3	13.61	98.5	35.8	52005	ND	ND	No
ILEU	LEESYTLNSDLAR	Yes	755.87	788.4	13.61	98.5	32.8	29539	ND	ND	No
ILEU	LEESYTLNSDLAR	Yes	755.87	889.5	13.61	98.5	41.8	58556	ND	ND	No
ILEU	LHEWTKPENLDFIEVNVSLPR	No									
ILEU	TFHFNTVEEVHSR	Yes	534.93	399.2	11.99	70	33.8	96788	ND	ND	No
ILEU	TFHFNTVEEVHSR	Yes	534.93	627.3	11.99	70	27.8	26312	ND	ND	No
ILEU	TFHFNTVEEVHSR	Yes	534.93	748.3	11.99	70	33.8	8253	ND	ND	No
ILEU	TFHFNTVEEVHSR	Yes	534.93	756.4	11.99	70	27.8	58624	ND	ND	No
ILEU	TYNFLPEFLVSTQK	Yes	843.94	379.2	23.33	109.9	42.6	134293	ND	ND	No
ILEU	TYNFLPEFLVSTQK	Yes	843.94	463.3	23.33	109.9	48.6	76077	ND	ND	No
ILEU	TYNFLPEFLVSTQK	Yes	843.94	526.2	23.33	109.9	36.6	99652	ND	ND	No
ILEU	TYNFLPEFLVSTQK	Yes	843.94	639.3	23.33	109.9	36.6	83064	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
ILK	GDDTPLHLAASHGHR	Yes	528.59	369.2	8.99	69.2	33.5	15851	ND	ND	No
ILK	GDDTPLHLAASHGHR	Yes	528.59	389.1	8.99	69.2	24.5	16815	ND	ND	No
ILK	GDDTPLHLAASHGHR	Yes	528.59	593.3	8.99	69.2	30.5	4816	ND	ND	No
ILK	GDDTPLHLAASHGHR	Yes	528.59	599.3	8.99	69.2	30.5	2965	ND	ND	No
ILK	HSGIDFK	Yes	402.21	294.2	8.60	52.9	20.2	698457	ND	ND	No
ILK	HSGIDFK	Yes	402.21	510.2	8.60	52.9	20.2	424385	ND	ND	No
ILK	HSGIDFK	Yes	402.21	579.3	8.60	52.9	20.2	35714	ND	ND	No
ILK	HSGIDFK	Yes	402.21	666.3	8.60	52.9	20.2	66989	ND	ND	No
ILK	LNENHSGELWK	Yes	663.83	333.2	10.69	86.6	37.7	38474	ND	ND	No
ILK	LNENHSGELWK	Yes	663.83	881.4	10.69	86.6	40.7	6337	ND	ND	No
ILK	LNENHSGELWK	Yes	663.83	970.5	10.69	86.6	34.7	2527	ND	ND	No
ILK	LNENHSGELWK	Yes	663.83	994.5	10.69	86.6	34.7	5663	ND	ND	No
ILK	QLNFLTK	Yes	432.25	361.2	14.39	56.8	18.5	194665	ND	ND	No
ILK	QLNFLTK	Yes	432.25	508.3	14.39	56.8	21.5	87923	ND	ND	No
ILK	QLNFLTK	Yes	432.25	622.4	14.39	56.8	21.5	124449	ND	ND	No
ILK	QLNFLTK	Yes	432.25	735.4	14.39	56.8	21.5	22933	ND	ND	No
ILK	WQGNDIVVK	Yes	529.79	315.1	11.74	69.3	25.8	150356	ND	7747	Yes (Based on Transition Ratios)
ILK	WQGNDIVVK	Yes	529.79	458.3	11.74	69.3	31.8	16642	ND	9488	Yes (Based on Transition Ratios)
ILK	WQGNDIVVK	Yes	529.79	744.4	11.74	69.3	25.8	115132	ND	7321	Yes (Based on Transition Ratios)

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
ILK	WQGNDIVVK	Yes	529.79	872.5	11.74	69.3	25.8	17728	ND	12593	Yes (Based on Transition Ratios)
INHBA	AEVWLFLK	Yes	503.29	407.3	22.33	65.9	33.6	38492	ND	ND	No
INHBA	AEVWLFLK	Yes	503.29	706.4	22.33	65.9	24.6	52506	ND	2940	No
INHBA	AEVWLFLK	Yes	503.29	746.4	22.33	65.9	21.6	3395	ND	ND	No
INHBA	AEVWLFLK	Yes	503.29	805.5	22.33	65.9	24.6	84876	ND	ND	No
INHBA	EGSDLSVVER	Yes	545.77	304.2	10.24	71.4	26.5	93615	5400	7015	No
INHBA	EGSDLSVVER	Yes	545.77	403.2	10.24	71.4	26.5	147317	11830	8135	No
INHBA	EGSDLSVVER	Yes	545.77	702.4	10.24	71.4	35.5	40694	1240	3294	No
INHBA	EGSDLSVVER	Yes	545.77	904.5	10.24	71.4	29.5	9963	1190	911	No
INHBA	GHSPFANLK	Yes	485.76	282.1	10.87	63.7	23.9	158066	ND	ND	No
INHBA	GHSPFANLK	Yes	485.76	445.3	10.87	63.7	32.9	26907	ND	ND	No
INHBA	GHSPFANLK	Yes	485.76	689.4	10.87	63.7	23.9	65911	ND	ND	No
INHBA	GHSPFANLK	Yes	485.76	776.4	10.87	63.7	23.9	67364	ND	ND	No
INHBA	HPQGSLDTGEEAEEVGLK	Yes	632.64	416.3	11.80	82.6	35.8	9673	ND	ND	No
INHBA	HPQGSLDTGEEAEEVGLK	Yes	632.64	735.3	11.80	82.6	29.8	8734	ND	ND	No
INHBA	HPQGSLDTGEEAEEVGLK	Yes	632.64	745.4	11.80	82.6	29.8	18961	ND	ND	No
INHBA	HPQGSLDTGEEAEEVGLK	Yes	632.64	874.5	11.80	82.6	29.8	8328	ND	ND	No
INHBA	SELLLSEK	Yes	459.76	330.2	12.20	60.3	22.7	161591	ND	ND	No
INHBA	SELLLSEK	Yes	459.76	363.2	12.20	60.3	31.7	313350	ND	ND	No
INHBA	SELLLSEK	Yes	459.76	589.4	12.20	60.3	22.7	203305	ND	ND	No
INHBA	SELLLSEK	Yes	459.76	702.4	12.20	60.3	22.7	283090	ND	ND	No
ISLR	ALPGTPVASSQPR	Yes	640.85	440.3	9.47	83.7	27.7	22301	12350	10861	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
ISLR	ALPGTPVASSQPR	Yes	640.85	574.3	9.47	83.7	39.7	ND	9576	14346	Yes (Based on Manual Review)
ISLR	ALPGTPVASSQPR	Yes	640.85	841.5	9.47	83.7	33.7	52305	41276	25572	No
ISLR	ALPGTPVASSQPR	Yes	640.85	999.5	9.47	83.7	39.7	5655	5632	3394	No
ISLR	EVPLLQSLWLAHNEIR	Yes	640.02	531.3	24.17	83.6	33.2	6290	ND	ND	No
ISLR	EVPLLQSLWLAHNEIR	Yes	640.02	668.3	24.17	83.6	36.2	ND	9659	7219	Yes (Based on Manual Review)
ISLR	EVPLLQSLWLAHNEIR	Yes	640.02	739.4	24.17	83.6	39.2	14933	18937	14255	No
ISLR	EVPLLQSLWLAHNEIR	Yes	640.02	852.5	24.17	83.6	36.2	10871	10689	13863	No
ISLR	LPGLPEGAFR	Yes	528.8	268.2	16.32	69.2	28.8	128034	ND	ND	No
ISLR	LPGLPEGAFR	Yes	528.8	381.3	16.32	69.2	25.8	63086	ND	ND	No
ISLR	LPGLPEGAFR	Yes	528.8	676.3	16.32	69.2	28.8	133401	ND	ND	No
ISLR	LPGLPEGAFR	Yes	528.8	846.4	16.32	69.2	34.8	25708	ND	ND	No
ISLR	SLDLSHNLISDFAWSDLHNLSALQLLK	No									
ISLR	TVAAGALASLSHLK	Yes	446.93	343.2	16.74	58.7	17.3	ND	ND	ND	No
ISLR	TVAAGALASLSHLK	Yes	446.93	684.4	16.74	58.7	23.3	35935	24016	ND	No
ISLR	TVAAGALASLSHLK	Yes	446.93	755.4	16.74	58.7	23.3	32109	15086	ND	No
ISLR	TVAAGALASLSHLK	Yes	446.93	868.5	16.74	58.7	29.3	4735	ND	ND	No
ITA5	DLDGNGYPDLIVGSFGVDK	Yes	990.98	709.4	21.27	128.8	46.1	8351	ND	ND	No
ITA5	DLDGNGYPDLIVGSFGVDK	Yes	990.98	735.3	21.27	128.8	43.1	7567	ND	ND	No
ITA5	DLDGNGYPDLIVGSFGVDK	Yes	990.98	808.4	21.27	128.8	55.1	8448	ND	ND	No
ITA5	DLDGNGYPDLIVGSFGVDK	Yes	990.98	921.5	21.27	128.8	46.1	2014	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
ITA5	LLESSLSSSEGEEPVEYK	Yes	991.98	310.2	13.41	129	43.1	24259	ND	ND	No
ITA5	LLESSLSSSEGEEPVEYK	Yes	991.98	635.3	13.41	129	49.1	26647	ND	ND	No
ITA5	LLESSLSSSEGEEPVEYK	Yes	991.98	764.4	13.41	129	46.1	7011	ND	ND	No
ITA5	LLESSLSSSEGEEPVEYK	Yes	991.98	950.4	13.41	129	46.1	9191	ND	ND	No
ITA5	SLQWFGATVR	Yes	582.81	503.3	18.49	76.2	28.1	168786	ND	ND	No
ITA5	SLQWFGATVR	Yes	582.81	650.4	18.49	76.2	31.1	134563	ND	ND	No
ITA5	SLQWFGATVR	Yes	582.81	836.4	18.49	76.2	25.1	132308	ND	ND	No
ITA5	SLQWFGATVR	Yes	582.81	964.5	18.49	76.2	28.1	30271	ND	ND	No
ITA5	SSASSGPQILK	Yes	537.79	655.4	9.86	70.4	26.2	82326	ND	ND	No
ITA5	SSASSGPQILK	Yes	537.79	742.4	9.86	70.4	26.2	100723	ND	ND	No
ITA5	SSASSGPQILK	Yes	537.79	829.5	9.86	70.4	26.2	121745	ND	ND	No
ITA5	SSASSGPQILK	Yes	537.79	900.5	9.86	70.4	26.2	54813	ND	ND	No
ITA5	VTAPPEAEYSGLVR	Yes	744.89	595.3	13.70	97.1	35.3	8818	ND	ND	No
ITA5	VTAPPEAEYSGLVR	Yes	744.89	694.4	13.70	97.1	44.3	40720	ND	ND	No
ITA5	VTAPPEAEYSGLVR	Yes	744.89	823.4	13.70	97.1	44.3	27125	ND	ND	No
ITA5	VTAPPEAEYSGLVR	Yes	744.89	894.5	13.70	97.1	44.3	44354	ND	ND	No
ITAM	LFTALFPFEK	Yes	606.84	520.3	23.93	79.3	38.2	1249540	ND	ND	No
ITAM	LFTALFPFEK	Yes	606.84	667.3	23.93	79.3	26.2	426000	ND	ND	No
ITAM	LFTALFPFEK	Yes	606.84	780.4	23.93	79.3	29.2	392187	ND	ND	No
ITAM	LFTALFPFEK	Yes	606.84	952.5	23.93	79.3	29.2	670268	ND	ND	No
ITAM	SLPISLVFLVPVR	Yes	720.45	371.2	24.67	93.9	31.2	26267	ND	ND	No
ITAM	SLPISLVFLVPVR	Yes	720.45	470.3	24.67	93.9	31.2	15641	ND	ND	No
ITAM	SLPISLVFLVPVR	Yes	720.45	829.5	24.67	93.9	34.2	12632	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
ITAM	SLPISLVFLVPVR	Yes	720.45	942.6	24.67	93.9	31.2	3587	ND	ND	No
ITAM	SLVKPITQLLGR	Yes	662.92	300.2	17.98	86.5	34.7	23343	ND	ND	No
ITAM	SLVKPITQLLGR	Yes	662.92	687.4	17.98	86.5	40.7	6935	ND	ND	No
ITAM	SLVKPITQLLGR	Yes	662.92	800.5	17.98	86.5	40.7	6175	ND	ND	No
ITAM	SLVKPITQLLGR	Yes	662.92	897.6	17.98	86.5	34.7	60157	ND	ND	No
ITAM	VQSLVLGAPR	Yes	520.32	400.2	12.69	68.1	25.4	70475	ND	ND	No
ITAM	VQSLVLGAPR	Yes	520.32	428.3	12.69	68.1	25.4	32132	ND	ND	No
ITAM	VQSLVLGAPR	Yes	520.32	612.4	12.69	68.1	34.4	30547	ND	ND	No
ITAM	VQSLVLGAPR	Yes	520.32	812.5	12.69	68.1	25.4	78077	ND	ND	No
ITAM	YVIGVGDAFR	Yes	548.79	263.1	16.38	71.8	23.6	245291	ND	ND	No
ITAM	YVIGVGDAFR	Yes	548.79	664.3	16.38	71.8	23.6	21630	ND	ND	No
ITAM	YVIGVGDAFR	Yes	548.79	721.4	16.38	71.8	26.6	113474	ND	ND	No
ITAM	YVIGVGDAFR	Yes	548.79	834.4	16.38	71.8	26.6	115677	ND	ND	No
K0090	ALVQTEDHLLLFLQQLAGK	Yes	713.07	516.3	24.63	93	39.9	9930	ND	ND	No
K0090	ALVQTEDHLLLFLQQLAGK	Yes	713.07	644.4	24.63	93	30.9	16897	ND	ND	No
K0090	ALVQTEDHLLLFLQQLAGK	Yes	713.07	894.4	24.63	93	33.9	3722	ND	ND	No
K0090	ALVQTEDHLLLFLQQLAGK	Yes	713.07	904.5	24.63	93	30.9	13159	ND	ND	No
K0090	FNVEDGEIVQQVR	Yes	766.89	262.1	14.70	99.9	42.2	13880	ND	ND	No
K0090	FNVEDGEIVQQVR	Yes	766.89	530.3	14.70	99.9	33.2	4706	ND	ND	No
K0090	FNVEDGEIVQQVR	Yes	766.89	629.4	14.70	99.9	33.2	2069	ND	ND	No
K0090	FNVEDGEIVQQVR	Yes	766.89	742.5	14.70	99.9	45.2	1892	ND	ND	No
K0090	HLLIGLPSGAILSLPK	Yes	543.68	251.2	22.36	71.1	34.3	136112	ND	ND	No
K0090	HLLIGLPSGAILSLPK	Yes	543.68	647.4	22.36	71.1	22.3	175329	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
K0090	HLLIGLPSGAILSLPK	Yes	543.68	798.5	22.36	71.1	22.3	36313	ND	ND	No
K0090	HLLIGLPSGAILSLPK	Yes	543.68	885.5	22.36	71.1	25.3	34664	ND	ND	No
K0090	LFGIESSSGTILWK	Yes	769.42	318.2	21.94	100.3	36.4	17680	ND	ND	No
K0090	LFGIESSSGTILWK	Yes	769.42	446.3	21.94	100.3	45.4	7423	ND	ND	No
K0090	LFGIESSSGTILWK	Yes	769.42	804.5	21.94	100.3	36.4	3868	ND	ND	No
K0090	LFGIESSSGTILWK	Yes	769.42	978.5	21.94	100.3	36.4	6206	ND	ND	No
K0090	VLLLIDDEYK	Yes	610.84	310.2	18.50	79.8	35.4	11110	ND	ND	No
K0090	VLLLIDDEYK	Yes	610.84	326.2	18.50	79.8	29.4	26490	ND	ND	No
K0090	VLLLIDDEYK	Yes	610.84	669.3	18.50	79.8	29.4	11266	ND	ND	No
K0090	VLLLIDDEYK	Yes	610.84	895.4	18.50	79.8	26.4	12582	ND	ND	No
K1C18	DWSHYFK	Yes	491.72	457.2	15.23	64.4	27.1	40257	ND	ND	No
K1C18	DWSHYFK	Yes	491.72	594.3	15.23	64.4	27.1	25845	ND	ND	No
K1C18	DWSHYFK	Yes	491.72	681.3	15.23	64.4	24.1	80298	ND	ND	No
K1C18	DWSHYFK	Yes	491.72	689.3	15.23	64.4	24.1	12235	ND	ND	No
K1C18	GLQAQIASSGLTVEVDAPK	No									
K1C18	LASYLDR	Yes	419.23	272.2	10.26	55.1	17.9	14751	ND	ND	No
K1C18	LASYLDR	Yes	419.23	566.3	10.26	55.1	20.9	19922	ND	ND	No
K1C18	LASYLDR	Yes	419.23	653.3	10.26	55.1	20.9	119038	ND	ND	No
K1C18	LASYLDR	Yes	419.23	724.4	10.26	55.1	20.9	41326	ND	ND	No
K1C18	LQLETEIEALK	Yes	643.86	331.2	18.73	84.1	39.8	43408	ND	ND	No
K1C18	LQLETEIEALK	Yes	643.86	355.2	18.73	84.1	30.8	40800	ND	ND	No
K1C18	LQLETEIEALK	Yes	643.86	803.5	18.73	84.1	30.8	41703	ND	ND	No
K1C18	LQLETEIEALK	Yes	643.86	932.5	18.73	84.1	30.8	37581	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
K1C18	VVSETNDTK	Yes	496.75	578.3	5.44	65.1	33.4	125330	ND	ND	No
K1C18	VVSETNDTK	Yes	496.75	707.3	5.44	65.1	24.4	31118	ND	ND	No
K1C18	VVSETNDTK	Yes	496.75	794.4	5.44	65.1	24.4	843799	ND	ND	No
K1C18	VVSETNDTK	Yes	496.75	893.4	5.44	65.1	24.4	42506	ND	ND	No
K1C19	APSIHGGSGGR	Yes	498.25	369.2	5.57	65.3	27.4	15471	ND	ND	No
K1C19	APSIHGGSGGR	Yes	498.25	627.3	5.57	65.3	30.4	90666	ND	ND	No
K1C19	APSIHGGSGGR	Yes	498.25	740.4	5.57	65.3	33.4	13319	ND	ND	No
K1C19	APSIHGGSGGR	Yes	498.25	827.4	5.57	65.3	27.4	27170	ND	ND	No
K1C19	FGAQLAHIQALISGIEAQLGDVR	Yes	803.11	274.2	24.71	104.6	47.5	89819	ND	88592	No
K1C19	FGAQLAHIQALISGIEAQLGDVR	Yes	803.11	559.3	24.71	104.6	35.5	19055	ND	29939	No
K1C19	FGAQLAHIQALISGIEAQLGDVR	Yes	803.11	758.4	24.71	104.6	38.5	30564	ND	28236	No
K1C19	FGAQLAHIQALISGIEAQLGDVR	Yes	803.11	887.5	24.71	104.6	38.5	33427	ND	14423	Yes (Based on Transition Ratios)
K1C19	FGPGVAFR	Yes	425.73	393.2	13.69	55.9	24.2	525916	ND	ND	No
K1C19	FGPGVAFR	Yes	425.73	549.3	13.69	55.9	27.2	805317	ND	ND	No
K1C19	FGPGVAFR	Yes	425.73	646.4	13.69	55.9	21.2	250479	ND	ND	No
K1C19	FGPGVAFR	Yes	425.73	703.4	13.69	55.9	21.2	224365	ND	ND	No
K1C19	GQVGGQVSVEVDSAPGTDLAK	Yes	1007.51	626.3	13.35	131	43.8	2994	ND	ND	No
K1C19	GQVGGQVSVEVDSAPGTDLAK	Yes	1007.51	701.4	13.35	131	52.8	13037	ND	ND	No
K1C19	GQVGGQVSVEVDSAPGTDLAK	Yes	1007.51	713.4	13.35	131	52.8	ND	ND	ND	No
K1C19	GQVGGQVSVEVDSAPGTDLAK	Yes	1007.51	772.4	13.35	131	52.8	2761	ND	ND	No
K1C19	SLLEGQEDHYNNLSASK	Yes	635.64	305.2	11.76	83	39	60901	ND	ND	No
K1C19	SLLEGQEDHYNNLSASK	Yes	635.64	314.2	11.76	83	30	63871	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
K1C19	SLLEGQEDHYNNLSASK	Yes	635.64	392.2	11.76	83	39	63359	ND	ND	No
K1C19	SLLEGQEDHYNNLSASK	Yes	635.64	505.3	11.76	83	39	11258	ND	ND	No
K2C8	ISSSSFSR	Yes	435.72	496.3	8.16	57.2	24.7	4503	ND	ND	No
K2C8	ISSSSFSR	Yes	435.72	583.3	8.16	57.2	18.7	3436	ND	ND	No
K2C8	ISSSSFSR	Yes	435.72	670.3	8.16	57.2	21.7	17199	ND	ND	No
K2C8	ISSSSFSR	Yes	435.72	757.3	8.16	57.2	21.7	20185	ND	ND	No
K2C8	LQAEIEGLK	Yes	500.79	559.3	12.46	65.6	33.5	143551	ND	ND	No
K2C8	LQAEIEGLK	Yes	500.79	688.4	12.46	65.6	24.5	134266	ND	ND	No
K2C8	LQAEIEGLK	Yes	500.79	759.4	12.46	65.6	24.5	719265	ND	ND	No
K2C8	LQAEIEGLK	Yes	500.79	887.5	12.46	65.6	24.5	57094	ND	ND	No
K2C8	SYTSGPGSR	Yes	456.21	352.2	5.81	59.9	28.6	6414	ND	ND	No
K2C8	SYTSGPGSR	Yes	456.21	416.2	5.81	59.9	25.6	12098	ND	ND	No
K2C8	SYTSGPGSR	Yes	456.21	560.3	5.81	59.9	22.6	17279	ND	ND	No
K2C8	SYTSGPGSR	Yes	456.21	661.3	5.81	59.9	22.6	35569	ND	ND	No
K2C8	WSLLQQQK	Yes	515.79	403.2	14.99	67.5	25.2	67964	ND	ND	No
K2C8	WSLLQQQK	Yes	515.79	644.4	14.99	67.5	25.2	138081	ND	ND	No
K2C8	WSLLQQQK	Yes	515.79	757.5	14.99	67.5	25.2	173442	ND	ND	No
K2C8	WSLLQQQK	Yes	515.79	844.5	14.99	67.5	25.2	128903	ND	ND	No
K2C8	YEELQSLAGK	Yes	569.29	293.1	12.27	74.4	27.5	1240348	ND	ND	No
K2C8	YEELQSLAGK	Yes	569.29	603.3	12.27	74.4	27.5	150415	ND	ND	No
K2C8	YEELQSLAGK	Yes	569.29	716.4	12.27	74.4	27.5	186212	ND	ND	No
K2C8	YEELQSLAGK	Yes	569.29	845.5	12.27	74.4	27.5	320810	ND	ND	No
KIT	INSVGSTASSSQPLLVHDDV	Yes	1013.51	485.2	14.66	131.7	50.1	5751	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
KIT	INSVGSTASSSQPLLVHDDV	Yes	1013.51	584.3	14.66	131.7	50.1	4006	ND	ND	No
KIT	INSVGSTASSSQPLLVHDDV	Yes	1013.51	697.4	14.66	131.7	47.1	2625	ND	ND	No
KIT	INSVGSTASSSQPLLVHDDV	Yes	1013.51	907.5	14.66	131.7	50.1	5732	ND	ND	No
KIT	LVVQSSIDSSAFK	Yes	690.87	312.2	14.14	90.1	32.9	52555	ND	ND	No
KIT	LVVQSSIDSSAFK	Yes	690.87	654.3	14.14	90.1	35.9	31514	ND	ND	No
KIT	LVVQSSIDSSAFK	Yes	690.87	854.4	14.14	90.1	32.9	27168	ND	ND	No
KIT	LVVQSSIDSSAFK	Yes	690.87	941.5	14.14	90.1	32.9	66812	ND	ND	No
KIT	QATLTISSAR	Yes	524.29	420.2	10.03	68.6	25.6	38107	13022	17652	No
KIT	QATLTISSAR	Yes	524.29	634.4	10.03	68.6	31.6	42789	18723	29114	No
KIT	QATLTISSAR	Yes	524.29	747.4	10.03	68.6	34.6	10636	3154	5379	No
KIT	QATLTISSAR	Yes	524.29	848.5	10.03	68.6	34.6	14442	4368	3889	No
KIT	TSAYFNFAFK	Yes	598.29	294.2	19.64	78.2	37.8	91192	ND	ND	No
KIT	TSAYFNFAFK	Yes	598.29	626.3	19.64	78.2	28.8	56801	ND	ND	No
KIT	TSAYFNFAFK	Yes	598.29	773.4	19.64	78.2	28.8	183342	ND	ND	No
KIT	TSAYFNFAFK	Yes	598.29	936.5	19.64	78.2	28.8	88407	ND	ND	No
KIT	YVSELHLTR	Yes	373.21	263.1	11.35	49.1	16.6	34985	22684	21209	No
KIT	YVSELHLTR	Yes	373.21	276.2	11.35	49.1	25.6	ND	23722	22228	Yes (Based on Manual Review)
KIT	YVSELHLTR	Yes	373.21	526.3	11.35	49.1	22.6	34436	28917	29088	No
KIT	YVSELHLTR	Yes	373.21	639.4	11.35	49.1	19.6	8194	8203	4369	No
KITH	EVEVIGGADK	Yes	508.77	447.2	9.14	66.6	24.9	559336	ND	ND	No
KITH	EVEVIGGADK	Yes	508.77	560.3	9.14	66.6	24.9	393080	ND	ND	No
KITH	EVEVIGGADK	Yes	508.77	659.4	9.14	66.6	24.9	118363	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
KITH	EVEVIGGADK	Yes	508.77	788.4	9.14	66.6	24.9	187970	ND	ND	No
KITH	KPFGAILNLVPLAESVVK	Yes	632.38	727.5	24.56	82.6	38.8	29076	ND	ND	No
KITH	KPFGAILNLVPLAESVVK	Yes	632.38	841.5	24.56	82.6	26.8	75609	ND	ND	No
KITH	KPFGAILNLVPLAESVVK	Yes	632.38	842.5	24.56	82.6	29.8	366451	ND	ND	No
KITH	KPFGAILNLVPLAESVVK	Yes	632.38	954.6	24.56	82.6	29.8	71281	ND	ND	No
KLK11	ILQLILLALATGLVGGETR	No									
KLK11	LPHTLR	Yes	368.73	389.3	7.50	48.6	21.7	5039	ND	ND	No
KLK11	LPHTLR	Yes	368.73	526.3	7.50	48.6	27.7	7015	ND	ND	No
KLK11	LPHTLR	Yes	368.73	623.4	7.50	48.6	27.7	3491	ND	ND	No
KLK11	TATESFPHPGFNNSLPNK	Yes	979.47	261.2	13.44	127.4	51.6	6384	ND	ND	No
KLK11	TATESFPHPGFNNSLPNK	Yes	979.47	358.2	13.44	127.4	51.6	45350	ND	ND	No
KLK11	TATESFPHPGFNNSLPNK	Yes	979.47	637.3	13.44	127.4	48.6	2694	ND	ND	No
KLK11	TATESFPHPGFNNSLPNK	Yes	979.47	871.4	13.44	127.4	54.6	3904	ND	ND	No
KLK11	YIVHLGQHNLQK	Yes	725.4	513.3	10.52	94.6	40.4	4541	ND	ND	No
KLK11	YIVHLGQHNLQK	Yes	725.4	626.4	10.52	94.6	37.4	3854	ND	ND	No
KLK11	YIVHLGQHNLQK	Yes	725.4	824.4	10.52	94.6	37.4	3914	ND	ND	No
KLK11	YIVHLGQHNLQK	Yes	725.4	948.5	10.52	94.6	34.4	ND	ND	ND	No
KLK13	VEAGEQVR	Yes	444.23	274.2	8.26	58.3	25	3770	ND	ND	No
KLK13	VEAGEQVR	Yes	444.23	588.3	8.26	58.3	19	ND	ND	ND	No
KLK13	VEAGEQVR	Yes	444.23	659.3	8.26	58.3	22	61655	ND	ND	No
KLK13	VEAGEQVR	Yes	444.23	788.4	8.26	58.3	19	13572	ND	ND	No
KLK13	VSGWGTTTSPQVNYPK	Yes	861.43	407.2	13.20	112.1	43.4	11581	ND	ND	No
KLK13	VSGWGTTTSPQVNYPK	Yes	861.43	430.2	13.20	112.1	40.4	11795	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
KLK13	VSGWGTTTSPQVNYPK	Yes	861.43	521.3	13.20	112.1	49.4	18144	ND	ND	No
KLK13	VSGWGTTTSPQVNYPK	Yes	861.43	932.5	13.20	112.1	40.4	10007	ND	ND	No
KLK13	YVLWIR	Yes	425.25	288.2	18.52	55.9	27.2	6388	ND	ND	No
KLK13	YVLWIR	Yes	425.25	474.3	18.52	55.9	21.2	9332	ND	ND	No
KLK13	YVLWIR	Yes	425.25	587.4	18.52	55.9	21.2	10059	ND	ND	No
KLK13	YVLWIR	Yes	425.25	686.4	18.52	55.9	24.2	3135	ND	ND	No
KLK14	QVTHPNYNSR	Yes	608.3	329.2	8.11	79.5	38.3	774	ND	ND	No
KLK14	QVTHPNYNSR	Yes	608.3	750.4	8.11	79.5	35.3	ND	ND	ND	No
KLK14	QVTHPNYNSR	Yes	608.3	887.4	8.11	79.5	35.3	ND	ND	ND	No
KLK14	QVTHPNYNSR	Yes	608.3	988.5	8.11	79.5	26.3	ND	ND	ND	No
KLK14	VLGSGTWPSAPK	Yes	600.32	499.3	13.43	78.4	37.9	379716	ND	ND	No
KLK14	VLGSGTWPSAPK	Yes	600.32	843.4	13.43	78.4	28.9	52969	ND	ND	No
KLK14	VLGSGTWPSAPK	Yes	600.32	930.5	13.43	78.4	28.9	21865	ND	ND	No
KLK14	VLGSGTWPSAPK	Yes	600.32	987.5	13.43	78.4	28.9	197324	ND	ND	No
KLK14	VSGWGTISSPIAR	Yes	665.86	630.4	15.91	86.9	40.8	53321	ND	ND	No
KLK14	VSGWGTISSPIAR	Yes	665.86	743.4	15.91	86.9	40.8	17320	ND	ND	No
KLK14	VSGWGTISSPIAR	Yes	665.86	844.5	15.91	86.9	40.8	10069	ND	ND	No
KLK14	VSGWGTISSPIAR	Yes	665.86	901.5	15.91	86.9	31.8	21485	ND	ND	No
KLK6	ESSQEQSSVVR	Yes	618.3	460.3	6.14	80.8	38.7	12017	ND	ND	No
KLK6	ESSQEQSSVVR	Yes	618.3	547.3	6.14	80.8	29.7	23469	ND	ND	No
KLK6	ESSQEQSSVVR	Yes	618.3	675.4	6.14	80.8	29.7	19304	ND	ND	No
KLK6	ESSQEQSSVVR	Yes	618.3	804.4	6.14	80.8	38.7	23341	ND	ND	No
KLK6	LSELIQPLPLER	Yes	469.95	443.3	18.96	61.6	21.5	28406	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
KLK6	LSELIQPLPLER	Yes	469.95	514.3	18.96	61.6	21.5	136672	10147	11839	No
KLK6	LSELIQPLPLER	Yes	469.95	684.4	18.96	61.6	21.5	28951	ND	ND	No
KLK6	LSELIQPLPLER	Yes	469.95	724.4	18.96	61.6	18.5	32845	2425	3820	No
KLK6	YTNWIQK	Yes	476.75	388.3	11.67	62.5	32.5	56570	ND	ND	No
KLK6	YTNWIQK	Yes	476.75	574.3	11.67	62.5	23.5	28362	ND	ND	No
KLK6	YTNWIQK	Yes	476.75	688.4	11.67	62.5	23.5	95829	ND	ND	No
KLK6	YTNWIQK	Yes	476.75	789.4	11.67	62.5	23.5	71778	ND	ND	No
KNG1	DFVQPPTK	Yes	466.25	263.1	9.53	61.1	23	1236466	98770	104063	Yes (Based on Transition Ratios)
KNG1	DFVQPPTK	Yes	466.25	442.3	9.53	61.1	26	1129015	11706	14598	No
KNG1	DFVQPPTK	Yes	466.25	570.3	9.53	61.1	23	388951	3410	ND	No
KNG1	DFVQPPTK	Yes	466.25	669.4	9.53	61.1	23	ND	4565	5393	Yes (Based on Manual Review)
KNG1	DIPTNSPELEETLTHTITK	Yes	713.7	361.2	17.85	93.1	39.9	12783	ND	ND	No
KNG1	DIPTNSPELEETLTHTITK	Yes	713.7	462.3	17.85	93.1	39.9	19736	ND	ND	No
KNG1	DIPTNSPELEETLTHTITK	Yes	713.7	599.4	17.85	93.1	42.9	24620	ND	ND	No
KNG1	DIPTNSPELEETLTHTITK	Yes	713.7	914.5	17.85	93.1	36.9	6774	ND	ND	No
KNG1	GHGLGHGHEQQHGLGHGHK	No									
KNG1	LDDDLEHQGGHVLDHGHK	Yes	674.65	459.2	9.44	88	38	7477	ND	ND	No
KNG1	LDDDLEHQGGHVLDHGHK	Yes	674.65	478.3	9.44	88	38	16114	ND	ND	No
KNG1	LDDDLEHQGGHVLDHGHK	Yes	674.65	706.4	9.44	88	35	6625	ND	ND	No
KNG1	LDDDLEHQGGHVLDHGHK	Yes	674.65	805.4	9.44	88	38	3411	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
KNG1	TVGSDTFYSFK	Yes	626.3	381.2	15.27	81.8	39.1	ND	ND	ND	Yes (Based on Manual Review)
KNG1	TVGSDTFYSFK	Yes	626.3	544.3	15.27	81.8	39.1	69557	ND	3102	No
KNG1	TVGSDTFYSFK	Yes	626.3	907.4	15.27	81.8	39.1	12474	ND	1609	No
KNG1	TVGSDTFYSFK	Yes	626.3	994.5	15.27	81.8	27.1	13356	ND	ND	No
KPYM	APIIAVTR	Yes	420.77	375.2	11.03	55.3	21	ND	ND	ND	Yes (Based on Manual Review)
KPYM	APIIAVTR	Yes	420.77	446.3	11.03	55.3	24	13824	11987	13415	No
KPYM	APIIAVTR	Yes	420.77	559.4	11.03	55.3	24	16235	18137	18611	No
KPYM	APIIAVTR	Yes	420.77	672.4	11.03	55.3	30	6723	5703	5676	No
KPYM	DPVQEAWAEDVDLR	Yes	821.89	288.2	17.96	107	44.7	43742	ND	ND	No
KPYM	DPVQEAWAEDVDLR	Yes	821.89	440.2	17.96	107	38.7	22107	ND	ND	No
KPYM	DPVQEAWAEDVDLR	Yes	821.89	569.3	17.96	107	38.7	23435	ND	ND	No
KPYM	DPVQEAWAEDVDLR	Yes	821.89	640.3	17.96	107	38.7	19925	ND	ND	No
KPYM	GDYPLEAVR	No									
KPYM	IYVDDGLISLQVK	Yes	731.91	277.2	19.53	95.4	34.7	79444	ND	ND	No
KPYM	IYVDDGLISLQVK	Yes	731.91	574.4	19.53	95.4	34.7	24805	ND	ND	No
KPYM	IYVDDGLISLQVK	Yes	731.91	687.4	19.53	95.4	34.7	14174	ND	ND	No
KPYM	IYVDDGLISLQVK	Yes	731.91	857.5	19.53	95.4	31.7	6678	ND	ND	No
KPYM	LDIDSPPITAR	Yes	599.33	557.3	13.47	78.3	37.9	59710	ND	ND	No
KPYM	LDIDSPPITAR	Yes	599.33	654.4	13.47	78.3	28.9	86057	ND	ND	No
KPYM	LDIDSPPITAR	Yes	599.33	856.5	13.47	78.3	28.9	71258	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
KPYM	LDIDSPPITAR	Yes	599.33	969.5	13.47	78.3	28.9	8662	ND	ND	No
KRT35	DALESTLAETEAR	Yes	703.34	605.3	14.91	91.7	30.4	30039	ND	ND	No
KRT35	DALESTLAETEAR	Yes	703.34	676.3	14.91	91.7	33.4	52495	ND	ND	No
KRT35	DALESTLAETEAR	Yes	703.34	890.5	14.91	91.7	33.4	15115	ND	ND	No
KRT35	DALESTLAETEAR	Yes	703.34	977.5	14.91	91.7	42.4	31088	ND	ND	No
KRT35	LNVEVDAAPPVDLNR	Yes	811.43	402.2	15.29	105.7	47.2	28240	ND	ND	No
KRT35	LNVEVDAAPPVDLNR	Yes	811.43	456.2	15.29	105.7	38.2	16699	ND	ND	No
KRT35	LNVEVDAAPPVDLNR	Yes	811.43	881.5	15.29	105.7	38.2	16309	ND	ND	No
KRT35	LNVEVDAAPPVDLNR	Yes	811.43	952.5	15.29	105.7	47.2	18142	ND	ND	No
KRT35	LPSLSPVAR	Yes	470.29	442.3	12.83	61.7	32.2	31679	ND	ND	No
KRT35	LPSLSPVAR	Yes	470.29	529.3	12.83	61.7	32.2	32161	ND	ND	No
KRT35	LPSLSPVAR	Yes	470.29	729.4	12.83	61.7	26.2	34667	ND	ND	No
KRT35	LPSLSPVAR	Yes	470.29	826.5	12.83	61.7	26.2	7606	ND	ND	No
KRT35	LVVEIDNAK	Yes	500.79	447.2	11.69	65.6	33.5	62498	ND	ND	No
KRT35	LVVEIDNAK	Yes	500.79	560.3	11.69	65.6	30.5	127119	ND	ND	No
KRT35	LVVEIDNAK	Yes	500.79	689.3	11.69	65.6	24.5	138189	ND	ND	No
KRT35	LVVEIDNAK	Yes	500.79	788.4	11.69	65.6	24.5	468157	ND	ND	No
KRT35	YETEVSLR	Yes	498.75	293.1	10.54	65.3	21.4	77784	ND	ND	No
KRT35	YETEVSLR	Yes	498.75	375.2	10.54	65.3	27.4	21917	ND	ND	No
KRT35	YETEVSLR	Yes	498.75	603.3	10.54	65.3	24.4	10712	ND	ND	No
KRT35	YETEVSLR	Yes	498.75	704.4	10.54	65.3	24.4	51786	ND	ND	No
LAMB2	DTEQTLYQVQER	Yes	755.36	432.2	11.36	98.4	32.7	5251	ND	ND	No
LAMB2	DTEQTLYQVQER	Yes	755.36	531.3	11.36	98.4	44.7	5717	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
LAMB2	DTEQTLYQVQER	Yes	755.36	822.4	11.36	98.4	35.7	9826	ND	ND	No
LAMB2	DTEQTLYQVQER	Yes	755.36	935.5	11.36	98.4	44.7	2753	ND	ND	No
LAMB2	IQGTLQPHAR	Yes	374.21	400.2	6.88	49.3	19.6	14207	ND	ND	No
LAMB2	IQGTLQPHAR	Yes	374.21	480.3	6.88	49.3	19.6	92467	ND	ND	No
LAMB2	IQGTLQPHAR	Yes	374.21	608.3	6.88	49.3	19.6	17760	ND	ND	No
LAMB2	IQGTLQPHAR	Yes	374.21	721.4	6.88	49.3	19.6	5954	ND	ND	No
LAMB2	SLADVDAILAR	Yes	572.32	359.2	18.21	74.8	27.7	37687	ND	ND	No
LAMB2	SLADVDAILAR	Yes	572.32	658.4	18.21	74.8	27.7	88202	ND	ND	No
LAMB2	SLADVDAILAR	Yes	572.32	872.5	18.21	74.8	27.7	42046	ND	ND	No
LAMB2	SLADVDAILAR	Yes	572.32	943.5	18.21	74.8	27.7	64504	ND	ND	No
LAMB2	TGGSAQPETPYSGPGLLIDSLVLLPR	No									
LAMB2	VLELSIPASAEQIQHLAGAIAER	Yes	806.11	342.2	24.26	105	38.7	39506	36383	36885	No
LAMB2	VLELSIPASAEQIQHLAGAIAER	Yes	806.11	687.4	24.26	105	47.7	ND	ND	9208	Yes (Based on Manual Review)
LAMB2	VLELSIPASAEQIQHLAGAIAER	Yes	806.11	937.5	24.26	105	44.7	12616	16384	25218	No
LAMB2	VLELSIPASAEQIQHLAGAIAER	Yes	806.11	981.6	24.26	105	35.7	27106	11850	12378	Yes (Based on Transition Ratios)
LDHA	DQLIYNLLK	Yes	560.32	357.2	20.42	73.3	27.2	25011	ND	ND	No
LDHA	DQLIYNLLK	Yes	560.32	650.4	20.42	73.3	24.2	16189	ND	ND	No
LDHA	DQLIYNLLK	Yes	560.32	763.5	20.42	73.3	27.2	17424	ND	ND	No
LDHA	DQLIYNLLK	Yes	560.32	876.6	20.42	73.3	27.2	12726	ND	ND	No
LDHA	FIIPNVVK	Yes	465.29	261.2	17.21	61	23	1933498	ND	11302	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
LDHA	FIIPNVVK	Yes	465.29	556.3	17.21	61	23	868755	ND	12862	No
LDHA	FIIPNVVK	Yes	465.29	669.4	17.21	61	23	896224	ND	6658	No
LDHA	FIIPNVVK	Yes	465.29	782.5	17.21	61	23	84111	ND	6705	Yes (Based on Transition Ratios)
LDHA	LLIVSNPVDILTYVAWK	No									
LDHA	LVIITAGAR	Yes	457.3	588.3	12.59	60	22.6	19819	22203	13114	No
LDHA	LVIITAGAR	Yes	457.3	611.4	12.59	60	22.6	ND	ND	ND	No
LDHA	LVIITAGAR	Yes	457.3	701.4	12.59	60	22.6	27515	17314	17684	No
LDHA	LVIITAGAR	Yes	457.3	800.5	12.59	60	31.6	3427	ND	ND	No
LDHA	TLHPDLGTDK	Yes	548.79	352.2	8.60	71.8	26.6	308794	ND	ND	No
LDHA	TLHPDLGTDK	Yes	548.79	745.4	8.60	71.8	29.6	380094	ND	ND	No
LDHA	TLHPDLGTDK	Yes	548.79	882.4	8.60	71.8	26.6	24002	ND	ND	No
LDHA	TLHPDLGTDK	Yes	548.79	950.5	8.60	71.8	23.6	5241	ND	ND	No
LDHB	DYSVTANSK	Yes	492.74	348.2	6.86	64.6	24.2	166048	ND	ND	No
LDHB	DYSVTANSK	Yes	492.74	520.3	6.86	64.6	24.2	277228	ND	ND	No
LDHB	DYSVTANSK	Yes	492.74	619.3	6.86	64.6	24.2	124715	ND	ND	No
LDHB	DYSVTANSK	Yes	492.74	706.4	6.86	64.6	24.2	534865	ND	ND	No
LDHB	FIIPQIVK	Yes	479.31	261.2	18.83	62.8	20.6	2856545	31893	24401	No
LDHB	FIIPQIVK	Yes	479.31	584.4	18.83	62.8	23.6	2076534	15977	9895	No
LDHB	FIIPQIVK	Yes	479.31	697.5	18.83	62.8	23.6	1499614	9592	5535	No
LDHB	FIIPQIVK	Yes	479.31	810.5	18.83	62.8	23.6	112512	ND	ND	No
LDHB	GLTSVINQK	Yes	480.28	502.3	11.16	63	23.6	34272	38720	50584	No
LDHB	GLTSVINQK	Yes	480.28	601.4	11.16	63	20.6	7963	7740	11686	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
LDHB	GLTSVINQK	Yes	480.28	688.4	11.16	63	23.6	19348	24315	33281	No
LDHB	GLTSVINQK	Yes	480.28	789.4	11.16	63	23.6	19341	22798	31126	No
LDHB	LIAPVAEEEATVPNNK	Yes	847.95	472.3	12.76	110.4	39.8	235885	ND	ND	No
LDHB	LIAPVAEEEATVPNNK	Yes	847.95	571.3	12.76	110.4	39.8	18849	ND	ND	No
LDHB	LIAPVAEEEATVPNNK	Yes	847.95	672.4	12.76	110.4	39.8	13133	ND	ND	No
LDHB	LIAPVAEEEATVPNNK	Yes	847.95	743.4	12.76	110.4	39.8	12400	ND	ND	No
LDHB	NVNVFK	Yes	360.71	294.2	10.27	47.5	24.4	384495	ND	ND	No
LDHB	NVNVFK	Yes	360.71	393.3	10.27	47.5	21.4	42997	ND	ND	No
LDHB	NVNVFK	Yes	360.71	507.3	10.27	47.5	18.4	393612	ND	ND	No
LDHB	NVNVFK	Yes	360.71	606.4	10.27	47.5	18.4	33557	ND	ND	No
LEG1	DGGAWGTEQR	Yes	538.74	301.1	8.23	70.5	23.2	71395	1299	3506	No
LEG1	DGGAWGTEQR	Yes	538.74	487.2	8.23	70.5	23.2	25754	1277	2562	No
LEG1	DGGAWGTEQR	Yes	538.74	590.3	8.23	70.5	26.2	95799	5423	1835	No
LEG1	DGGAWGTEQR	Yes	538.74	776.4	8.23	70.5	29.2	80735	2871	2232	No
LEG1	GEVAPDAK	Yes	393.7	286.1	5.68	51.8	19.8	30360	ND	ND	No
LEG1	GEVAPDAK	Yes	393.7	430.2	5.68	51.8	28.8	48786	ND	ND	No
LEG1	GEVAPDAK	Yes	393.7	501.3	5.68	51.8	16.8	41607	ND	ND	No
LEG1	GEVAPDAK	Yes	393.7	600.3	5.68	51.8	16.8	63357	ND	ND	No
LEG1	LPDGYEFK	Yes	484.74	294.2	12.61	63.5	29.8	171318	13004	ND	No
LEG1	LPDGYEFK	Yes	484.74	643.3	12.61	63.5	32.8	66836	ND	ND	No
LEG1	LPDGYEFK	Yes	484.74	758.3	12.61	63.5	32.8	119898	1572	ND	No
LEG1	LPDGYEFK	Yes	484.74	855.4	12.61	63.5	23.8	76508	2506	ND	No
LEG1	SFVLNLGK	Yes	439.26	317.2	16.42	57.7	30.8	169729	ND	ND	No

Table S5. MRM assay of individual proteins.											
Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
LEG1	SFVLNLGK	Yes	439.26	334.2	16.42	57.7	21.8	184051	7381	6391	No
LEG1	SFVLNLGK	Yes	439.26	544.3	16.42	57.7	21.8	391583	7952	11326	No
LEG1	SFVLNLGK	Yes	439.26	643.4	16.42	57.7	21.8	564059	13318	14045	No
LEG3	GNDVAFHFNPR	Yes	637.31	272.2	12.96	83.2	33.5	54834	ND	ND	No
LEG3	GNDVAFHFNPR	Yes	637.31	533.3	12.96	83.2	39.5	3401	ND	ND	No
LEG3	GNDVAFHFNPR	Yes	637.31	670.3	12.96	83.2	30.5	5562	ND	ND	No
LEG3	GNDVAFHFNPR	Yes	637.31	817.4	12.96	83.2	30.5	ND	ND	ND	No
LEG3	IALDFQR	Yes	431.74	303.2	13.91	56.7	21.5	ND	ND	ND	No
LEG3	IALDFQR	Yes	431.74	565.3	13.91	56.7	21.5	72512	1784	ND	No
LEG3	IALDFQR	Yes	431.74	678.4	13.91	56.7	21.5	122905	3207	ND	No
LEG3	IALDFQR	Yes	431.74	749.4	13.91	56.7	21.5	76568	861	ND	No
LEG3	IQVLVEPDHFK	Yes	442.25	341.2	14.17	58.1	23.1	130009	ND	ND	No
LEG3	IQVLVEPDHFK	Yes	442.25	643.3	14.17	58.1	23.1	158083	ND	ND	No
LEG3	IQVLVEPDHFK	Yes	442.25	772.4	14.17	58.1	20.1	32729	ND	ND	No
LEG3	IQVLVEPDHFK	Yes	442.25	871.4	14.17	58.1	20.1	29542	ND	ND	No
LEG3	LDNNWGR	Yes	437.71	532.3	9.07	57.5	24.8	14005	ND	ND	No
LEG3	LDNNWGR	Yes	437.71	643.3	9.07	57.5	21.8	1451	ND	ND	No
LEG3	LDNNWGR	Yes	437.71	646.3	9.07	57.5	21.8	46398	ND	ND	No
LEG3	LDNNWGR	Yes	437.71	761.3	9.07	57.5	21.8	30198	ND	ND	No
LEG3	VAVNDAHLLQYNHR	No									
LEG9	FAVNFQTGFSGNDIAFHFNPR	No									
LEG9	FDENAVVR	Yes	475.24	373.3	9.70	62.3	23.4	48964	ND	ND	No
LEG9	FDENAVVR	Yes	475.24	558.3	9.70	62.3	23.4	50659	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
LEG9	FDENAVVR	Yes	475.24	687.4	9.70	62.3	23.4	81623	ND	ND	No
LEG9	FDENAVVR	Yes	475.24	802.4	9.70	62.3	32.4	63970	ND	ND	No
LEG9	NTQIDNSWGSEER	Yes	768.34	344.2	10.71	100.1	36.3	16804	ND	ND	No
LEG9	NTQIDNSWGSEER	Yes	768.34	457.2	10.71	100.1	36.3	7648	ND	ND	No
LEG9	NTQIDNSWGSEER	Yes	768.34	577.3	10.71	100.1	36.3	14174	ND	ND	No
LEG9	NTQIDNSWGSEER	Yes	768.34	964.4	10.71	100.1	42.3	5828	ND	ND	No
LEG9	SILLSGTVLPSAQR	Yes	721.42	314.2	17.11	94.1	34.2	169161	ND	ND	No
LEG9	SILLSGTVLPSAQR	Yes	721.42	558.3	17.11	94.1	34.2	153890	97881	ND	Yes (Based on Transition Ratios)
LEG9	SILLSGTVLPSAQR	Yes	721.42	671.4	17.11	94.1	34.2	67569	5865	ND	Yes (Based on Transition Ratios)
LEG9	SILLSGTVLPSAQR	Yes	721.42	928.5	17.11	94.1	43.2	40370	ND	ND	No
LEG9	VAVDGQHLFEYYHR	Yes	578.62	475.2	14.57	75.6	33.1	7545	ND	ND	No
LEG9	VAVDGQHLFEYYHR	Yes	578.62	638.3	14.57	75.6	36.1	5378	ND	ND	No
LEG9	VAVDGQHLFEYYHR	Yes	578.62	767.3	14.57	75.6	30.1	3430	ND	ND	No
LEG9	VAVDGQHLFEYYHR	Yes	578.62	914.4	14.57	75.6	33.1	7963	ND	ND	No
LG3BP	ASHEEVEGLVEK	Yes	442.89	545.3	9.84	58.1	20.1	177073	155092	74004	No
LG3BP	ASHEEVEGLVEK	Yes	442.89	554.2	9.84	58.1	23.1	179713	155835	82769	No
LG3BP	ASHEEVEGLVEK	Yes	442.89	653.3	9.84	58.1	20.1	65271	48020	33798	No
LG3BP	ASHEEVEGLVEK	Yes	442.89	674.4	9.84	58.1	20.1	69101	65386	35399	No
LG3BP	AVDTWSWGER	No									
LG3BP	STHTLDLSR	Yes	343.85	262.2	8.72	45.4	18.1	274082	106162	66357	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
LG3BP	STHTLDLSR	Yes	343.85	375.2	8.72	45.4	21.1	129737	70593	42255	No
LG3BP	STHTLDLSR	Yes	343.85	490.3	8.72	45.4	18.1	104379	40109	21212	No
LG3BP	STHTLDLSR	Yes	343.85	655.3	8.72	45.4	12.1	18611	8512	4854	No
LG3BP	VEIFYR	Yes	413.73	338.2	13.15	54.4	23.7	17352	87391	57119	No
LG3BP	VEIFYR	Yes	413.73	485.3	13.15	54.4	20.7	43469	270184	145630	No
LG3BP	VEIFYR	Yes	413.73	598.3	13.15	54.4	20.7	84212	553115	281282	No
LG3BP	VEIFYR	Yes	413.73	727.4	13.15	54.4	29.7	19449	96362	43018	No
LG3BP	YSSDYFQAPSDYR	Yes	799.84	637.3	13.84	104.2	37.7	69372	89355	50893	No
LG3BP	YSSDYFQAPSDYR	Yes	799.84	708.3	13.84	104.2	40.7	48250	68355	35509	No
LG3BP	YSSDYFQAPSDYR	Yes	799.84	836.4	13.84	104.2	37.7	36624	32633	28911	No
LG3BP	YSSDYFQAPSDYR	Yes	799.84	983.5	13.84	104.2	37.7	26559	28215	22605	No
LPLC3	AQLAPSATK	Yes	443.75	313.2	6.51	58.2	19	181006	ND	ND	No
LPLC3	AQLAPSATK	Yes	443.75	503.3	6.51	58.2	31	396390	ND	ND	No
LPLC3	AQLAPSATK	Yes	443.75	574.3	6.51	58.2	22	283578	ND	ND	No
LPLC3	AQLAPSATK	Yes	443.75	687.4	6.51	58.2	22	493503	ND	ND	No
LPLC3	LEEWLSHVVGAVYAPK	Yes	599.99	315.2	21.32	78.4	37.1	14987	ND	ND	No
LPLC3	LEEWLSHVVGAVYAPK	Yes	599.99	705.4	21.32	78.4	25.1	19688	ND	ND	No
LPLC3	LEEWLSHVVGAVYAPK	Yes	599.99	804.5	21.32	78.4	28.1	14958	ND	ND	No
LPLC3	LEEWLSHVVGAVYAPK	Yes	599.99	903.5	21.32	78.4	28.1	4215	ND	ND	No
LPLC3	LNVALDVGIPLPK	Yes	674.91	454.3	20.58	88.1	38.2	66477	ND	ND	No
LPLC3	LNVALDVGIPLPK	Yes	674.91	624.4	20.58	88.1	29.2	33271	ND	ND	No
LPLC3	LNVALDVGIPLPK	Yes	674.91	838.5	20.58	88.1	32.2	43288	ND	ND	No
LPLC3	LNVALDVGIPLPK	Yes	674.91	951.6	20.58	88.1	29.2	27106	ND	ND	No

Table S5. MRM assay of individual proteins.											
Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
LPLC3	SVAGDIIDFPK	Yes	581.31	506.3	17.97	76	37.1	77332	ND	ND	No
LPLC3	SVAGDIIDFPK	Yes	581.31	619.3	17.97	76	28.1	70252	ND	ND	No
LPLC3	SVAGDIIDFPK	Yes	581.31	904.5	17.97	76	28.1	50297	ND	ND	No
LPLC3	SVAGDIIDFPK	Yes	581.31	975.5	17.97	76	28.1	126670	ND	ND	No
LPLC3	VLNINFSNSVLEIVENAVVLTVAS	No									
LPLC4	GLLPNLVDNLVNR	Yes	718.91	501.3	22.90	93.7	43.1	2956	62357	62953	Yes (Based on Transition Ratios)
LPLC4	GLLPNLVDNLVNR	Yes	718.91	615.4	22.90	93.7	43.1	9116	12773	15366	No
LPLC4	GLLPNLVDNLVNR	Yes	718.91	829.5	22.90	93.7	37.1	11589	22285	20208	No
LPLC4	GLLPNLVDNLVNR	Yes	718.91	942.5	22.90	93.7	40.1	4020	5291	6093	No
LPLC4	ILNIDFSNADIDVLEDLLVLSA	No									
LPLC4	IVELTLPR	Yes	470.8	342.2	16.08	61.7	23.2	32311	ND	ND	No
LPLC4	IVELTLPR	Yes	470.8	599.4	16.08	61.7	32.2	25665	ND	ND	No
LPLC4	IVELTLPR	Yes	470.8	728.4	16.08	61.7	26.2	77373	ND	ND	No
LPLC4	IVELTLPR	Yes	470.8	827.5	16.08	61.7	23.2	3861	ND	ND	No
LPLC4	LLPGVGVYLSLYTR	Yes	775.95	439.2	24.03	101.1	39.6	3860	ND	ND	No
LPLC4	LLPGVGVYLSLYTR	Yes	775.95	639.3	24.03	101.1	45.6	5641	ND	ND	No
LPLC4	LLPGVGVYLSLYTR	Yes	775.95	752.4	24.03	101.1	33.6	ND	ND	ND	No
LPLC4	LLPGVGVYLSLYTR	Yes	775.95	915.5	24.03	101.1	45.6	8726	ND	ND	No
LPLC4	YGEILESEGSIR	Yes	676.84	350.1	13.60	88.3	35.3	134141	ND	ND	No
LPLC4	YGEILESEGSIR	Yes	676.84	463.2	13.60	88.3	32.3	45772	ND	ND	No
LPLC4	YGEILESEGSIR	Yes	676.84	561.3	13.60	88.3	32.3	16433	ND	ND	No
LPLC4	YGEILESEGSIR	Yes	676.84	890.5	13.60	88.3	38.3	82912	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
LPPRC	DAGIEPGPDTYLALLNAYAEK	Yes	1111.06	357.2	24.07	144.3	48.4	27977	ND	ND	No
LPPRC	DAGIEPGPDTYLALLNAYAEK	Yes	1111.06	486.2	24.07	144.3	48.4	31675	ND	ND	No
LPPRC	DAGIEPGPDTYLALLNAYAEK	Yes	1111.06	921.5	24.07	144.3	60.4	12513	ND	ND	No
LPPRC	DAGIEPGPDTYLALLNAYAEK	Yes	1111.06	992.5	24.07	144.3	57.4	14151	ND	ND	No
LPPRC	NVQGIIEILK	Yes	376.23	260.2	20.11	49.5	25.7	4671	ND	ND	No
LPPRC	NVQGIIEILK	Yes	376.23	342.2	20.11	49.5	13.7	ND	ND	ND	No
LPPRC	NVQGIIEILK	Yes	376.23	399.2	20.11	49.5	13.7	1101	ND	ND	No
LPPRC	NVQGIIEILK	Yes	376.23	502.3	20.11	49.5	16.7	1878	ND	ND	No
LPPRC	SGGLGGSHALLLLR	Yes	450.93	401.3	17.16	59.2	29.5	50835	ND	ND	No
LPPRC	SGGLGGSHALLLLR	Yes	450.93	514.4	17.16	59.2	29.5	60806	ND	ND	No
LPPRC	SGGLGGSHALLLLR	Yes	450.93	627.5	17.16	59.2	26.5	74755	ND	ND	No
LPPRC	SGGLGGSHALLLLR	Yes	450.93	698.5	17.16	59.2	26.5	89945	ND	ND	No
LPPRC	TVLDQQQTPSR	Yes	636.83	359.2	7.75	83.2	33.5	50717	ND	ND	No
LPPRC	TVLDQQQTPSR	Yes	636.83	460.3	7.75	83.2	30.5	18077	ND	ND	No
LPPRC	TVLDQQQTPSR	Yes	636.83	844.4	7.75	83.2	39.5	12496	ND	ND	No
LPPRC	TVLDQQQTPSR	Yes	636.83	959.5	7.75	83.2	30.5	14823	ND	ND	No
LPPRC	TVQLTSSELESTLETLK	Yes	940	329.2	21.16	122.3	43.9	9934	ND	ND	No
LPPRC	TVQLTSSELESTLETLK	Yes	940	442.3	21.16	122.3	40.9	3253	ND	ND	No
LPPRC	TVQLTSSELESTLETLK	Yes	940	490.3	21.16	122.3	46.9	2436	ND	ND	No
LPPRC	TVQLTSSELESTLETLK	Yes	940	791.5	21.16	122.3	40.9	3885	ND	ND	No
LRP1	AALSGANVLTLIEK	Yes	700.4	1057.6	22.80	100	36.3	ND	ND	ND	No
LRP1	AALSGANVLTLIEK	Yes	700.4	1144.7	22.80	100	36.3	ND	ND	ND	No
LRP1	AALSGANVLTLIEK	Yes	700.4	716.5	22.80	100	36.3	ND	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
LRP1	AALSGANVLTLIEK	Yes	700.4	929.6	22.80	100	36.3	ND	ND	ND	No
LRP1	TVLWPNGLSLDIPAGR	Yes	854.972	1209.7	21.11	100	43.1	ND	8174	4835	No
LRP1	TVLWPNGLSLDIPAGR	Yes	854.972	400.231	21.11	100	37.1	ND	166746	59574	No
LRP1	TVLWPNGLSLDIPAGR	Yes	854.972	500.3	21.11	100	43.1	ND	15454	11382	No
LRP1	TVLWPNGLSLDIPAGR	Yes	854.972	605.333	21.11	100	43.1	ND	30940	18227	No
LRP1	VFFTDYGQIPK	Yes	657.84	1068.54	16.06	100	28.4	ND	9497	10537	No
LRP1	VFFTDYGQIPK	Yes	657.84	244.2	16.06	100	34.4	ND	ND	ND	No
LRP1	VFFTDYGQIPK	Yes	657.84	820.4	16.06	100	34.4	ND	9479	5914	No
LRP1	VFFTDYGQIPK	Yes	657.84	921.468	16.06	100	28.4	ND	11791	11505	No
LUM	LPSGLPVSLLTLYLDNNK	No									
LUM	NIPTVNENLENYYLEVNQLEK	Yes	846.09	517.3	21.16	110.1	49.7	3641	52183	66686	Yes (Based on Transition Ratios)
LUM	NIPTVNENLENYYLEVNQLEK	Yes	846.09	631.3	21.16	110.1	40.7	4560	218572	201687	No
LUM	NIPTVNENLENYYLEVNQLEK	Yes	846.09	730.4	21.16	110.1	43.7	3742	200882	182907	No
LUM	NIPTVNENLENYYLEVNQLEK	Yes	846.09	972.5	21.16	110.1	40.7	3898	231659	220149	No
LUM	NNQIDHIDEK	Yes	409.2	276.2	7.44	53.8	24.4	105424	264912	244943	No
LUM	NNQIDHIDEK	Yes	409.2	504.3	7.44	53.8	27.4	17958	41787	36561	No
LUM	NNQIDHIDEK	Yes	409.2	756.4	7.44	53.8	21.4	7836	26246	15348	No
LUM	NNQIDHIDEK	Yes	409.2	869.4	7.44	53.8	27.4	ND	ND	ND	No
LUM	SLEDLQLTHNK	Yes	433.23	398.2	12.04	56.9	25.6	52207	359476	342909	No
LUM	SLEDLQLTHNK	Yes	433.23	499.3	12.04	56.9	22.6	44358	411092	358230	No
LUM	SLEDLQLTHNK	Yes	433.23	612.3	12.04	56.9	22.6	30311	311966	279144	No
LUM	SLEDLQLTHNK	Yes	433.23	740.4	12.04	56.9	28.6	7885	53248	65875	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
LUM	SLEYLDLSFNQIAR	Yes	834.93	330.2	21.78	108.7	42.2	7204	2226673	1964607	Yes (Based on Transition Ratios)
LUM	SLEYLDLSFNQIAR	Yes	834.93	601.3	21.78	108.7	48.2	3311	460676	436255	Yes (Based on Transition Ratios)
LUM	SLEYLDLSFNQIAR	Yes	834.93	748.4	21.78	108.7	42.2	4021	959380	841757	Yes (Based on Transition Ratios)
LUM	SLEYLDLSFNQIAR	Yes	834.93	948.5	21.78	108.7	42.2	3014	762620	733922	Yes (Based on Transition Ratios)
LY6K	DPEDSQR	Yes	423.68	342.1	5.30	55.7	21.1	7653	ND	ND	No
LY6K	DPEDSQR	Yes	423.68	390.2	5.30	55.7	30.1	18729	ND	544	No
LY6K	DPEDSQR	Yes	423.68	505.2	5.30	55.7	27.1	17624	ND	834	No
LY6K	DPEDSQR	Yes	423.68	634.3	5.30	55.7	30.1	19303	ND	ND	No
LY6K	TDEGDNR	Yes	403.67	289.2	5.59	53.1	20.3	ND	ND	ND	
LY6K	TDEGDNR	Yes	403.67	461.2	5.59	53.1	20.3	ND	ND	ND	
LY6K	TDEGDNR	Yes	403.67	590.3	5.59	53.1	20.3	ND	ND	ND	
LY6K	TDEGDNR	Yes	403.67	705.3	5.59	53.1	23.3	ND	ND	ND	
LY6K	VWTDANLTAR	Yes	573.8	286.2	12.56	75	27.7	65045	ND	ND	No
LY6K	VWTDANLTAR	Yes	573.8	460.3	12.56	75	27.7	7776	ND	ND	No
LY6K	VWTDANLTAR	Yes	573.8	760.4	12.56	75	33.7	12057	ND	ND	No
LY6K	VWTDANLTAR	Yes	573.8	861.4	12.56	75	27.7	37753	ND	ND	No
LYAM2	NWAPGEPNNR	Yes	577.77	301.1	8.90	75.5	24.9	91435	ND	ND	No
LYAM2	NWAPGEPNNR	Yes	577.77	372.2	8.90	75.5	24.9	88736	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
LYAM2	NWAPGEPNNR	Yes	577.77	783.4	8.90	75.5	27.9	99497	ND	ND	No
LYAM2	NWAPGEPNNR	Yes	577.77	854.4	8.90	75.5	27.9	22249	ND	ND	No
LYAM2	QPQNGSVR	Yes	443.23	361.2	5.37	58.2	25	2688	ND	ND	No
LYAM2	QPQNGSVR	Yes	443.23	418.2	5.37	58.2	31	4725	ND	ND	No
LYAM2	QPQNGSVR	Yes	443.23	532.3	5.37	58.2	22	3171	ND	ND	No
LYAM2	QPQNGSVR	Yes	443.23	660.3	5.37	58.2	31	2517	ND	ND	No
LYAM2	YTHLVAIQNK	Yes	396.22	502.3	9.62	52.1	17.8	130444	ND	2813	No
LYAM2	YTHLVAIQNK	Yes	396.22	515.3	9.62	52.1	17.8	81145	ND	ND	No
LYAM2	YTHLVAIQNK	Yes	396.22	573.3	9.62	52.1	17.8	215425	3408	7990	No
LYAM2	YTHLVAIQNK	Yes	396.22	685.4	9.62	52.1	17.8	76545	2723	1413	No
LYAM3	EVAAWTYHYSTK	Yes	485.9	335.2	12.48	63.7	31.3	25418	ND	ND	No
LYAM3	EVAAWTYHYSTK	Yes	485.9	635.3	12.48	63.7	31.3	11064	ND	ND	No
LYAM3	EVAAWTYHYSTK	Yes	485.9	798.4	12.48	63.7	31.3	12250	ND	ND	No
LYAM3	EVAAWTYHYSTK	Yes	485.9	899.4	12.48	63.7	31.3	8269	ND	ND	No
LYAM3	NEIDYLNK	Yes	504.75	261.2	11.00	66.1	33.7	82723	ND	ND	No
LYAM3	NEIDYLNK	Yes	504.75	537.3	11.00	66.1	30.7	15041	ND	ND	No
LYAM3	NEIDYLNK	Yes	504.75	652.3	11.00	66.1	24.7	29335	ND	ND	No
LYAM3	NEIDYLNK	Yes	504.75	765.4	11.00	66.1	24.7	49728	ND	ND	No
LYAM3	YTDLVAIQNK	Yes	582.82	380.1	12.20	76.2	28.1	22399	ND	ND	No
LYAM3	YTDLVAIQNK	Yes	582.82	672.4	12.20	76.2	28.1	15775	ND	ND	No
LYAM3	YTDLVAIQNK	Yes	582.82	785.5	12.20	76.2	28.1	5433	ND	ND	No
LYAM3	YTDLVAIQNK	Yes	582.82	900.5	12.20	76.2	28.1	9707	ND	ND	No
LYOX	HWFQAGYSTSR	Yes	447.21	324.1	11.68	58.7	26.4	24639	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
LYOX	HWFQAGYSTSR	Yes	447.21	363.2	11.68	58.7	20.4	13915	ND	ND	No
LYOX	HWFQAGYSTSR	Yes	447.21	613.3	11.68	58.7	20.4	7609	ND	ND	No
LYOX	HWFQAGYSTSR	Yes	447.21	727.3	11.68	58.7	20.4	8570	ND	ND	No
LYOX	NQGTSDFLPSRPR	Yes	737.87	272.2	11.04	96.2	41	11495	ND	ND	No
LYOX	NQGTSDFLPSRPR	Yes	737.87	603.2	11.04	96.2	44	4649	ND	ND	No
LYOX	NQGTSDFLPSRPR	Yes	737.87	612.4	11.04	96.2	44	10648	ND	ND	No
LYOX	NQGTSDFLPSRPR	Yes	737.87	872.5	11.04	96.2	38	5202	ND	ND	No
LYOX	TPILLIR	Yes	413.28	288.2	16.41	54.3	29.7	ND	ND	ND	No
LYOX	TPILLIR	Yes	413.28	514.4	16.41	54.3	23.7	45132	ND	ND	No
LYOX	TPILLIR	Yes	413.28	627.5	16.41	54.3	29.7	23694	ND	ND	No
LYOX	TPILLIR	Yes	413.28	724.5	16.41	54.3	20.7	4756	ND	ND	No
LYOX	VSVNPSYLVPESDYTNNVVR	Yes	751.38	702.4	17.17	97.9	35.9	18908	ND	ND	No
LYOX	VSVNPSYLVPESDYTNNVVR	Yes	751.38	860.5	17.17	97.9	35.9	9758	ND	ND	No
LYOX	VSVNPSYLVPESDYTNNVVR	Yes	751.38	865.5	17.17	97.9	44.9	15247	ND	ND	No
LYOX	VSVNPSYLVPESDYTNNVVR	Yes	751.38	959.5	17.17	97.9	32.9	9636	ND	ND	No
LYOX	YRPGYGTGYFQYGLPDLVADPYYIQASTYVQK	No									
LYPD3	GGPQQPHNK	Yes	481.74	261.2	5.25	63.1	29.7	18379	ND	ND	No
LYPD3	GGPQQPHNK	Yes	481.74	623.3	5.25	63.1	26.7	4401	ND	ND	No
LYPD3	GGPQQPHNK	Yes	481.74	702.3	5.25	63.1	23.7	2579	ND	ND	No
LYPD3	GGPQQPHNK	Yes	481.74	848.4	5.25	63.1	29.7	1785	ND	ND	No
LYPD3	LNLTSR	Yes	352.21	262.2	8.82	46.4	18	39393	ND	ND	No
LYPD3	LNLTSR	Yes	352.21	442.3	8.82	46.4	15	2617	ND	ND	No
LYPD3	LNLTSR	Yes	352.21	476.3	8.82	46.4	18	64140	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
LYPD3	LNLTSR	Yes	352.21	590.3	8.82	46.4	18	36783	ND	ND	No
LYPD3	LTGGAAGHQDR	Yes	541.77	612.3	5.34	70.9	35.3	17776	ND	ND	No
LYPD3	LTGGAAGHQDR	Yes	541.77	683.3	5.34	70.9	32.3	11638	ND	ND	No
LYPD3	LTGGAAGHQDR	Yes	541.77	868.4	5.34	70.9	26.3	18786	ND	ND	No
LYPD3	LTGGAAGHQDR	Yes	541.77	969.5	5.34	70.9	29.3	4076	ND	ND	No
LYPD3	SNSGQYPAK	Yes	476.23	315.2	5.50	62.4	29.5	153724	ND	ND	No
LYPD3	SNSGQYPAK	Yes	476.23	606.3	5.50	62.4	23.5	12950	ND	ND	No
LYPD3	SNSGQYPAK	Yes	476.23	663.3	5.50	62.4	26.5	43279	ND	ND	No
LYPD3	SNSGQYPAK	Yes	476.23	750.4	5.50	62.4	23.5	116086	ND	ND	No
LYPD3	TYFSPR	Yes	385.7	272.2	9.30	50.8	22.5	19136	ND	ND	No
LYPD3	TYFSPR	Yes	385.7	359.2	9.30	50.8	19.5	50476	ND	ND	No
LYPD3	TYFSPR	Yes	385.7	506.3	9.30	50.8	19.5	215501	ND	ND	No
LYPD3	TYFSPR	Yes	385.7	669.3	9.30	50.8	22.5	10716	ND	ND	No
MAGA4	EAALLEEEEGV	Yes	594.79	304.2	15.23	77.7	28.7	31519	ND	ND	No
MAGA4	EAALLEEEEGV	Yes	594.79	385.2	15.23	77.7	28.7	32908	ND	ND	No
MAGA4	EAALLEEEEGV	Yes	594.79	498.3	15.23	77.7	25.7	32309	ND	ND	No
MAGA4	EAALLEEEEGV	Yes	594.79	627.3	15.23	77.7	25.7	25125	ND	ND	No
MAGA4	IAYPSLR	Yes	410.24	375.2	12.34	53.9	23.6	ND	ND	ND	No
MAGA4	IAYPSLR	Yes	410.24	472.3	12.34	53.9	23.6	89709	ND	ND	No
MAGA4	IAYPSLR	Yes	410.24	635.4	12.34	53.9	20.6	36055	ND	ND	No
MAGA4	IAYPSLR	Yes	410.24	706.4	12.34	53.9	20.6	19063	ND	ND	No
MAGA4	QPNEGSSSQEEEGPSTSPDAESLFR	No									
MAGA4	VLEHVVR	No									

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
MAGA4	YEFLWGPR	Yes	534.27	293.1	19.61	69.9	23	139934	ND	ND	No
MAGA4	YEFLWGPR	Yes	534.27	329.2	19.61	69.9	23	81067	ND	ND	No
MAGA4	YEFLWGPR	Yes	534.27	628.4	19.61	69.9	29	32050	ND	ND	No
MAGA4	YEFLWGPR	Yes	534.27	775.4	19.61	69.9	26	115949	ND	ND	No
MASP1	APEPISTQSHSVLILFHSDNSGENR	No									
MASP1	APGELEHGLITFSTR	Yes	543.29	363.2	16.62	71.1	31.3	36430	39596	25550	No
MASP1	APGELEHGLITFSTR	Yes	543.29	510.3	16.62	71.1	34.3	46641	32351	47145	No
MASP1	APGELEHGLITFSTR	Yes	543.29	611.3	16.62	71.1	28.3	113112	99581	93240	No
MASP1	APGELEHGLITFSTR	Yes	543.29	724.4	16.62	71.1	34.3	56143	36735	42148	No
MASP1	DSDLLSPSDFK	Yes	612.29	318.1	16.20	80	29.4	1924996	ND	ND	No
MASP1	DSDLLSPSDFK	Yes	612.29	431.2	16.20	80	29.4	836505	ND	ND	No
MASP1	DSDLLSPSDFK	Yes	612.29	680.3	16.20	80	29.4	1435521	ND	ND	No
MASP1	DSDLLSPSDFK	Yes	612.29	793.4	16.20	80	29.4	1052588	ND	ND	No
MASP1	SDENEQHLGVK	Yes	628.3	303.2	6.73	82.1	33.1	63611	ND	ND	No
MASP1	SDENEQHLGVK	Yes	628.3	416.3	6.73	82.1	39.1	44759	ND	ND	No
MASP1	SDENEQHLGVK	Yes	628.3	553.3	6.73	82.1	39.1	38455	ND	ND	No
MASP1	SDENEQHLGVK	Yes	628.3	924.5	6.73	82.1	30.1	16918	ND	ND	No
MASP1	TGVITSPDFPNPYPK	Yes	816.92	258.1	15.73	106.4	38.4	727424	1103949	902990	No
MASP1	TGVITSPDFPNPYPK	Yes	816.92	504.3	15.73	106.4	47.4	139749	206259	190205	No
MASP1	TGVITSPDFPNPYPK	Yes	816.92	715.4	15.73	106.4	44.4	144683	223602	202212	No
MASP1	TGVITSPDFPNPYPK	Yes	816.92	862.4	15.73	106.4	47.4	109708	153710	131787	No
MDHC	ESAFEFLSSA	No									
MDHC	GEFVTTVQQR	Yes	582.8	431.2	10.20	76.2	28.1	4812	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
MDHC	GEFVTTVQQR	Yes	582.8	631.4	10.20	76.2	25.1	4454	ND	ND	No
MDHC	GEFVTTVQQR	Yes	582.8	732.4	10.20	76.2	28.1	12877	ND	ND	No
MDHC	GEFVTTVQQR	Yes	582.8	831.5	10.20	76.2	37.1	2953	ND	ND	No
MDHC	LGVTANDVK	Yes	458.76	546.3	8.83	60.2	22.7	141263	ND	ND	No
MDHC	LGVTANDVK	Yes	458.76	647.3	8.83	60.2	22.7	324542	ND	ND	No
MDHC	LGVTANDVK	Yes	458.76	746.4	8.83	60.2	22.7	88975	ND	ND	No
MDHC	LGVTANDVK	Yes	458.76	803.4	8.83	60.2	22.7	181219	ND	ND	No
MDHC	NVIIWGNHSSTQYPDVNHAK	No									
MDHC	VLVTGAAGQIAYSLLYSIGNGSVFGK	Yes	862.47	351.2	24.71	112.3	50.5	21540	ND	ND	No
MDHC	VLVTGAAGQIAYSLLYSIGNGSVFGK	Yes	862.47	594.3	24.71	112.3	44.5	8105	ND	ND	No
MDHC	VLVTGAAGQIAYSLLYSIGNGSVFGK	Yes	862.47	765.4	24.71	112.3	38.5	34614	ND	ND	No
MDHC	VLVTGAAGQIAYSLLYSIGNGSVFGK	Yes	862.47	965.5	24.71	112.3	41.5	12905	ND	ND	No
MDHM	LTLYDIAHTPGVAADLSHIETK	No									
MDHM	VAVLGASGGIGQPLSLLLK	Yes	897.05	511.3	24.44	116.7	39	61532	ND	ND	No
MDHM	VAVLGASGGIGQPLSLLLK	Yes	897.05	783.5	24.44	116.7	39	120996	ND	ND	No
MDHM	VAVLGASGGIGQPLSLLLK	Yes	897.05	825.5	24.44	116.7	39	82705	ND	ND	No
MDHM	VAVLGASGGIGQPLSLLLK	Yes	897.05	968.6	24.44	116.7	39	101342	ND	ND	No
MDHM	VDFPQDQLTALTGR	Yes	780.9	333.2	18.20	101.7	36.9	19352	10494	10516	No
MDHM	VDFPQDQLTALTGR	Yes	780.9	517.3	18.20	101.7	39.9	12481	16111	10468	No
MDHM	VDFPQDQLTALTGR	Yes	780.9	618.4	18.20	101.7	42.9	15848	3453	3966	Yes (Based on Transition Ratios)
MDHM	VDFPQDQLTALTGR	Yes	780.9	731.4	18.20	101.7	45.9	10874	10382	12236	No
MDHM	VNVPVIGGHAGK	Yes	383.22	526.3	11.39	50.4	20.1	57546	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
MDHM	VNVPVIGGHAGK	Yes	383.22	639.4	11.39	50.4	20.1	73908	ND	ND	No
MDHM	VNVPVIGGHAGK	Yes	383.22	738.4	11.39	50.4	26.1	16021	ND	ND	No
MDHM	VNVPVIGGHAGK	Yes	383.22	835.5	11.39	50.4	26.1	ND	ND	ND	No
MDHM	VSSFEEK	Yes	413.2	276.2	6.99	54.3	29.7	233734	ND	ND	No
MDHM	VSSFEEK	Yes	413.2	552.3	6.99	54.3	23.7	60137	ND	ND	No
MDHM	VSSFEEK	Yes	413.2	639.3	6.99	54.3	20.7	321445	ND	ND	No
MDHM	VSSFEEK	Yes	413.2	726.3	6.99	54.3	20.7	396475	ND	88843	No
MIF	IGGAQNR	Yes	358.2	417.2	5.39	47.2	21.3	19091	ND	ND	No
MIF	IGGAQNR	Yes	358.2	488.3	5.39	47.2	18.3	8220	ND	ND	No
MIF	IGGAQNR	Yes	358.2	545.3	5.39	47.2	18.3	74631	ND	ND	No
MIF	IGGAQNR	Yes	358.2	602.3	5.39	47.2	18.3	183307	ND	ND	No
MLH1	HEVHFLHEESILER	Yes	592.3	267.1	13.23	77.4	33.8	21223	ND	ND	No
MLH1	HEVHFLHEESILER	Yes	592.3	503.2	13.23	77.4	33.8	8119	ND	ND	No
MLH1	HEVHFLHEESILER	Yes	592.3	746.4	13.23	77.4	30.8	5859	ND	ND	No
MLH1	HEVHFLHEESILER	Yes	592.3	763.4	13.23	77.4	30.8	3607	ND	ND	No
MLH1	HFTEDGNILQLANLPDLYK	Yes	734.38	635.3	22.79	95.7	32	71535	ND	ND	No
MLH1	HFTEDGNILQLANLPDLYK	Yes	734.38	801.3	22.79	95.7	32	66312	ND	ND	No
MLH1	HFTEDGNILQLANLPDLYK	Yes	734.38	914.4	22.79	95.7	35	62863	ND	ND	No
MLH1	HFTEDGNILQLANLPDLYK	Yes	734.38	933.5	22.79	95.7	32	42425	ND	ND	No
MLH1	LQSFEDLASISTYGFR	Yes	611.97	379.2	22.27	79.9	28.8	42551	ND	ND	No
MLH1	LQSFEDLASISTYGFR	Yes	611.97	542.3	22.27	79.9	25.8	51431	ND	ND	No
MLH1	LQSFEDLASISTYGFR	Yes	611.97	643.3	22.27	79.9	28.8	37097	ND	ND	No
MLH1	LQSFEDLASISTYGFR	Yes	611.97	730.4	22.27	79.9	28.8	120609	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
MLH1	TLPNASTVDNIR	Yes	650.85	717.4	12.02	85	40.1	65486	ND	ND	No
MLH1	TLPNASTVDNIR	Yes	650.85	804.4	12.02	85	37.1	72828	ND	ND	No
MLH1	TLPNASTVDNIR	Yes	650.85	875.5	12.02	85	40.1	60709	ND	ND	No
MLH1	TLPNASTVDNIR	Yes	650.85	989.5	12.02	85	40.1	37338	ND	ND	No
MLH1	WTVEHIVYK	Yes	392.21	310.2	13.70	51.6	23.6	112963	ND	ND	No
MLH1	WTVEHIVYK	Yes	392.21	522.3	13.70	51.6	17.6	41875	ND	ND	No
MLH1	WTVEHIVYK	Yes	392.21	659.4	13.70	51.6	26.6	13370	ND	ND	No
MLH1	WTVEHIVYK	Yes	392.21	788.4	13.70	51.6	17.6	9596	ND	ND	No
MMP1	DGFFYFFHGTR	Yes	465.22	333.2	21.85	61	30.3	110793	ND	ND	No
MMP1	DGFFYFFHGTR	Yes	465.22	617.3	21.85	61	27.3	117915	ND	ND	No
MMP1	DGFFYFFHGTR	Yes	465.22	764.4	21.85	61	24.3	99831	ND	ND	No
MMP1	DGFFYFFHGTR	Yes	465.22	927.4	21.85	61	24.3	18787	ND	ND	No
MMP1	DIYSSFGFPR	Yes	594.79	623.3	19.60	77.7	25.7	51817	ND	ND	No
MMP1	DIYSSFGFPR	Yes	594.79	710.4	19.60	77.7	28.7	93929	ND	ND	No
MMP1	DIYSSFGFPR	Yes	594.79	797.4	19.60	77.7	28.7	156922	ND	ND	No
MMP1	DIYSSFGFPR	Yes	594.79	960.5	19.60	77.7	28.7	123041	ND	ND	No
MMP1	IENYTPDLPR	Yes	406.54	385.3	12.64	53.4	27.3	37689	ND	ND	No
MMP1	IENYTPDLPR	Yes	406.54	500.3	12.64	53.4	21.3	10038	ND	ND	No
MMP1	IENYTPDLPR	Yes	406.54	597.3	12.64	53.4	18.3	25405	ND	ND	No
MMP1	IENYTPDLPR	Yes	406.54	698.4	12.64	53.4	27.3	1376	ND	ND	No
MMP1	LTFDAITTIR	Yes	575.83	603.4	18.12	75.3	27.8	52776	ND	ND	No
MMP1	LTFDAITTIR	Yes	575.83	674.4	18.12	75.3	36.8	86940	ND	ND	No
MMP1	LTFDAITTIR	Yes	575.83	789.4	18.12	75.3	36.8	96433	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
MMP1	LTFDAITTIR	Yes	575.83	936.5	18.12	75.3	27.8	65870	ND	ND	No
MMP1	SQNPVQPIGPQTPK	Yes	497.6	526.3	9.71	65.2	19.9	23711	ND	ND	No
MMP1	SQNPVQPIGPQTPK	Yes	497.6	627.3	9.71	65.2	22.9	31005	ND	ND	No
MMP1	SQNPVQPIGPQTPK	Yes	497.6	654.3	9.71	65.2	19.9	21005	ND	ND	No
MMP1	SQNPVQPIGPQTPK	Yes	497.6	837.5	9.71	65.2	22.9	28630	ND	ND	No
MMP11	FPVHAALVWGPEK	Yes	484.27	430.2	16.94	63.5	31.2	267325	ND	ND	No
MMP11	FPVHAALVWGPEK	Yes	484.27	616.3	16.94	63.5	22.2	351672	ND	ND	No
MMP11	FPVHAALVWGPEK	Yes	484.27	623.3	16.94	63.5	25.2	81320	ND	ND	No
MMP11	FPVHAALVWGPEK	Yes	484.27	736.4	16.94	63.5	22.2	133970	ND	ND	No
MMP11	FPWQLVQEQVR	Yes	715.38	999.6	19.93	93.3	43	33211	ND	ND	No
MMP11	FPWQLVQEQVR	Yes	715.38	659.3	19.93	93.3	37	23921	ND	ND	No
MMP11	FPWQLVQEQVR	Yes	715.38	758.4	19.93	93.3	43	42918	ND	ND	No
MMP11	FPWQLVQEQVR	Yes	715.38	871.5	19.93	93.3	43	40193	ND	ND	No
MMP11	GGQLQPGYPALASR	No									
MMP11	GVPSEIDAAFQDADGYAYFLR	Yes	1153.04	435.3	24.44	149.7	56.2	3603	ND	ND	No
MMP11	GVPSEIDAAFQDADGYAYFLR	Yes	1153.04	583.3	24.44	149.7	50.2	2974	ND	ND	No
MMP11	GVPSEIDAAFQDADGYAYFLR	Yes	1153.04	669.4	24.44	149.7	50.2	2918	ND	ND	No
MMP11	GVPSEIDAAFQDADGYAYFLR	Yes	1153.04	889.5	24.44	149.7	62.2	5670	ND	ND	No
MMP11	VWSDVTPLTFTEVHEGR	Yes	658.33	286.2	19.08	85.9	28.1	107147	ND	ND	No
MMP11	VWSDVTPLTFTEVHEGR	Yes	658.33	498.2	19.08	85.9	40.1	17507	ND	ND	No
MMP11	VWSDVTPLTFTEVHEGR	Yes	658.33	827.4	19.08	85.9	37.1	20023	ND	ND	No
MMP11	VWSDVTPLTFTEVHEGR	Yes	658.33	974.5	19.08	85.9	40.1	12800	ND	ND	No
MMP12	FLLILLLQATASGALPLNSSTSLEK	Yes	867.5	261.2	24.91	112.9	50.8	18533	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
MMP12	FLLILLLQATASGALPLNSSTSLEK	Yes	867.5	374.2	24.91	112.9	50.8	13961	ND	ND	No
MMP12	FLLILLLQATASGALPLNSSTSLEK	Yes	867.5	600.4	24.91	112.9	38.8	7379	ND	ND	No
MMP12	FLLILLLQATASGALPLNSSTSLEK	Yes	867.5	713.5	24.91	112.9	41.8	6579	ND	ND	No
MMP12	GIQSLYGDPK	Yes	539.28	416.2	11.62	70.6	26.2	70544	ND	ND	No
MMP12	GIQSLYGDPK	Yes	539.28	579.3	11.62	70.6	26.2	135678	ND	ND	No
MMP12	GIQSLYGDPK	Yes	539.28	779.4	11.62	70.6	26.2	102090	ND	ND	No
MMP12	GIQSLYGDPK	Yes	539.28	907.5	11.62	70.6	26.2	22236	ND	ND	No
MMP12	IDAVFYSK	Yes	471.75	544.3	12.51	61.9	23.3	232771	ND	ND	No
MMP12	IDAVFYSK	Yes	471.75	643.3	12.51	61.9	23.3	70813	ND	ND	No
MMP12	IDAVFYSK	Yes	471.75	714.4	12.51	61.9	23.3	360847	ND	ND	No
MMP12	IDAVFYSK	Yes	471.75	829.4	12.51	61.9	23.3	238489	ND	ND	No
MMP12	TSVNLISSLWPTLPSGIEAAYEIEAR	No									
MMP12	YYYFFQGSNQFEYDFLLQR	No									
MMP14	AVDSEYPK	Yes	454.72	407.2	6.98	59.7	31.5	37676	ND	3288	No
MMP14	AVDSEYPK	Yes	454.72	623.3	6.98	59.7	22.5	37275	ND	ND	No
MMP14	AVDSEYPK	Yes	454.72	738.3	6.98	59.7	22.5	256132	ND	ND	No
MMP14	AVDSEYPK	Yes	454.72	837.4	6.98	59.7	25.5	8681	ND	ND	No
MMP14	FNEELR	Yes	404.2	262.1	9.05	53.1	20.3	135371	ND	ND	No
MMP14	FNEELR	Yes	404.2	288.2	9.05	53.1	29.3	214919	ND	ND	No
MMP14	FNEELR	Yes	404.2	546.3	9.05	53.1	20.3	201543	ND	ND	No
MMP14	FNEELR	Yes	404.2	660.3	9.05	53.1	23.3	140316	ND	ND	No
MMP14	FYGLQVTGK	Yes	506.78	305.2	14.01	66.4	33.8	469691	ND	ND	No
MMP14	FYGLQVTGK	Yes	506.78	532.3	14.01	66.4	24.8	132174	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
MMP14	FYGLQVTGK	Yes	506.78	702.4	14.01	66.4	24.8	870546	ND	ND	No
MMP14	FYGLQVTGK	Yes	506.78	865.5	14.01	66.4	24.8	115041	ND	ND	No
MMP14	HWVFDEASLEPGYPK	Yes	592.29	561.3	17.81	77.4	27.8	71765	ND	ND	No
MMP14	HWVFDEASLEPGYPK	Yes	592.29	685.3	17.81	77.4	30.8	12207	ND	ND	No
MMP14	HWVFDEASLEPGYPK	Yes	592.29	690.3	17.81	77.4	27.8	15325	ND	ND	No
MMP14	HWVFDEASLEPGYPK	Yes	592.29	814.4	17.81	77.4	27.8	20873	ND	ND	No
MMP14	VWESATPLR	Yes	529.79	286.2	13.56	69.3	22.8	326867	ND	ND	No
MMP14	VWESATPLR	Yes	529.79	385.3	13.56	69.3	34.8	59982	ND	ND	No
MMP14	VWESATPLR	Yes	529.79	644.4	13.56	69.3	31.8	143165	ND	ND	No
MMP14	VWESATPLR	Yes	529.79	773.4	13.56	69.3	25.8	254432	ND	ND	No
MMP2	AFQVWSDVTPLR	Yes	709.88	385.3	19.51	92.6	30.7	116100	47640	36708	No
MMP2	AFQVWSDVTPLR	Yes	709.88	446.2	19.51	92.6	30.7	95786	44821	40207	No
MMP2	AFQVWSDVTPLR	Yes	709.88	787.4	19.51	92.6	33.7	90093	47031	41343	No
MMP2	AFQVWSDVTPLR	Yes	709.88	973.5	19.51	92.6	33.7	92369	55899	36803	No
MMP2	IDAVYEAPQEEK	Yes	696.34	300.2	10.05	90.8	33.1	327613	ND	ND	No
MMP2	IDAVYEAPQEEK	Yes	696.34	630.3	10.05	90.8	42.1	186710	ND	ND	No
MMP2	IDAVYEAPQEEK	Yes	696.34	830.4	10.05	90.8	33.1	81042	ND	ND	No
MMP2	IDAVYEAPQEEK	Yes	696.34	993.5	10.05	90.8	33.1	117243	ND	ND	No
MMP2	IIGYTPDLDPETVDDAFAR	Yes	703.34	579.3	20.02	91.7	42.4	66500	25850	26685	No
MMP2	IIGYTPDLDPETVDDAFAR	Yes	703.34	793.4	20.02	91.7	33.4	50786	18593	11285	No
MMP2	IIGYTPDLDPETVDDAFAR	Yes	703.34	894.4	20.02	91.7	33.4	48775	19484	11214	No
MMP2	IIGYTPDLDPETVDDAFAR	Yes	703.34	988.5	20.02	91.7	30.4	38072	11375	12136	No
MMP2	LIADAWNAIPDNLDAVVDLQGGGHSYFFK	No									

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
MMP2	QDIVFDGIAQIR	Yes	687.87	357.2	18.84	89.7	32.8	30699	ND	ND	No
MMP2	QDIVFDGIAQIR	Yes	687.87	657.4	18.84	89.7	41.8	22622	ND	ND	No
MMP2	QDIVFDGIAQIR	Yes	687.87	772.4	18.84	89.7	41.8	14785	ND	ND	No
MMP2	QDIVFDGIAQIR	Yes	687.87	919.5	18.84	89.7	41.8	18807	ND	ND	No
MMP26	DSIYNAVSIWSNVTPLIFQQVQNGDADIK	No									
MMP26	HTLTYR	No									
MMP26	IQHLYGEK	Yes	494.27	333.2	7.61	64.8	33.2	65528	ND	ND	No
MMP26	IQHLYGEK	Yes	494.27	379.2	7.61	64.8	30.2	78159	ND	ND	No
MMP26	IQHLYGEK	Yes	494.27	609.3	7.61	64.8	30.2	45281	ND	ND	No
MMP26	IQHLYGEK	Yes	494.27	746.4	7.61	64.8	24.2	152435	ND	ND	No
MMP26	TFQLSADDIQR	Yes	647.33	377.2	13.98	84.5	31	223036	ND	ND	No
MMP26	TFQLSADDIQR	Yes	647.33	717.4	13.98	84.5	31	65420	ND	ND	No
MMP26	TFQLSADDIQR	Yes	647.33	804.4	13.98	84.5	31	201775	ND	ND	No
MMP26	TFQLSADDIQR	Yes	647.33	917.5	13.98	84.5	31	92289	ND	ND	No
MMP7	DLPHITVDR	Yes	355.86	389.2	12.53	46.9	21.7	19320	3024	3676	Yes (Based on Transition Ratios)
MMP7	DLPHITVDR	Yes	355.86	490.3	12.53	46.9	18.7	46942	1325	1008	No
MMP7	DLPHITVDR	Yes	355.86	603.3	12.53	46.9	18.7	65451	1578	955	No
MMP7	DLPHITVDR	Yes	355.86	740.4	12.53	46.9	24.7	1903	ND	ND	No
MMP7	IVSYTR	Yes	369.71	276.2	7.07	48.7	27.8	1251	ND	ND	No
MMP7	IVSYTR	Yes	369.71	439.2	7.07	48.7	24.8	2030	ND	ND	No
MMP7	IVSYTR	Yes	369.71	526.3	7.07	48.7	18.8	37190	ND	ND	No
MMP7	IVSYTR	Yes	369.71	625.3	7.07	48.7	15.8	3761	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
MMP7	LSQDDIK	Yes	409.72	260.2	7.22	53.9	20.5	328658	14291	14420	No
MMP7	LSQDDIK	Yes	409.72	490.3	7.22	53.9	20.5	65467	6784	3377	No
MMP7	LSQDDIK	Yes	409.72	618.3	7.22	53.9	20.5	287697	27205	8643	No
MMP7	LSQDDIK	Yes	409.72	705.3	7.22	53.9	20.5	400775	20169	9966	No
MMP7	NANSLEAK	Yes	423.72	347.2	5.94	55.7	30.1	61619	ND	ND	No
MMP7	NANSLEAK	Yes	423.72	547.3	5.94	55.7	21.1	56992	ND	ND	No
MMP7	NANSLEAK	Yes	423.72	661.4	5.94	55.7	21.1	154879	3655	2989	No
MMP7	NANSLEAK	Yes	423.72	732.4	5.94	55.7	18.1	20588	ND	ND	No
MMP9	AFALWSAVTPLTFTR	Yes	840.96	290.2	24.56	109.5	45.5	240899	6471	19474	No
MMP9	AFALWSAVTPLTFTR	Yes	840.96	589.3	24.56	109.5	36.5	66916	6294	8999	No
MMP9	AFALWSAVTPLTFTR	Yes	840.96	734.4	24.56	109.5	36.5	96715	4397	6688	No
MMP9	AFALWSAVTPLTFTR	Yes	840.96	934.5	24.56	109.5	39.5	58168	1343	4688	No
MMP9	AVIDDAFAR	No									
MMP9	FQTFEGDLK	Yes	542.77	260.2	13.68	71	29.4	513634	7030	8373	No
MMP9	FQTFEGDLK	Yes	542.77	276.1	13.68	71	26.4	1094219	5340	7019	No
MMP9	FQTFEGDLK	Yes	542.77	708.4	13.68	71	26.4	106525	4205	3253	No
MMP9	FQTFEGDLK	Yes	542.77	809.4	13.68	71	26.4	588069	6680	10178	No
MMP9	LGLGADVAQVTGALR	Yes	480.94	416.3	19.40	63	22.1	100682	ND	1668	No
MMP9	LGLGADVAQVTGALR	Yes	480.94	517.3	19.40	63	22.1	132472	ND	7427	No
MMP9	LGLGADVAQVTGALR	Yes	480.94	616.4	19.40	63	25.1	60868	ND	ND	No
MMP9	LGLGADVAQVTGALR	Yes	480.94	744.4	19.40	63	22.1	20479	ND	ND	No
MMP9	SLGPALLLLQK	Yes	576.87	501.3	21.17	75.4	30.9	127931	15350	10300	No
MMP9	SLGPALLLLQK	Yes	576.87	614.4	21.17	75.4	27.9	199743	19436	20700	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
MMP9	SLGPALLLLQK	Yes	576.87	727.5	21.17	75.4	27.9	100930	10072	11148	No
MMP9	SLGPALLLLQK	Yes	576.87	952.6	21.17	75.4	27.9	246793	27558	21083	No
MOGS	EQILGDEAR	No									
MOGS	SLAASSSFYGQR	Yes	637.31	360.2	11.38	83.2	30.5	20789	ND	ND	No
MOGS	SLAASSSFYGQR	Yes	637.31	523.3	11.38	83.2	39.5	18290	ND	ND	No
MOGS	SLAASSSFYGQR	Yes	637.31	844.4	11.38	83.2	30.5	22732	ND	ND	No
MOGS	SLAASSSFYGQR	Yes	637.31	931.4	11.38	83.2	30.5	27301	ND	ND	No
MOGS	TLPSGLDDYPR	Yes	617.31	550.3	13.12	80.6	38.7	35444	10444	11359	No
MOGS	TLPSGLDDYPR	Yes	617.31	665.3	13.12	80.6	35.7	22456	12587	11900	Yes (Based on Transition Ratios)
MOGS	TLPSGLDDYPR	Yes	617.31	835.4	13.12	80.6	29.7	24175	2157	ND	No
MOGS	TLPSGLDDYPR	Yes	617.31	922.4	13.12	80.6	38.7	33504	5109	4047	No
MOGS	VDPALFPPVPLFTAVPSR	No									
MOGS	VPPEFLVQR	No									
MPRI	FLHQDIDSGQGIR	Yes	743.38	398.2	10.80	96.9	41.2	22065	ND	ND	No
MPRI	FLHQDIDSGQGIR	Yes	743.38	526.3	10.80	96.9	35.2	4725	ND	ND	No
MPRI	FLHQDIDSGQGIR	Yes	743.38	617.3	10.80	96.9	44.2	11364	ND	ND	No
MPRI	FLHQDIDSGQGIR	Yes	743.38	960.5	10.80	96.9	44.2	7383	ND	ND	No
MPRI	GHQAFDVGQPR	Yes	606.3	323.1	9.07	79.2	38.2	6951	ND	ND	No
MPRI	GHQAFDVGQPR	Yes	606.3	394.2	9.07	79.2	32.2	3263	ND	ND	No
MPRI	GHQAFDVGQPR	Yes	606.3	556.3	9.07	79.2	38.2	7319	ND	ND	No
MPRI	GHQAFDVGQPR	Yes	606.3	889.5	9.07	79.2	35.2	3902	ND	ND	No
MPRI	TYHSVGDSVLR	Yes	617.32	402.2	9.96	80.6	32.7	28554	4063	8276	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
MPRI	TYHSVGDSVLR	Yes	617.32	646.4	9.96	80.6	38.7	16551	4071	3772	No
MPRI	TYHSVGDSVLR	Yes	617.32	745.4	9.96	80.6	38.7	ND	4053	7113	Yes (Based on Manual Review)
MPRI	TYHSVGDSVLR	Yes	617.32	832.5	9.96	80.6	35.7	29936	11114	9351	No
MPRI	VPIDGPPIDIGR	Yes	624.85	345.2	15.16	81.6	39	211432	7930	14045	No
MPRI	VPIDGPPIDIGR	Yes	624.85	767.4	15.16	81.6	39	90960	7363	ND	No
MPRI	VPIDGPPIDIGR	Yes	624.85	824.5	15.16	81.6	39	248933	14749	9207	No
MPRI	VPIDGPPIDIGR	Yes	624.85	939.5	15.16	81.6	30	87668	2041	3001	No
MPRI	YVDQVLQLVYK	No									
MRP3	ADGALTQEEK	Yes	531.26	276.2	6.59	69.5	34.9	35586	ND	ND	No
MRP3	ADGALTQEEK	Yes	531.26	634.3	6.59	69.5	22.9	113429	ND	ND	No
MRP3	ADGALTQEEK	Yes	531.26	747.4	6.59	69.5	25.9	140668	ND	ND	No
MRP3	ADGALTQEEK	Yes	531.26	875.4	6.59	69.5	22.9	52452	ND	ND	No
MRP3	DFEIISDTK	Yes	534.27	450.2	14.50	69.9	26	181453	ND	ND	No
MRP3	DFEIISDTK	Yes	534.27	563.3	14.50	69.9	26	223872	ND	ND	No
MRP3	DFEIISDTK	Yes	534.27	676.4	14.50	69.9	26	155409	ND	ND	No
MRP3	DFEIISDTK	Yes	534.27	805.4	14.50	69.9	26	189160	ND	ND	No
MRP3	GVVAEFDSPANLIAAR	Yes	543.96	317.2	19.25	71.2	25.3	34676	ND	ND	No
MRP3	GVVAEFDSPANLIAAR	Yes	543.96	430.3	19.25	71.2	25.3	32492	ND	ND	No
MRP3	GVVAEFDSPANLIAAR	Yes	543.96	657.4	19.25	71.2	22.3	9061	ND	ND	No
MRP3	GVVAEFDSPANLIAAR	Yes	543.96	825.5	19.25	71.2	31.3	12222	ND	ND	No
MRP3	IDGLNVADIGLHDLR	Yes	540.96	288.2	19.34	70.8	34.1	268263	ND	ND	No
MRP3	IDGLNVADIGLHDLR	Yes	540.96	612.3	19.34	70.8	22.1	85148	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
MRP3	IDGLNVADIGLHDLR	Yes	540.96	710.4	19.34	70.8	34.1	97348	ND	ND	No
MRP3	IDGLNVADIGLHDLR	Yes	540.96	938.5	19.34	70.8	34.1	42186	ND	ND	No
MRP3	NVDPNPYPETSAGFLSR	Yes	621.97	426.2	15.38	81.2	29.3	8805	ND	ND	No
MRP3	NVDPNPYPETSAGFLSR	Yes	621.97	540.2	15.38	81.2	32.3	18595	ND	ND	No
MRP3	NVDPNPYPETSAGFLSR	Yes	621.97	579.3	15.38	81.2	29.3	15460	ND	ND	No
MRP3	NVDPNPYPETSAGFLSR	Yes	621.97	838.4	15.38	81.2	38.3	9606	ND	ND	No
MUC1	EGTINVHDVETQFNQYK	No									
MUC1	QGGFLGLSNIK	No									
MUC1	SSVPSSTEK	Yes	461.23	551.3	5.53	60.5	28.8	72549	ND	ND	No
MUC1	SSVPSSTEK	Yes	461.23	648.3	5.53	60.5	22.8	634207	ND	ND	No
MUC1	SSVPSSTEK	Yes	461.23	747.4	5.53	60.5	19.8	49854	ND	ND	No
MUC1	SSVPSSTEK	Yes	461.23	834.4	5.53	60.5	19.8	4442	ND	ND	No
MUC1	VSAGNGGSSLSYTNPAVAATSANL	No									
MUC1	YVPPSSTDR	Yes	511.25	263.1	6.42	67	22	59146	ND	ND	No
MUC1	YVPPSSTDR	Yes	511.25	565.3	6.42	67	31	28658	ND	ND	No
MUC1	YVPPSSTDR	Yes	511.25	662.3	6.42	67	28	46822	ND	ND	No
MUC1	YVPPSSTDR	Yes	511.25	759.4	6.42	67	22	52354	ND	ND	No
MUC16	ALFSSNLDPSLVEQVFLDK	No									
MUC16	DSLYVNGFNPR	Yes	641.32	479.2	14.27	83.7	30.7	31956	ND	ND	No
MUC16	DSLYVNGFNPR	Yes	641.32	590.3	14.27	83.7	30.7	29684	ND	ND	No
MUC16	DSLYVNGFNPR	Yes	641.32	704.3	14.27	83.7	30.7	63346	ND	ND	No
MUC16	DSLYVNGFNPR	Yes	641.32	803.4	14.27	83.7	30.7	53429	ND	ND	No
MUC16	LTLLRPEK	Yes	323.87	373.2	11.36	42.8	23.1	84315	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
MUC16	LTLLRPEK	Yes	323.87	529.3	11.36	42.8	17.1	30670	ND	ND	No
MUC16	LTLLRPEK	Yes	323.87	642.4	11.36	42.8	17.1	125596	ND	ND	No
MUC16	LTLLRPEK	Yes	323.87	755.5	11.36	42.8	23.1	ND	ND	ND	No
MUC16	VLQGLLTPLFR	Yes	628.89	532.3	24.07	82.1	30.2	401319	ND	ND	No
MUC16	VLQGLLTPLFR	Yes	628.89	746.5	24.07	82.1	27.2	441639	ND	ND	No
MUC16	VLQGLLTPLFR	Yes	628.89	859.5	24.07	82.1	30.2	96071	ND	ND	No
MUC16	VLQGLLTPLFR	Yes	628.89	916.6	24.07	82.1	30.2	406284	ND	ND	No
MUC16	VPTGTITEVSSTGVNSSSK	Yes	925.97	569.3	10.98	120.5	52.2	3873	ND	ND	No
MUC16	VPTGTITEVSSTGVNSSSK	Yes	925.97	779.4	10.98	120.5	52.2	2057	ND	ND	No
MUC16	VPTGTITEVSSTGVNSSSK	Yes	925.97	866.4	10.98	120.5	46.2	2579	ND	ND	No
MUC16	VPTGTITEVSSTGVNSSSK	Yes	925.97	953.5	10.98	120.5	52.2	2647	ND	ND	No
MUC4	FLNSNSGLQGLQFYR	Yes	872.44	485.3	19.12	113.5	40.9	11202	ND	ND	No
MUC4	FLNSNSGLQGLQFYR	Yes	872.44	613.3	19.12	113.5	40.9	12869	ND	ND	No
MUC4	FLNSNSGLQGLQFYR	Yes	872.44	783.4	19.12	113.5	40.9	17275	ND	ND	No
MUC4	FLNSNSGLQGLQFYR	Yes	872.44	911.5	19.12	113.5	46.9	10697	ND	ND	No
MUC4	IGLASALQPR	Yes	513.31	584.4	14.42	67.2	25.1	138110	ND	ND	No
MUC4	IGLASALQPR	Yes	513.31	671.4	14.42	67.2	25.1	317012	ND	ND	No
MUC4	IGLASALQPR	Yes	513.31	742.4	14.42	67.2	25.1	232520	ND	ND	No
MUC4	IGLASALQPR	Yes	513.31	912.5	14.42	67.2	34.1	93209	ND	ND	No
MUC4	NDVVFQPISGEDVR	Yes	787.89	274.2	15.27	102.6	46.2	211965	ND	ND	No
MUC4	NDVVFQPISGEDVR	Yes	787.89	329.1	15.27	102.6	37.2	537222	ND	ND	No
MUC4	NDVVFQPISGEDVR	Yes	787.89	428.2	15.27	102.6	34.2	201661	ND	ND	No
MUC4	NDVVFQPISGEDVR	Yes	787.89	872.4	15.27	102.6	46.2	179861	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
MUC4	SLEPFTLEILAR	Yes	694.89	472.3	23.53	90.6	42.1	49657	ND	ND	No
MUC4	SLEPFTLEILAR	Yes	694.89	601.4	23.53	90.6	39.1	87622	ND	ND	No
MUC4	SLEPFTLEILAR	Yes	694.89	815.5	23.53	90.6	42.1	130922	ND	ND	No
MUC4	SLEPFTLEILAR	Yes	694.89	962.6	23.53	90.6	33.1	21971	ND	ND	No
MUC4	STAAPIPILPER	Yes	632.87	331.2	15.61	82.6	27.3	1023965	ND	ND	No
MUC4	STAAPIPILPER	Yes	632.87	401.2	15.61	82.6	30.3	154319	ND	ND	No
MUC4	STAAPIPILPER	Yes	632.87	724.4	15.61	82.6	39.3	754726	ND	ND	No
MUC4	STAAPIPILPER	Yes	632.87	934.6	15.61	82.6	30.3	539313	ND	ND	No
MUC5B	AVTLSLDGGDTAIR	Yes	463.58	288.2	15.65	60.8	30.2	3362	ND	ND	No
MUC5B	AVTLSLDGGDTAIR	Yes	463.58	359.2	15.65	60.8	18.2	6272	ND	ND	No
MUC5B	AVTLSLDGGDTAIR	Yes	463.58	689.4	15.65	60.8	24.2	4275	ND	ND	No
MUC5B	AVTLSLDGGDTAIR	Yes	463.58	804.4	15.65	60.8	24.2	3459	ND	ND	No
MUC5B	LTDPNSAFSR	Yes	554.28	681.3	10.10	72.5	35.9	19279	ND	ND	No
MUC5B	LTDPNSAFSR	Yes	554.28	778.4	10.10	72.5	35.9	87683	ND	ND	No
MUC5B	LTDPNSAFSR	Yes	554.28	893.4	10.10	72.5	26.9	15571	ND	ND	No
MUC5B	LTDPNSAFSR	Yes	554.28	994.5	10.10	72.5	26.9	5077	ND	ND	No
MUC5B	LTPLQFGNLQK	Yes	629.86	559.3	16.72	82.3	39.2	173917	ND	ND	No
MUC5B	LTPLQFGNLQK	Yes	629.86	706.4	16.72	82.3	33.2	257300	ND	ND	No
MUC5B	LTPLQFGNLQK	Yes	629.86	834.4	16.72	82.3	33.2	275213	ND	ND	No
MUC5B	LTPLQFGNLQK	Yes	629.86	947.5	16.72	82.3	39.2	53434	ND	ND	No
MUC5B	SVVGDALEFGNSWK	Yes	503.58	529.3	20.78	66	23.2	27173	ND	ND	No
MUC5B	SVVGDALEFGNSWK	Yes	503.58	591.3	20.78	66	20.2	64009	ND	ND	No
MUC5B	SVVGDALEFGNSWK	Yes	503.58	738.4	20.78	66	23.2	56748	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
MUC5B	SVVGDALEFGNSWK	Yes	503.58	867.4	20.78	66	23.2	30652	ND	ND	No
MUC5B	TGLLVEQSGDYIK	Yes	711.88	272.2	15.21	92.8	36.8	466660	ND	ND	No
MUC5B	TGLLVEQSGDYIK	Yes	711.88	385.2	15.21	92.8	33.8	154026	ND	ND	No
MUC5B	TGLLVEQSGDYIK	Yes	711.88	682.3	15.21	92.8	33.8	49894	ND	ND	No
MUC5B	TGLLVEQSGDYIK	Yes	711.88	939.4	15.21	92.8	33.8	145601	ND	ND	No
MUCL1	WVGDLPNGR	No									
NAMPT	EHFQDDVFNEK	Yes	469.88	390.2	12.15	61.6	21.5	153590	ND	ND	No
NAMPT	EHFQDDVFNEK	Yes	469.88	537.3	12.15	61.6	18.5	466876	ND	ND	No
NAMPT	EHFQDDVFNEK	Yes	469.88	636.3	12.15	61.6	21.5	79831	ND	ND	No
NAMPT	EHFQDDVFNEK	Yes	469.88	772.3	12.15	61.6	21.5	164613	ND	ND	No
NAMPT	GDLEEYGQDLLHTVFK	Yes	621.98	294.2	24.55	81.2	35.3	146764	ND	ND	No
NAMPT	GDLEEYGQDLLHTVFK	Yes	621.98	494.3	24.55	81.2	35.3	58470	ND	ND	No
NAMPT	GDLEEYGQDLLHTVFK	Yes	621.98	857.5	24.55	81.2	32.3	26345	ND	ND	No
NAMPT	GDLEEYGQDLLHTVFK	Yes	621.98	972.6	24.55	81.2	29.3	27109	ND	ND	No
NAMPT	STQAPLIIRPDSGNPLDTVLK	Yes	745.75	388.2	19.69	97.2	32.6	359771	ND	ND	No
NAMPT	STQAPLIIRPDSGNPLDTVLK	Yes	745.75	460.3	19.69	97.2	41.6	57620	ND	ND	No
NAMPT	STQAPLIIRPDSGNPLDTVLK	Yes	745.75	688.4	19.69	97.2	44.6	19195	ND	ND	No
NAMPT	STQAPLIIRPDSGNPLDTVLK	Yes	745.75	785.5	19.69	97.2	44.6	32476	ND	ND	No
NAMPT	YDGHLPIEIK	Yes	395.55	260.2	14.14	52	23.7	562251	ND	ND	No
NAMPT	YDGHLPIEIK	Yes	395.55	473.2	14.14	52	20.7	397679	ND	ND	No
NAMPT	YDGHLPIEIK	Yes	395.55	599.4	14.14	52	20.7	604269	ND	ND	No
NAMPT	YDGHLPIEIK	Yes	395.55	712.5	14.14	52	20.7	83418	ND	ND	No
NAMPT	YLLETSGNLDGLEYK	Yes	857.93	277.2	17.83	111.7	40.2	177000	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
NAMPT	YLLETSGNLDGLEYK	Yes	857.93	439.2	17.83	111.7	37.2	27028	ND	ND	No
NAMPT	YLLETSGNLDGLEYK	Yes	857.93	519.3	17.83	111.7	37.2	32833	ND	ND	No
NAMPT	YLLETSGNLDGLEYK	Yes	857.93	609.3	17.83	111.7	49.2	53788	ND	ND	No
NAPSA	ASSSFQANGTK	Yes	549.26	618.3	6.20	71.9	29.7	33762	ND	ND	No
NAPSA	ASSSFQANGTK	Yes	549.26	765.4	6.20	71.9	26.7	25716	ND	ND	No
NAPSA	ASSSFQANGTK	Yes	549.26	852.4	6.20	71.9	26.7	16843	ND	ND	No
NAPSA	ASSSFQANGTK	Yes	549.26	939.5	6.20	71.9	23.7	16040	ND	ND	No
NAPSA	FAIQYGTGR	Yes	506.76	390.2	12.01	66.4	24.8	95432	ND	ND	No
NAPSA	FAIQYGTGR	Yes	506.76	553.3	12.01	66.4	24.8	162297	ND	ND	No
NAPSA	FAIQYGTGR	Yes	506.76	681.3	12.01	66.4	24.8	87139	ND	ND	No
NAPSA	FAIQYGTGR	Yes	506.76	794.4	12.01	66.4	33.8	44812	ND	ND	No
NAPSA	GADLGWGETAQAQFPG	No									
NAPSA	LGAPSPGDKPIFVPLSNYR	Yes	676.7	539.3	17.46	88.3	41.1	107088	ND	ND	No
NAPSA	LGAPSPGDKPIFVPLSNYR	Yes	676.7	652.3	17.46	88.3	41.1	50469	ND	ND	No
NAPSA	LGAPSPGDKPIFVPLSNYR	Yes	676.7	749.4	17.46	88.3	41.1	417724	ND	ND	No
NAPSA	LGAPSPGDKPIFVPLSNYR	Yes	676.7	995.5	17.46	88.3	41.1	29253	ND	ND	No
NAPSA	VDGILSEDK	Yes	488.25	272.1	10.52	64	24	191311	ND	ND	No
NAPSA	VDGILSEDK	Yes	488.25	591.3	10.52	64	24	392191	ND	ND	No
NAPSA	VDGILSEDK	Yes	488.25	761.4	10.52	64	24	288399	ND	ND	No
NAPSA	VDGILSEDK	Yes	488.25	876.4	10.52	64	24	127825	ND	ND	No
NCF4	AEALFDFTGNSK	Yes	650.31	272.1	17.56	84.9	31.1	1168850	9131	7149	No
NCF4	AEALFDFTGNSK	Yes	650.31	506.3	17.56	84.9	40.1	138024	ND	ND	No
NCF4	AEALFDFTGNSK	Yes	650.31	768.4	17.56	84.9	31.1	339064	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
NCF4	AEALFDFTGNSK	Yes	650.31	915.4	17.56	84.9	31.1	288902	ND	ND	No
NCF4	DAEGDLVR	Yes	437.72	274.2	8.73	57.5	30.8	37785	5800	9617	No
NCF4	DAEGDLVR	Yes	437.72	387.3	8.73	57.5	30.8	49757	10145	9025	No
NCF4	DAEGDLVR	Yes	437.72	559.3	8.73	57.5	21.8	ND	7230	16116	Yes (Based on Manual Review)
NCF4	DAEGDLVR	Yes	437.72	688.4	8.73	57.5	21.8	ND	14739	12739	Yes (Based on Manual Review)
NCF4	DIAVEEDLSSTPLLK	Yes	815.43	300.2	18.97	106.2	38.4	94425	ND	ND	No
NCF4	DIAVEEDLSSTPLLK	Yes	815.43	470.3	18.97	106.2	44.4	35463	ND	ND	No
NCF4	DIAVEEDLSSTPLLK	Yes	815.43	658.4	18.97	106.2	41.4	12674	ND	ND	No
NCF4	DIAVEEDLSSTPLLK	Yes	815.43	745.4	18.97	106.2	41.4	24291	ND	ND	No
NCF4	GATGIFPLSFVK	Yes	618.85	400.2	22.59	80.8	26.7	931769	ND	ND	No
NCF4	GATGIFPLSFVK	Yes	618.85	690.4	22.59	80.8	29.7	1125742	14540	13952	No
NCF4	GATGIFPLSFVK	Yes	618.85	837.5	22.59	80.8	26.7	2093331	18333	17691	No
NCF4	GATGIFPLSFVK	Yes	618.85	950.6	22.59	80.8	29.7	163767	ND	ND	No
NCF4	SVSPQGNSVDR	Yes	573.28	274.1	6.01	75	24.7	39983	ND	ND	No
NCF4	SVSPQGNSVDR	Yes	573.28	647.3	6.01	75	33.7	53236	ND	ND	No
NCF4	SVSPQGNSVDR	Yes	573.28	872.4	6.01	75	24.7	40242	ND	ND	No
NCF4	SVSPQGNSVDR	Yes	573.28	959.5	6.01	75	24.7	24588	ND	ND	No
NDKA	DRPFFAGLVK	Yes	383.89	416.3	17.74	50.5	17.1	39302	ND	ND	No
NDKA	DRPFFAGLVK	Yes	383.89	487.3	17.74	50.5	17.1	215020	ND	ND	No
NDKA	DRPFFAGLVK	Yes	383.89	516.3	17.74	50.5	17.1	343811	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
NDKA	DRPFFAGLVK	Yes	383.89	663.3	17.74	50.5	17.1	118186	ND	ND	No
NDKA	EHYVDLK	Yes	301.82	260.2	8.44	39.9	15.9	181060	ND	ND	No
NDKA	EHYVDLK	Yes	301.82	267.1	8.44	39.9	18.9	544700	ND	ND	No
NDKA	EHYVDLK	Yes	301.82	375.2	8.44	39.9	15.9	32544	ND	ND	No
NDKA	EHYVDLK	Yes	301.82	430.2	8.44	39.9	15.9	77243	ND	ND	No
NDKA	NIIHGSDSVESAEK	Yes	495.91	347.2	8.58	65	28.8	9282	ND	1729	No
NDKA	NIIHGSDSVESAEK	Yes	495.91	434.2	8.58	65	28.8	21374	ND	5702	No
NDKA	NIIHGSDSVESAEK	Yes	495.91	563.3	8.58	65	22.8	35600	ND	2424	No
NDKA	NIIHGSDSVESAEK	Yes	495.91	824.4	8.58	65	25.8	6514	ND	ND	No
NDKA	TFIAIKPDGVQR	Yes	672.89	433.2	12.59	87.8	35.1	17931	ND	ND	No
NDKA	TFIAIKPDGVQR	Yes	672.89	574.3	12.59	87.8	38.1	5174	ND	ND	No
NDKA	TFIAIKPDGVQR	Yes	672.89	799.4	12.59	87.8	35.1	9504	ND	ND	No
NDKA	TFIAIKPDGVQR	Yes	672.89	983.6	12.59	87.8	41.1	9191	ND	ND	No
NDKB	ASEEHLK	Yes	407.21	526.3	5.44	53.5	20.4	18643	ND	ND	No
NDKB	ASEEHLK	Yes	407.21	554.2	5.44	53.5	17.4	2721	ND	ND	No
NDKB	ASEEHLK	Yes	407.21	655.3	5.44	53.5	20.4	40322	ND	ND	No
NDKB	ASEEHLK	Yes	407.21	742.4	5.44	53.5	20.4	35148	ND	ND	No
NDKB	DRPFFPGLVK	Yes	588.33	663.3	16.91	76.9	37.4	44765	ND	ND	No
NDKB	DRPFFPGLVK	Yes	588.33	817.4	16.91	76.9	37.4	122003	ND	ND	No
NDKB	DRPFFPGLVK	Yes	588.33	904.5	16.91	76.9	28.4	11157	ND	ND	No
NDKB	DRPFFPGLVK	Yes	588.33	930.5	16.91	76.9	31.4	61316	ND	ND	No
NDKB	EISLWFKPEELVDYK	Yes	948.49	310.2	22.85	123.4	47.2	21007	ND	ND	No
NDKB	EISLWFKPEELVDYK	Yes	948.49	425.2	22.85	123.4	53.2	15336	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
NDKB	EISLWFKPEELVDYK	Yes	948.49	629.3	22.85	123.4	47.2	5121	ND	ND	No
NDKB	EISLWFKPEELVDYK	Yes	948.49	992.5	22.85	123.4	53.2	10326	ND	ND	No
NDKB	NIIHGSDSVK	Yes	357.19	333.2	7.44	47.1	21.8	61877	ND	ND	No
NDKB	NIIHGSDSVK	Yes	357.19	448.2	7.44	47.1	18.8	17914	ND	ND	No
NDKB	NIIHGSDSVK	Yes	357.19	592.3	7.44	47.1	21.8	109839	ND	ND	No
NDKB	NIIHGSDSVK	Yes	357.19	729.4	7.44	47.1	15.8	5021	ND	ND	No
NDKB	TFIAIKPDGVQR	Yes	672.89	433.2	12.59	87.8	35.1	17931	ND	ND	No
NDKB	TFIAIKPDGVQR	Yes	672.89	574.3	12.59	87.8	38.1	5174	ND	ND	No
NDKB	TFIAIKPDGVQR	Yes	672.89	799.4	12.59	87.8	35.1	9504	ND	ND	No
NDKB	TFIAIKPDGVQR	Yes	672.89	983.6	12.59	87.8	41.1	9191	ND	ND	No
NDUS1	FEAPLFNAR	Yes	532.78	277.1	16.55	69.7	22.9	400859	ND	ND	No
NDUS1	FEAPLFNAR	Yes	532.78	620.4	16.55	69.7	34.9	59944	ND	ND	No
NDUS1	FEAPLFNAR	Yes	532.78	717.4	16.55	69.7	25.9	186451	ND	ND	No
NDUS1	FEAPLFNAR	Yes	532.78	788.4	16.55	69.7	25.9	149875	ND	ND	No
NDUS1	ILQDIASGSHPFSQVLK	Yes	614	260.2	16.73	80.2	34.9	58074	ND	ND	No
NDUS1	ILQDIASGSHPFSQVLK	Yes	614	355.2	16.73	80.2	25.9	44616	ND	ND	No
NDUS1	ILQDIASGSHPFSQVLK	Yes	614	798.4	16.73	80.2	28.9	43598	ND	ND	No
NDUS1	ILQDIASGSHPFSQVLK	Yes	614	818.5	16.73	80.2	31.9	71281	ND	ND	No
NDUS1	LVNQQLLADPLVPPQLTIK	Yes	700.75	583.3	22.00	91.4	42.3	19647	ND	ND	No
NDUS1	LVNQQLLADPLVPPQLTIK	Yes	700.75	796.5	22.00	91.4	33.3	196921	ND	ND	No
NDUS1	LVNQQLLADPLVPPQLTIK	Yes	700.75	895.6	22.00	91.4	30.3	18233	ND	ND	No
NDUS1	LVNQQLLADPLVPPQLTIK	Yes	700.75	995.6	22.00	91.4	33.3	24154	ND	ND	No
NDUS1	NDGAAILAAVSSIAQK	Yes	764.92	358.1	21.61	99.7	39.2	9564	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
NDUS1	NDGAAILAAVSSIAQK	Yes	764.92	803.5	21.61	99.7	36.2	10046	ND	ND	No
NDUS1	NDGAAILAAVSSIAQK	Yes	764.92	874.5	21.61	99.7	36.2	11971	ND	ND	No
NDUS1	NDGAAILAAVSSIAQK	Yes	764.92	987.6	21.61	99.7	36.2	11525	ND	ND	No
NDUS1	SATYVNTEGR	Yes	549.26	260.1	7.00	71.9	29.7	22303	ND	ND	No
NDUS1	SATYVNTEGR	Yes	549.26	576.3	7.00	71.9	26.7	31630	ND	ND	No
NDUS1	SATYVNTEGR	Yes	549.26	675.3	7.00	71.9	26.7	24082	ND	ND	No
NDUS1	SATYVNTEGR	Yes	549.26	838.4	7.00	71.9	35.7	12690	ND	ND	No
NEBL	EPAVIGRPDFEHAVEASK	Yes	651.33	305.2	13.28	85	36.8	17500	ND	ND	No
NEBL	EPAVIGRPDFEHAVEASK	Yes	651.33	533.3	13.28	85	39.8	9949	ND	ND	No
NEBL	EPAVIGRPDFEHAVEASK	Yes	651.33	604.3	13.28	85	39.8	12040	ND	ND	No
NEBL	EPAVIGRPDFEHAVEASK	Yes	651.33	741.4	13.28	85	36.8	7302	ND	ND	No
NEBL	GFTPVVDDPVTER	No									
NEBL	GNAVLQSQVK	Yes	522.3	461.3	8.42	68.4	28.5	30077	ND	ND	No
NEBL	GNAVLQSQVK	Yes	522.3	589.3	8.42	68.4	25.5	38635	ND	ND	No
NEBL	GNAVLQSQVK	Yes	522.3	702.4	8.42	68.4	25.5	66022	ND	ND	No
NEBL	GNAVLQSQVK	Yes	522.3	801.5	8.42	68.4	25.5	28433	ND	ND	No
NEBL	NIGAFISEAK	Yes	525.29	434.2	15.00	68.8	34.6	173200	ND	ND	No
NEBL	NIGAFISEAK	Yes	525.29	547.3	15.00	68.8	34.6	89146	ND	ND	No
NEBL	NIGAFISEAK	Yes	525.29	694.4	15.00	68.8	25.6	106367	ND	ND	No
NEBL	NIGAFISEAK	Yes	525.29	822.4	15.00	68.8	25.6	546877	ND	ND	No
NEBL	TDPGSIFDLDPLEDNIQSR	Yes	1066.51	458.2	22.84	138.6	49.4	5076	ND	ND	No
NEBL	TDPGSIFDLDPLEDNIQSR	Yes	1066.51	571.3	22.84	138.6	49.4	15324	ND	ND	No
NEBL	TDPGSIFDLDPLEDNIQSR	Yes	1066.51	617.3	22.84	138.6	58.4	23221	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
NEBL	TDPGSIFDLDPLEDNIQSR	Yes	1066.51	718.3	22.84	138.6	49.4	6104	ND	ND	No
NEK4	DSVSDGFVQENQPR	Yes	789.36	272.2	10.99	102.8	37.2	57113	ND	ND	No
NEK4	DSVSDGFVQENQPR	Yes	789.36	514.3	10.99	102.8	46.2	10844	ND	ND	No
NEK4	DSVSDGFVQENQPR	Yes	789.36	643.3	10.99	102.8	46.2	10199	ND	ND	No
NEK4	DSVSDGFVQENQPR	Yes	789.36	870.4	10.99	102.8	37.2	17124	ND	ND	No
NEK4	DYSPELAELIR	Yes	653.34	366.1	19.23	85.3	28.2	116585	ND	ND	No
NEK4	DYSPELAELIR	Yes	653.34	601.4	19.23	85.3	40.2	74525	ND	ND	No
NEK4	DYSPELAELIR	Yes	653.34	714.5	19.23	85.3	37.2	82006	ND	ND	No
NEK4	DYSPELAELIR	Yes	653.34	940.5	19.23	85.3	31.2	76736	ND	ND	No
NEK4	GSYGEVTLVK	Yes	526.79	460.3	11.97	69	34.7	77566	ND	ND	No
NEK4	GSYGEVTLVK	Yes	526.79	559.4	11.97	69	25.7	92467	ND	ND	No
NEK4	GSYGEVTLVK	Yes	526.79	745.4	11.97	69	25.7	279011	ND	ND	No
NEK4	GSYGEVTLVK	Yes	526.79	908.5	11.97	69	25.7	30037	ND	ND	No
NEK4	LLGSSDSPASASR	Yes	624.32	588.3	8.62	81.5	36	62360	ND	ND	No
NEK4	LLGSSDSPASASR	Yes	624.32	675.3	8.62	81.5	39	62604	ND	ND	No
NEK4	LLGSSDSPASASR	Yes	624.32	790.4	8.62	81.5	30	26427	ND	ND	No
NEK4	LLGSSDSPASASR	Yes	624.32	877.4	8.62	81.5	30	27635	ND	ND	No
NEK4	VDVTSTQK	Yes	439.24	463.3	5.86	57.7	21.8	180833	ND	ND	No
NEK4	VDVTSTQK	Yes	439.24	564.3	5.86	57.7	21.8	541220	ND	ND	No
NEK4	VDVTSTQK	Yes	439.24	663.4	5.86	57.7	21.8	543235	ND	ND	No
NEK4	VDVTSTQK	Yes	439.24	778.4	5.86	57.7	21.8	413686	ND	ND	No
NET1	AGDWWK	Yes	381.68	333.2	13.78	50.2	25.3	80626	ND	ND	No
NET1	AGDWWK	Yes	381.68	519.3	13.78	50.2	19.3	39367	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
NET1	AGDWWK	Yes	381.68	634.3	13.78	50.2	19.3	12156	ND	ND	No
NET1	AGDWWK	Yes	381.68	691.3	13.78	50.2	19.3	85335	ND	ND	No
NET1	DSYFYAVSDLQVGGR	No									
NET1	FTVNIISVYK	No									
NET1	LHTFGDENEDDSELAR	No									
NET1	SSLVIQWR	Yes	494.78	361.2	16.56	64.8	21.3	7652	ND	ND	No
NET1	SSLVIQWR	Yes	494.78	387.2	16.56	64.8	24.3	14263	ND	ND	No
NET1	SSLVIQWR	Yes	494.78	602.3	16.56	64.8	24.3	38726	ND	ND	No
NET1	SSLVIQWR	Yes	494.78	701.4	16.56	64.8	24.3	18553	ND	ND	No
NEU2	LVQLAGAPEPFEPAQPDAY	Yes	1007	341.2	18.83	130.9	52.8	3883	ND	ND	No
NEU2	LVQLAGAPEPFEPAQPDAY	Yes	1007	465.2	18.83	130.9	46.8	15176	ND	ND	No
NEU2	LVQLAGAPEPFEPAQPDAY	Yes	1007	653.4	18.83	130.9	46.8	3746	ND	ND	No
NEU2	LVQLAGAPEPFEPAQPDAY	Yes	1007	761.3	18.83	130.9	43.8	5825	ND	ND	No
NEU2	SNATQLDGPAGALLLR	Yes	798.94	401.3	18.66	104.1	34.7	45122	ND	ND	No
NEU2	SNATQLDGPAGALLLR	Yes	798.94	615.3	18.66	104.1	37.7	45534	ND	ND	No
NEU2	SNATQLDGPAGALLLR	Yes	798.94	867.5	18.66	104.1	46.7	145625	ND	ND	No
NEU2	SNATQLDGPAGALLLR	Yes	798.94	982.6	18.66	104.1	37.7	107522	ND	ND	No
NGAL	ELTSELK	Yes	410.23	260.2	9.33	53.9	29.5	649692	ND	ND	No
NGAL	ELTSELK	Yes	410.23	389.2	9.33	53.9	20.5	230717	ND	ND	No
NGAL	ELTSELK	Yes	410.23	476.3	9.33	53.9	20.5	682034	ND	ND	No
NGAL	ELTSELK	Yes	410.23	577.3	9.33	53.9	20.5	811206	ND	ND	No
NGAL	ITLYGR	Yes	361.71	395.2	10.64	47.7	18.4	39689	ND	ND	No
NGAL	ITLYGR	Yes	361.71	491.3	10.64	47.7	24.4	2866	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
NGAL	ITLYGR	Yes	361.71	508.3	10.64	47.7	18.4	98226	ND	ND	No
NGAL	ITLYGR	Yes	361.71	609.3	10.64	47.7	18.4	50881	ND	ND	No
NGAL	SYPGLTSYLVR	Yes	628.34	550.3	18.02	82.1	39.1	18355	ND	ND	No
NGAL	SYPGLTSYLVR	Yes	628.34	738.4	18.02	82.1	36.1	65125	ND	ND	No
NGAL	SYPGLTSYLVR	Yes	628.34	851.5	18.02	82.1	33.1	17776	ND	ND	No
NGAL	SYPGLTSYLVR	Yes	628.34	908.5	18.02	82.1	39.1	50119	ND	ND	No
NGAL	VPLQQNFQDNQFQGK	Yes	895.94	438.3	12.97	116.6	44.9	5491	ND	ND	No
NGAL	VPLQQNFQDNQFQGK	Yes	895.94	479.3	12.97	116.6	50.9	11106	ND	ND	No
NGAL	VPLQQNFQDNQFQGK	Yes	895.94	566.3	12.97	116.6	47.9	4887	ND	ND	No
NGAL	VPLQQNFQDNQFQGK	Yes	895.94	836.4	12.97	116.6	44.9	4801	ND	ND	No
NGAL	WYVVGLAGNAILR	Yes	716.41	350.2	21.96	93.4	34	97641	23864	21069	No
NGAL	WYVVGLAGNAILR	Yes	716.41	643.4	21.96	93.4	34	32062	7911	9971	No
NGAL	WYVVGLAGNAILR	Yes	716.41	884.5	21.96	93.4	34	51419	10277	14447	No
NGAL	WYVVGLAGNAILR	Yes	716.41	983.6	21.96	93.4	34	33148	6913	8718	No
NGLY1	GDGDVAWQHTQLFR	No									
NGLY1	IGNTAFSTR	Yes	483.75	510.3	9.38	63.4	20.8	46783	ND	ND	No
NGLY1	IGNTAFSTR	Yes	483.75	581.3	9.38	63.4	26.8	20819	ND	ND	No
NGLY1	IGNTAFSTR	Yes	483.75	682.4	9.38	63.4	32.8	7014	ND	ND	No
NGLY1	IGNTAFSTR	Yes	483.75	853.4	9.38	63.4	23.8	12367	ND	ND	No
NGLY1	IIVELVEFISPK	No									
NGLY1	LLLTYADNILR	Yes	435.59	288.2	21.10	57.2	19.8	14741	123868	113087	Yes (Based on Transition Ratios)
NGLY1	LLLTYADNILR	Yes	435.59	401.3	21.10	57.2	22.8	8921	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
NGLY1	LLLTYADNILR	Yes	435.59	515.3	21.10	57.2	19.8	7709	ND	3260	Yes (Based on Transition Ratios)
NGLY1	LLLTYADNILR	Yes	435.59	630.4	21.10	57.2	22.8	9041	ND	ND	No
NGLY1	SSQQPAASTQLPTTPSSNPSGLNQHTR	No									
NHRF1	SVDPDSPAEASGLR	Yes	700.836	1099.5	9.43	100	36.3	ND	ND	ND	No
NHRF1	SVDPDSPAEASGLR	Yes	700.836	550.273	9.43	100	33.3	ND	ND	ND	No
NHRF1	SVDPDSPAEASGLR	Yes	700.836	800.427	9.43	100	39.3	ND	ND	ND	No
NHRF1	SVDPDSPAEASGLR	Yes	700.836	887.5	9.43	100	36.3	ND	ND	ND	No
NIBAN	EFPVYLWQPFFR	Yes	814.92	566.3	24.71	106.1	38.4	77046	ND	ND	No
NIBAN	EFPVYLWQPFFR	Yes	814.92	694.4	24.71	106.1	35.4	38075	ND	ND	No
NIBAN	EFPVYLWQPFFR	Yes	814.92	880.4	24.71	106.1	38.4	76940	ND	ND	No
NIBAN	EFPVYLWQPFFR	Yes	814.92	993.5	24.71	106.1	38.4	37236	ND	ND	No
NIBAN	EVNEVSQNFQTTK	Yes	762.37	343.2	9.94	99.3	39	41691	ND	ND	No
NIBAN	EVNEVSQNFQTTK	Yes	762.37	349.2	9.94	99.3	36	30530	ND	ND	No
NIBAN	EVNEVSQNFQTTK	Yes	762.37	472.2	9.94	99.3	36	30506	ND	ND	No
NIBAN	EVNEVSQNFQTTK	Yes	762.37	953.5	9.94	99.3	36	52687	ND	ND	No
NIBAN	GESLSLPGPSPPPDGTEQVIISR	No									
NIBAN	NDYAVESYENK	Yes	666.29	393.1	9.51	87	31.8	123387	ND	ND	No
NIBAN	NDYAVESYENK	Yes	666.29	769.3	9.51	87	31.8	83476	ND	ND	No
NIBAN	NDYAVESYENK	Yes	666.29	868.4	9.51	87	31.8	47674	ND	ND	No
NIBAN	NDYAVESYENK	Yes	666.29	939.4	9.51	87	31.8	47448	ND	ND	No
NIBAN	VLTSEDEYNLLSDR	Yes	827.4	377.2	16.01	107.7	38.9	141220	ND	ND	No
NIBAN	VLTSEDEYNLLSDR	Yes	827.4	490.3	16.01	107.7	38.9	48121	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
NIBAN	VLTSEDEYNLLSDR	Yes	827.4	717.4	16.01	107.7	38.9	31856	ND	ND	No
NIBAN	VLTSEDEYNLLSDR	Yes	827.4	880.5	16.01	107.7	47.9	32230	ND	ND	No
NMU	GYFLFRPR	No									
NMU	VDEEFQSPFASQSR	Yes	813.87	344.1	15.06	106	38.3	14010	ND	ND	No
NMU	VDEEFQSPFASQSR	Yes	813.87	477.2	15.06	106	41.3	15782	ND	ND	No
NMU	VDEEFQSPFASQSR	Yes	813.87	792.4	15.06	106	44.3	38143	ND	ND	No
NMU	VDEEFQSPFASQSR	Yes	813.87	879.4	15.06	106	38.3	26697	ND	ND	No
NRP1	EGNKPVLFQGNTNPTDVVVAVFPKPLITR	No									
NRP1	FVSDYETHGAGFSIR	Yes	562.6	650.4	14.03	73.6	35.2	18383	4524	6843	No
NRP1	FVSDYETHGAGFSIR	Yes	562.6	707.4	14.03	73.6	32.2	80267	21877	12713	No
NRP1	FVSDYETHGAGFSIR	Yes	562.6	844.4	14.03	73.6	35.2	28337	2003	8003	No
NRP1	FVSDYETHGAGFSIR	Yes	562.6	945.5	14.03	73.6	35.2	13737	2553	2171	No
NRP1	FVTAVGTQGAISK	Yes	639.86	348.2	11.03	83.5	30.7	135957	ND	ND	No
NRP1	FVTAVGTQGAISK	Yes	639.86	761.4	11.03	83.5	30.7	247503	ND	ND	No
NRP1	FVTAVGTQGAISK	Yes	639.86	860.5	11.03	83.5	30.7	79923	ND	ND	No
NRP1	FVTAVGTQGAISK	Yes	639.86	931.5	11.03	83.5	30.7	27622	ND	ND	No
NRP1	IESPGYLTSPGYPHSYHPSEK	Yes	1173.56	460.2	12.24	152.4	60.1	4288	ND	ND	No
NRP1	IESPGYLTSPGYPHSYHPSEK	Yes	1173.56	597.3	12.24	152.4	60.1	1700	ND	ND	No
NRP1	IESPGYLTSPGYPHSYHPSEK	Yes	1173.56	647.3	12.24	152.4	60.1	2065	ND	ND	No
NRP1	IESPGYLTSPGYPHSYHPSEK	Yes	1173.56	948.5	12.24	152.4	63.1	ND	ND	ND	No
NRP1	SFEGNNNYDTPELR	Yes	828.37	514.3	12.32	107.9	38.9	59545	41023	14610	No
NRP1	SFEGNNNYDTPELR	Yes	828.37	615.3	12.32	107.9	47.9	42045	21452	24182	No
NRP1	SFEGNNNYDTPELR	Yes	828.37	730.4	12.32	107.9	38.9	25260	17890	11653	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
NRP1	SFEGNNNYDTPELR	Yes	828.37	893.4	12.32	107.9	47.9	8328	2836	3516	No
ODAM	EAINFR	No									
ODAM	IIILLGFLGATLSAPLIPQR	No									
ODAM	SPQQTR	Yes	358.69	276.2	5.19	47.3	21.3	6724	ND	ND	No
ODAM	SPQQTR	Yes	358.69	404.2	5.19	47.3	27.3	9329	ND	ND	No
ODAM	SPQQTR	Yes	358.69	532.3	5.19	47.3	21.3	14966	ND	ND	No
ODAM	SPQQTR	Yes	358.69	629.3	5.19	47.3	15.3	681	ND	ND	No
OSTP	AIPVAQDLNAPSDWDSR	Yes	618.97	262.2	16.26	80.8	38.1	97920	14649	ND	No
OSTP	AIPVAQDLNAPSDWDSR	Yes	618.97	563.3	16.26	80.8	38.1	24744	ND	ND	No
OSTP	AIPVAQDLNAPSDWDSR	Yes	618.97	765.3	16.26	80.8	32.1	23711	ND	ND	No
OSTP	AIPVAQDLNAPSDWDSR	Yes	618.97	862.4	16.26	80.8	29.1	55163	4282	ND	No
OSTP	DSYETSQLDDQSAETHSHK	Yes	726.65	284.2	7.96	94.7	43.6	2533	ND	ND	No
OSTP	DSYETSQLDDQSAETHSHK	Yes	726.65	371.2	7.96	94.7	37.6	3122	ND	ND	No
OSTP	DSYETSQLDDQSAETHSHK	Yes	726.65	495.2	7.96	94.7	31.6	3085	ND	ND	No
OSTP	DSYETSQLDDQSAETHSHK	Yes	726.65	609.3	7.96	94.7	37.6	2552	ND	ND	No
OSTP	GDSVVYGLR	No									
OSTP	ISHELDSASSEVN	No									
OSTP	YPDAVATWLNPDPSQK	Yes	901.44	459.3	19.07	117.3	48.2	69608	ND	ND	No
OSTP	YPDAVATWLNPDPSQK	Yes	901.44	546.3	19.07	117.3	42.2	15034	ND	ND	No
OSTP	YPDAVATWLNPDPSQK	Yes	901.44	671.3	19.07	117.3	51.2	22155	ND	ND	No
OSTP	YPDAVATWLNPDPSQK	Yes	901.44	785.4	19.07	117.3	48.2	16750	ND	ND	No
OVOS2	DGEAFLLTN	No									
OVOS2	QGVLDLPNDVVEGSAR	Yes	834.93	285.2	17.63	108.7	45.2	35055	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
OVOS2	QGVLDLPNDVVEGSAR	Yes	834.93	390.2	17.63	108.7	48.2	13179	ND	ND	No
OVOS2	QGVLDLPNDVVEGSAR	Yes	834.93	513.3	17.63	108.7	39.2	8670	ND	ND	No
OVOS2	QGVLDLPNDVVEGSAR	Yes	834.93	626.4	17.63	108.7	36.2	9404	ND	ND	No
OVOS2	SDPLAFITFSAK	Yes	648.85	553.3	22.26	84.7	37	146280	ND	ND	No
OVOS2	SDPLAFITFSAK	Yes	648.85	813.5	22.26	84.7	31	359115	ND	ND	No
OVOS2	SDPLAFITFSAK	Yes	648.85	884.5	22.26	84.7	31	359408	ND	ND	No
OVOS2	SDPLAFITFSAK	Yes	648.85	997.6	22.26	84.7	34	73547	ND	ND	No
OVOS2	SEVTQAPGQYTVDVEGR	Yes	918.44	417.2	12.07	119.5	51.9	3914	ND	ND	No
OVOS2	SEVTQAPGQYTVDVEGR	Yes	918.44	460.3	12.07	119.5	51.9	10633	ND	ND	No
OVOS2	SEVTQAPGQYTVDVEGR	Yes	918.44	545.3	12.07	119.5	39.9	4741	ND	ND	No
OVOS2	SEVTQAPGQYTVDVEGR	Yes	918.44	616.3	12.07	119.5	39.9	26936	ND	ND	No
OVOS2	SFLVEPEGIEK	Yes	624.33	575.3	15.53	81.5	39	76355	ND	ND	No
OVOS2	SFLVEPEGIEK	Yes	624.33	672.4	15.53	81.5	30	952898	ND	ND	No
OVOS2	SFLVEPEGIEK	Yes	624.33	801.4	15.53	81.5	30	912815	ND	ND	No
OVOS2	SFLVEPEGIEK	Yes	624.33	900.5	15.53	81.5	30	672187	ND	ND	No
P5CS	DHVVSDFSEHGSLK	Yes	519.58	253.1	10.26	68	33	288139	ND	ND	No
P5CS	DHVVSDFSEHGSLK	Yes	519.58	352.2	10.26	68	33	98711	ND	ND	No
P5CS	DHVVSDFSEHGSLK	Yes	519.58	541.3	10.26	68	33	34055	ND	ND	No
P5CS	DHVVSDFSEHGSLK	Yes	519.58	653.3	10.26	68	27	36704	ND	ND	No
P5CS	FGLGAEVGISTSR	Yes	647.34	450.2	15.49	84.5	31	16100	ND	ND	No
P5CS	FGLGAEVGISTSR	Yes	647.34	620.3	15.49	84.5	31	34634	ND	ND	No
P5CS	FGLGAEVGISTSR	Yes	647.34	719.4	15.49	84.5	31	16461	ND	ND	No
P5CS	FGLGAEVGISTSR	Yes	647.34	919.5	15.49	84.5	28	ND	ND	ND	Yes (Based on

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
											Manual Review)
P5CS	GPVGLEGLLTTK	Yes	592.85	632.4	19.17	77.5	28.6	557712	ND	ND	No
P5CS	GPVGLEGLLTTK	Yes	592.85	761.4	19.17	77.5	28.6	802638	ND	ND	No
P5CS	GPVGLEGLLTTK	Yes	592.85	874.5	19.17	77.5	31.6	271923	ND	ND	No
P5CS	GPVGLEGLLTTK	Yes	592.85	931.5	19.17	77.5	28.6	930057	ND	ND	No
P5CS	HEILLSQSVR	No									
P5CS	ILHLLTQEALSIHGVK	Yes	591.35	364.2	17.71	77.3	36.7	34179	ND	ND	No
P5CS	ILHLLTQEALSIHGVK	Yes	591.35	640.4	17.71	77.3	30.7	17433	ND	ND	No
P5CS	ILHLLTQEALSIHGVK	Yes	591.35	753.5	17.71	77.3	30.7	14360	ND	ND	No
P5CS	ILHLLTQEALSIHGVK	Yes	591.35	953.5	17.71	77.3	30.7	2996	ND	ND	No
PA2GX	No peptide										
PAPP1	DIPHWLNPTR	Yes	416.89	373.2	16.11	54.8	21.8	73464	ND	ND	No
PAPP1	DIPHWLNPTR	Yes	416.89	487.3	16.11	54.8	27.8	22898	ND	ND	No
PAPP1	DIPHWLNPTR	Yes	416.89	600.3	16.11	54.8	27.8	35736	ND	ND	No
PAPP1	DIPHWLNPTR	Yes	416.89	786.4	16.11	54.8	24.8	49607	ND	ND	No
PAPP1	EQVDFQHHQLAEAFK	Yes	609.63	365.2	13.37	79.6	34.6	29972	ND	ND	No
PAPP1	EQVDFQHHQLAEAFK	Yes	609.63	565.3	13.37	79.6	34.6	13678	ND	ND	No
PAPP1	EQVDFQHHQLAEAFK	Yes	609.63	678.4	13.37	79.6	31.6	43407	ND	ND	No
PAPP1	EQVDFQHHQLAEAFK	Yes	609.63	806.4	13.37	79.6	31.6	8782	ND	ND	No
PAPP1	GYIEHFSLWK	Yes	640.33	333.2	18.45	83.6	36.7	16491	ND	ND	No
PAPP1	GYIEHFSLWK	Yes	640.33	747.3	18.45	83.6	39.7	4146	ND	ND	No
PAPP1	GYIEHFSLWK	Yes	640.33	817.4	18.45	83.6	30.7	10715	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PAPP1	GYIEHFSLWK	Yes	640.33	946.5	18.45	83.6	30.7	6842	ND	ND	No
PAPP1	LDGSTHLNIFFAK	Yes	488.26	365.2	18.30	64	31.5	94625	ND	ND	No
PAPP1	LDGSTHLNIFFAK	Yes	488.26	512.3	18.30	64	25.5	30804	ND	ND	No
PAPP1	LDGSTHLNIFFAK	Yes	488.26	838.4	18.30	64	31.5	25195	ND	ND	No
PAPP1	LDGSTHLNIFFAK	Yes	488.26	852.5	18.30	64	25.5	30991	ND	ND	No
PAPP1	VSFSSPLVAISGVALR	Yes	801.96	288.2	24.95	104.5	40.8	ND	ND	ND	No
PAPP1	VSFSSPLVAISGVALR	Yes	801.96	602.4	24.95	104.5	34.8	60724	ND	ND	No
PAPP1	VSFSSPLVAISGVALR	Yes	801.96	715.4	24.95	104.5	34.8	5656	ND	ND	No
PAPP1	VSFSSPLVAISGVALR	Yes	801.96	885.6	24.95	104.5	46.8	ND	ND	ND	No
PBIP1	ALESELQQLR	Yes	593.83	544.3	14.76	77.6	28.6	11154	ND	ND	No
PBIP1	ALESELQQLR	Yes	593.83	657.4	14.76	77.6	28.6	7259	ND	ND	No
PBIP1	ALESELQQLR	Yes	593.83	786.4	14.76	77.6	37.6	2674	ND	ND	No
PBIP1	ALESELQQLR	Yes	593.83	873.5	14.76	77.6	28.6	7691	ND	ND	No
PBIP1	ELPLSPAFFGEDGIFR	Yes	897.96	492.3	24.53	116.8	51	16553	ND	ND	No
PBIP1	ELPLSPAFFGEDGIFR	Yes	897.96	540.3	24.53	116.8	39	13446	ND	ND	No
PBIP1	ELPLSPAFFGEDGIFR	Yes	897.96	793.4	24.53	116.8	39	8678	ND	ND	No
PBIP1	ELPLSPAFFGEDGIFR	Yes	897.96	940.5	24.53	116.8	51	8188	ND	ND	No
PBIP1	EQEPELSFLK	Yes	610.31	407.3	17.31	79.7	29.4	114645	ND	ND	No
PBIP1	EQEPELSFLK	Yes	610.31	494.3	17.31	79.7	29.4	326100	ND	ND	No
PBIP1	EQEPELSFLK	Yes	610.31	833.5	17.31	79.7	29.4	681027	ND	ND	No
PBIP1	EQEPELSFLK	Yes	610.31	962.5	17.31	79.7	29.4	101819	ND	ND	No
PBIP1	GLEEENAQLR	No									
PBIP1	QEGLTFFGTELAPVR	Yes	832.94	371.2	21.75	108.4	36.1	50931	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
PBIP1	QEGLTFFGTELAPVR	Yes	832.94	428.2	21.75	108.4	39.1	13780	ND	ND	No
PBIP1	QEGLTFFGTELAPVR	Yes	832.94	442.3	21.75	108.4	36.1	20449	ND	ND	No
PBIP1	QEGLTFFGTELAPVR	Yes	832.94	989.5	21.75	108.4	39.1	25248	ND	ND	No
PCBP1	IANPVEGSSGR	Yes	543.78	463.2	8.18	71.1	35.4	38807	ND	ND	No
PCBP1	IANPVEGSSGR	Yes	543.78	592.3	8.18	71.1	35.4	39923	ND	ND	No
PCBP1	IANPVEGSSGR	Yes	543.78	788.4	8.18	71.1	26.4	71183	ND	ND	No
PCBP1	IANPVEGSSGR	Yes	543.78	902.4	8.18	71.1	35.4	7159	ND	ND	No
PCBP1	IITLTGPTNAIFK	Yes	694.91	328.2	19.52	90.6	33.1	171448	ND	ND	No
PCBP1	IITLTGPTNAIFK	Yes	694.91	790.4	19.52	90.6	33.1	86054	ND	ND	No
PCBP1	IITLTGPTNAIFK	Yes	694.91	847.5	19.52	90.6	33.1	179906	ND	ND	No
PCBP1	IITLTGPTNAIFK	Yes	694.91	948.5	19.52	90.6	33.1	119050	ND	ND	No
PCBP1	LNQVAR	Yes	350.71	455.3	5.74	46.2	23.9	9171	ND	ND	No
PCBP1	LNQVAR	Yes	350.71	473.3	5.74	46.2	17.9	96915	ND	ND	No
PCBP1	LNQVAR	Yes	350.71	526.3	5.74	46.2	17.9	1568	ND	ND	No
PCBP1	LNQVAR	Yes	350.71	587.3	5.74	46.2	20.9	93199	ND	ND	No
PCBP1	QGANINEIR	Yes	507.77	288.2	9.04	66.5	30.8	40412	ND	ND	No
PCBP1	QGANINEIR	Yes	507.77	417.2	9.04	66.5	24.8	10102	ND	ND	No
PCBP1	QGANINEIR	Yes	507.77	531.3	9.04	66.5	24.8	41668	ND	ND	No
PCBP1	QGANINEIR	Yes	507.77	644.4	9.04	66.5	27.8	10179	ND	ND	No
PCBP1	QVTITGSAASISLAQYLINAR	No									
PCBP2	AFAMIIDK	Yes	454.75	375.2	17.33	59.7	31.5	1699101	ND	ND	No
PCBP2	AFAMIIDK	Yes	454.75	488.3	17.33	59.7	25.5	641239	ND	ND	No
PCBP2	AFAMIIDK	Yes	454.75	619.3	17.33	59.7	22.5	1079234	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
PCBP2	AFAMIIDK	Yes	454.75	690.4	17.33	59.7	22.5	5406799	ND	ND	No
PCBP2	ESTGAQVQVAGDMLPNSTER	Yes	697.33	492.2	15.07	91	42.1	32411	ND	ND	No
PCBP2	ESTGAQVQVAGDMLPNSTER	Yes	697.33	801.4	15.07	91	42.1	23679	ND	ND	No
PCBP2	ESTGAQVQVAGDMLPNSTER	Yes	697.33	816.4	15.07	91	36.1	65077	ND	ND	No
PCBP2	ESTGAQVQVAGDMLPNSTER	Yes	697.33	947.5	15.07	91	36.1	15932	ND	ND	No
PCBP2	GVTIPYRPKPSSSPVIFAGGQDR	Yes	810.44	258.1	16.00	105.5	47.9	361948	ND	ND	No
PCBP2	GVTIPYRPKPSSSPVIFAGGQDR	Yes	810.44	532.2	16.00	105.5	41.9	118659	ND	ND	No
PCBP2	GVTIPYRPKPSSSPVIFAGGQDR	Yes	810.44	750.4	16.00	105.5	47.9	243287	ND	ND	No
PCBP2	GVTIPYRPKPSSSPVIFAGGQDR	Yes	810.44	863.4	16.00	105.5	44.9	124871	ND	ND	No
PCBP2	IANPVEGSTDR	Yes	579.79	535.2	9.91	75.8	37	623599	ND	ND	No
PCBP2	IANPVEGSTDR	Yes	579.79	664.3	9.91	75.8	37	638618	ND	ND	No
PCBP2	IANPVEGSTDR	Yes	579.79	860.4	9.91	75.8	31	1272109	ND	ND	No
PCBP2	IANPVEGSTDR	Yes	579.79	974.5	9.91	75.8	31	207583	ND	ND	No
PCBP2	IITLAGPTNAIFK	Yes	679.91	328.2	21.05	88.7	35.4	530954	ND	ND	No
PCBP2	IITLAGPTNAIFK	Yes	679.91	790.4	21.05	88.7	29.4	321938	ND	ND	No
PCBP2	IITLAGPTNAIFK	Yes	679.91	847.5	21.05	88.7	32.4	1030637	ND	ND	No
PCBP2	IITLAGPTNAIFK	Yes	679.91	918.5	21.05	88.7	41.4	338418	ND	ND	No
PCBP2	LHQLAMQQSHFPMTHGNTGFSGIESSSPEVK	No									
PCBP2	LSSETGGMGSS	No									
PCBP2	MDTGVIEGGLNVTLTIR	No									
PCBP2	QMSGAQIK	Yes	431.73	388.3	7.89	56.7	21.5	39309	ND	ND	No
PCBP2	QMSGAQIK	Yes	431.73	459.3	7.89	56.7	21.5	25250	ND	ND	No
PCBP2	QMSGAQIK	Yes	431.73	475.2	7.89	56.7	30.5	10236	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PCBP2	QMSGAQIK	Yes	431.73	516.3	7.89	56.7	21.5	59837	ND	3695	No
PCBP2	QVTITGSAASISLAQYLINVR	No									
PCD15	EGDSITYAIENGDPQR	Yes	882.91	400.2	13.81	114.9	47.3	55698	ND	ND	No
PCD15	EGDSITYAIENGDPQR	Yes	882.91	815.4	13.81	114.9	38.3	15432	ND	ND	No
PCD15	EGDSITYAIENGDPQR	Yes	882.91	928.4	13.81	114.9	38.3	10348	ND	ND	No
PCD15	EGDSITYAIENGDPQR	Yes	882.91	999.5	13.81	114.9	50.3	13094	ND	ND	No
PCD15	GGPPATIVAIDEESR	No									
PCD15	GTAGGPDPTIELSLK	Yes	728.39	347.2	15.68	95	34.5	92553	ND	ND	No
PCD15	GTAGGPDPTIELSLK	Yes	728.39	556.2	15.68	95	34.5	69295	ND	ND	No
PCD15	GTAGGPDPTIELSLK	Yes	728.39	589.4	15.68	95	43.5	78485	ND	ND	No
PCD15	GTAGGPDPTIELSLK	Yes	728.39	900.5	15.68	95	40.5	132716	ND	ND	No
PCD15	VGAVLLNLQATDR	Yes	685.39	440.3	16.65	89.4	32.7	10602	ND	ND	No
PCD15	VGAVLLNLQATDR	Yes	685.39	462.2	16.65	89.4	29.7	7805	ND	ND	No
PCD15	VGAVLLNLQATDR	Yes	685.39	817.4	16.65	89.4	32.7	14452	ND	ND	No
PCD15	VGAVLLNLQATDR	Yes	685.39	930.5	16.65	89.4	38.7	9159	ND	ND	No
PCD15	VQADSLEVVLANLR	Yes	763.93	473.3	23.58	99.5	33.1	22872	ND	ND	No
PCD15	VQADSLEVVLANLR	Yes	763.93	685.4	23.58	99.5	36.1	19802	ND	ND	No
PCD15	VQADSLEVVLANLR	Yes	763.93	784.5	23.58	99.5	45.1	22637	ND	ND	No
PCD15	VQADSLEVVLANLR	Yes	763.93	913.5	23.58	99.5	42.1	20899	ND	ND	No
PCNA	IEDEEGS	No									
PCNA	LSQTSNVDK	Yes	496.26	562.3	5.67	65	24.3	82978	ND	ND	No
PCNA	LSQTSNVDK	Yes	496.26	663.3	5.67	65	27.3	171780	ND	ND	No
PCNA	LSQTSNVDK	Yes	496.26	791.4	5.67	65	21.3	105708	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
PCNA	LSQTSNVDK	Yes	496.26	878.4	5.67	65	24.3	121975	ND	ND	No
PCNA	SEGFDTYR	Yes	487.71	439.2	9.61	63.9	24	6452	ND	ND	No
PCNA	SEGFDTYR	Yes	487.71	554.3	9.61	63.9	24	15037	ND	ND	No
PCNA	SEGFDTYR	Yes	487.71	701.3	9.61	63.9	27	4249	ND	ND	No
PCNA	SEGFDTYR	Yes	487.71	758.3	9.61	63.9	24	39400	ND	ND	No
PCNA	YLNFFTK	Yes	466.75	395.2	18.02	61.2	29	252908	ND	ND	No
PCNA	YLNFFTK	Yes	466.75	542.3	18.02	61.2	23	104995	ND	ND	No
PCNA	YLNFFTK	Yes	466.75	656.3	18.02	61.2	23	758229	5306	6853	No
PCNA	YLNFFTK	Yes	466.75	769.4	18.02	61.2	23	260631	ND	ND	No
PCNA	YYLAPK	Yes	377.71	315.2	9.26	49.7	19.1	195800	ND	ND	No
PCNA	YYLAPK	Yes	377.71	327.1	9.26	49.7	19.1	285437	ND	ND	No
PCNA	YYLAPK	Yes	377.71	428.3	9.26	49.7	19.1	559321	ND	ND	No
PCNA	YYLAPK	Yes	377.71	591.4	9.26	49.7	19.1	223250	ND	ND	No
PCYOX	FGLNTVLTTDNSDLFINSIGIVPSVR	No									
PCYOX	IAIIGAGIGGTSAAYYLR	Yes	883.99	298.2	20.05	115	41.4	69304	ND	ND	No
PCYOX	IAIIGAGIGGTSAAYYLR	Yes	883.99	596.4	20.05	115	41.4	45014	ND	ND	No
PCYOX	IAIIGAGIGGTSAAYYLR	Yes	883.99	709.5	20.05	115	38.4	26627	ND	ND	No
PCYOX	IAIIGAGIGGTSAAYYLR	Yes	883.99	843.4	20.05	115	47.4	8662	ND	ND	No
PCYOX	IFSQETLTK	Yes	533.79	591.3	11.26	69.9	35	39764	ND	ND	No
PCYOX	IFSQETLTK	Yes	533.79	719.4	11.26	69.9	26	31413	ND	ND	No
PCYOX	IFSQETLTK	Yes	533.79	806.4	11.26	69.9	26	240664	ND	ND	No
PCYOX	IFSQETLTK	Yes	533.79	953.5	11.26	69.9	26	49035	ND	ND	No
PCYOX	TLLETLQK	Yes	473.28	388.3	14.08	62.1	32.3	136984	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
PCYOX	TLLETLQK	Yes	473.28	618.3	14.08	62.1	23.3	295250	ND	ND	No
PCYOX	TLLETLQK	Yes	473.28	731.4	14.08	62.1	23.3	816104	ND	ND	No
PCYOX	TLLETLQK	Yes	473.28	844.5	14.08	62.1	23.3	23169	ND	ND	No
PCYOX	YQSHDYAFSSVEK	Yes	780.85	276.2	10.84	101.7	39.9	6497	ND	ND	No
PCYOX	YQSHDYAFSSVEK	Yes	780.85	292.1	10.84	101.7	39.9	6097	ND	ND	No
PCYOX	YQSHDYAFSSVEK	Yes	780.85	549.3	10.84	101.7	45.9	3721	ND	ND	No
PCYOX	YQSHDYAFSSVEK	Yes	780.85	930.5	10.84	101.7	45.9	ND	ND	ND	No
PDGFA	AHGVHATK	Yes	410.73	456.3	5.20	54	23.6	11852	ND	ND	No
PDGFA	AHGVHATK	Yes	410.73	573.3	5.20	54	23.6	13652	ND	ND	No
PDGFA	AHGVHATK	Yes	410.73	612.3	5.20	54	20.6	74747	ND	ND	No
PDGFA	AHGVHATK	Yes	410.73	674.3	5.20	54	20.6	6794	ND	ND	No
PDGFA	EEDTGRPR	No									
PDGFA	LLEIDSVGSEDSLDTSLR	Yes	974.99	356.2	18.06	126.8	48.4	30483	ND	ND	No
PDGFA	LLEIDSVGSEDSLDTSLR	Yes	974.99	476.3	18.06	126.8	54.4	17173	ND	ND	No
PDGFA	LLEIDSVGSEDSLDTSLR	Yes	974.99	591.3	18.06	126.8	45.4	6990	ND	ND	No
PDGFA	LLEIDSVGSEDSLDTSLR	Yes	974.99	791.4	18.06	126.8	54.4	11102	ND	ND	No
PDGFA	SQIHSIR	Yes	420.74	375.2	6.31	55.3	27	13144	ND	ND	No
PDGFA	SQIHSIR	Yes	420.74	512.3	6.31	55.3	24	16567	ND	ND	No
PDGFA	SQIHSIR	Yes	420.74	553.3	6.31	55.3	21	3071	3920	909	No
PDGFA	SQIHSIR	Yes	420.74	625.4	6.31	55.3	24	70712	26727	10148	No
PDGFA	TVIYEIPR	Yes	495.78	272.2	13.59	65	33.3	20672	ND	ND	No
PDGFA	TVIYEIPR	Yes	495.78	385.3	13.59	65	30.3	22678	ND	ND	No
PDGFA	TVIYEIPR	Yes	495.78	677.4	13.59	65	27.3	50856	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PDGFA	TVIYEIPR	Yes	495.78	790.4	13.59	65	24.3	55777	ND	ND	No
PDGFB	SFDDLQR	Yes	440.71	416.3	9.91	57.9	27.9	86177	ND	ND	No
PDGFB	SFDDLQR	Yes	440.71	531.3	9.91	57.9	21.9	52020	ND	ND	No
PDGFB	SFDDLQR	Yes	440.71	646.3	9.91	57.9	21.9	207193	ND	ND	No
PDGFB	SFDDLQR	Yes	440.71	793.4	9.91	57.9	30.9	4627	ND	ND	No
PDGFB	SHSGGELESLAR	Yes	414.87	446.3	10.25	54.5	18.7	258539	4665	7528	No
PDGFB	SHSGGELESLAR	Yes	414.87	555.2	10.25	54.5	18.7	210218	7001	4754	No
PDGFB	SHSGGELESLAR	Yes	414.87	575.3	10.25	54.5	18.7	109583	2142	4831	No
PDGFB	SHSGGELESLAR	Yes	414.87	668.3	10.25	54.5	18.7	72419	2831	1902	No
PDGFB	SPGGSQEQR	Yes	473.22	303.2	5.24	62	29.3	22973	ND	ND	No
PDGFB	SPGGSQEQR	Yes	473.22	647.3	5.24	62	23.3	3409	ND	ND	No
PDGFB	SPGGSQEQR	Yes	473.22	704.3	5.24	62	23.3	5151	ND	ND	No
PDGFB	SPGGSQEQR	Yes	473.22	761.4	5.24	62	29.3	56927	ND	ND	No
PDGFD	DTSATPQSASIK	Yes	603.3	476.2	6.98	78.8	26	280068	ND	ND	No
PDGFD	DTSATPQSASIK	Yes	603.3	730.4	6.98	78.8	29	519466	ND	ND	No
PDGFD	DTSATPQSASIK	Yes	603.3	831.5	6.98	78.8	29	205056	ND	ND	No
PDGFD	DTSATPQSASIK	Yes	603.3	989.5	6.98	78.8	29	80896	ND	ND	No
PDGFD	GNGYVQSPR	No									
PDGFD	LANVVFFPR	Yes	531.81	566.3	18.36	69.6	25.9	81235	ND	ND	No
PDGFD	LANVVFFPR	Yes	531.81	665.4	18.36	69.6	25.9	83697	ND	ND	No
PDGFD	LANVVFFPR	Yes	531.81	791.4	18.36	69.6	25.9	ND	ND	ND	No
PDGFD	LANVVFFPR	Yes	531.81	878.5	18.36	69.6	22.9	23640	ND	ND	No
PDGFD	SDDYFVAKPGFK	Yes	687.34	448.3	13.08	89.7	41.7	379278	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PDGFD	SDDYFVAKPGFK	Yes	687.34	647.4	13.08	89.7	35.7	90388	ND	ND	No
PDGFD	SDDYFVAKPGFK	Yes	687.34	746.5	13.08	89.7	35.7	120129	ND	ND	No
PDGFD	SDDYFVAKPGFK	Yes	687.34	893.5	13.08	89.7	35.7	64255	ND	ND	No
PDGFD	YDFVEVEDISETSTIIR	No									
PDIA3	DPNIVIAK	Yes	435.26	327.1	10.38	57.1	24.7	71278	ND	ND	No
PDIA3	DPNIVIAK	Yes	435.26	331.2	10.38	57.1	24.7	102404	ND	ND	No
PDIA3	DPNIVIAK	Yes	435.26	543.4	10.38	57.1	24.7	31792	ND	ND	No
PDIA3	DPNIVIAK	Yes	435.26	657.4	10.38	57.1	21.7	47949	ND	ND	No
PDIA3	ELSDFISYLQR	Yes	685.85	416.3	21.41	89.5	29.7	31061	4631	5077	No
PDIA3	ELSDFISYLQR	Yes	685.85	579.3	21.41	89.5	29.7	28683	4721	9583	No
PDIA3	ELSDFISYLQR	Yes	685.85	779.4	21.41	89.5	29.7	57622	11620	15477	No
PDIA3	ELSDFISYLQR	Yes	685.85	926.5	21.41	89.5	41.7	23290	5200	5652	No
PDIA3	FAHTNVESLVNEYDDNGEGIILFRPSHLTNK	No									
PDIA3	SEPIPESNDGPVK	Yes	684.84	314.1	9.23	89.3	32.6	395195	ND	ND	No
PDIA3	SEPIPESNDGPVK	Yes	684.84	400.3	9.23	89.3	41.6	200287	ND	ND	No
PDIA3	SEPIPESNDGPVK	Yes	684.84	427.2	9.23	89.3	29.6	345793	ND	ND	No
PDIA3	SEPIPESNDGPVK	Yes	684.84	942.5	9.23	89.3	32.6	445313	ND	ND	No
PDIA3	TVAYTEQK	Yes	470.24	505.3	6.22	61.7	26.2	96506	ND	ND	No
PDIA3	TVAYTEQK	Yes	470.24	668.3	6.22	61.7	23.2	96210	ND	ND	No
PDIA3	TVAYTEQK	Yes	470.24	739.4	6.22	61.7	23.2	727437	ND	ND	No
PDIA3	TVAYTEQK	Yes	470.24	838.4	6.22	61.7	20.2	12172	ND	ND	No
PDIA4	EENGVLVLNDANFDNFVADK	No									
PDIA4	EVSQPDWTPPPEVTLVLTK	No									

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
PDIA4	FDVSGYPTIK	Yes	563.79	458.3	14.32	73.7	36.3	650272	16222	28395	No
PDIA4	FDVSGYPTIK	Yes	563.79	678.4	14.32	73.7	27.3	220607	53579	45605	Yes (Based on Transition Ratios)
PDIA4	FDVSGYPTIK	Yes	563.79	765.4	14.32	73.7	27.3	651232	9515	9889	Yes (Based on Transition Ratios)
PDIA4	FDVSGYPTIK	Yes	563.79	864.5	14.32	73.7	27.3	255678	12697	21505	No
PDIA4	FHHTFSTEIAK	Yes	439.89	285.1	9.44	57.7	29	84563	5931	9235	No
PDIA4	FHHTFSTEIAK	Yes	439.89	460.3	9.44	57.7	23	25165	ND	ND	No
PDIA4	FHHTFSTEIAK	Yes	439.89	561.3	9.44	57.7	23	41636	ND	ND	No
PDIA4	FHHTFSTEIAK	Yes	439.89	648.4	9.44	57.7	20	60091	4621	3895	No
PDIA4	FIEEHATK	Yes	487.75	456.3	6.56	63.9	30	ND	3464	3956	Yes (Based on Manual Review)
PDIA4	FIEEHATK	Yes	487.75	585.3	6.56	63.9	27	46431	1854	ND	No
PDIA4	FIEEHATK	Yes	487.75	714.3	6.56	63.9	24	211267	2232	924	No
PDIA4	FIEEHATK	Yes	487.75	827.4	6.56	63.9	24	31880	ND	ND	No
PDIA6	GESPVDYDGGR	Yes	576.25	682.3	8.36	75.3	33.9	3571	ND	ND	No
PDIA6	GESPVDYDGGR	Yes	576.25	781.3	8.36	75.3	33.9	2138	ND	ND	No
PDIA6	GESPVDYDGGR	Yes	576.25	878.4	8.36	75.3	24.9	2862	ND	ND	No
PDIA6	GESPVDYDGGR	Yes	576.25	965.4	8.36	75.3	30.9	ND	ND	ND	No
PDIA6	HHSLGGQYGVQGFPTIK	Yes	609.32	458.3	14.15	79.6	37.6	70364	ND	ND	No
PDIA6	HHSLGGQYGVQGFPTIK	Yes	609.32	662.4	14.15	79.6	28.6	53209	ND	ND	No
PDIA6	HHSLGGQYGVQGFPTIK	Yes	609.32	717.3	14.15	79.6	31.6	38917	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PDIA6	HHSLGGQYGVQGFPTIK	Yes	609.32	790.4	14.15	79.6	28.6	38280	ND	ND	No
PDIA6	NLEPEWAAAASEVK	Yes	757.88	357.2	16.69	98.8	32.8	66832	ND	ND	No
PDIA6	NLEPEWAAAASEVK	Yes	757.88	533.3	16.69	98.8	41.8	5852	ND	ND	No
PDIA6	NLEPEWAAAASEVK	Yes	757.88	675.4	16.69	98.8	44.8	10088	ND	ND	No
PDIA6	NLEPEWAAAASEVK	Yes	757.88	932.5	16.69	98.8	44.8	5699	ND	ND	No
PDIA6	NRPEDYQGGR	Yes	596.28	271.2	5.56	77.9	34.7	7849	ND	ND	No
PDIA6	NRPEDYQGGR	Yes	596.28	497.2	5.56	77.9	34.7	2458	ND	ND	No
PDIA6	NRPEDYQGGR	Yes	596.28	695.3	5.56	77.9	34.7	ND	ND	ND	No
PDIA6	NRPEDYQGGR	Yes	596.28	921.4	5.56	77.9	37.7	8051	ND	ND	No
PDIA6	NSYLEVLLK	Yes	539.81	472.3	20.20	70.6	32.3	28962	ND	ND	No
PDIA6	NSYLEVLLK	Yes	539.81	601.4	20.20	70.6	26.3	68882	ND	ND	No
PDIA6	NSYLEVLLK	Yes	539.81	714.5	20.20	70.6	26.3	113961	ND	ND	No
PDIA6	NSYLEVLLK	Yes	539.81	877.5	20.20	70.6	23.3	71864	ND	ND	No
PECA1	DQNFVILEFPVEEQDR	Yes	989.48	358.1	22.19	128.6	55	5273	ND	ND	No
PECA1	DQNFVILEFPVEEQDR	Yes	989.48	505.2	22.19	128.6	43	5017	ND	ND	No
PECA1	DQNFVILEFPVEEQDR	Yes	989.48	604.3	22.19	128.6	43	4604	ND	ND	No
PECA1	DQNFVILEFPVEEQDR	Yes	989.48	872.4	22.19	128.6	46	6153	ND	ND	No
PECA1	EDTIVSQTQDFTK	Yes	756.37	346.1	13.27	98.6	41.8	17231	ND	ND	No
PECA1	EDTIVSQTQDFTK	Yes	756.37	510.3	13.27	98.6	44.8	3848	ND	ND	No
PECA1	EDTIVSQTQDFTK	Yes	756.37	867.4	13.27	98.6	35.8	1596	ND	ND	No
PECA1	EDTIVSQTQDFTK	Yes	756.37	954.5	13.27	98.6	38.8	10633	ND	ND	No
PECA1	SELVTVTESFSTPK	Yes	762.89	330.2	16.40	99.4	36.1	112887	ND	ND	No
PECA1	SELVTVTESFSTPK	Yes	762.89	429.2	16.40	99.4	33.1	30216	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PECA1	SELVTVTESFSTPK	Yes	762.89	896.4	16.40	99.4	33.1	16580	ND	ND	No
PECA1	SELVTVTESFSTPK	Yes	762.89	995.5	16.40	99.4	36.1	7480	ND	ND	No
PECA1	STESYFIPEVR	Yes	664.33	500.3	16.40	86.7	31.7	78886	ND	ND	No
PECA1	STESYFIPEVR	Yes	664.33	613.4	16.40	86.7	31.7	20436	ND	ND	No
PECA1	STESYFIPEVR	Yes	664.33	760.4	16.40	86.7	40.7	32123	ND	ND	No
PECA1	STESYFIPEVR	Yes	664.33	923.5	16.40	86.7	40.7	6542	ND	ND	No
PECA1	VIAPVDEVQISILSSK	Yes	849.49	434.3	20.03	110.6	45.9	15708	ND	ND	No
PECA1	VIAPVDEVQISILSSK	Yes	849.49	634.4	20.03	110.6	48.9	22340	ND	ND	No
PECA1	VIAPVDEVQISILSSK	Yes	849.49	747.5	20.03	110.6	48.9	14905	ND	ND	No
PECA1	VIAPVDEVQISILSSK	Yes	849.49	875.5	20.03	110.6	42.9	17371	ND	ND	No
PEDF	DTDTGALLFIGK	Yes	417.56	317.2	18.84	54.9	15.8	7801	80115	89177	No
PEDF	DTDTGALLFIGK	Yes	417.56	464.3	18.84	54.9	18.8	24294	228559	278980	No
PEDF	DTDTGALLFIGK	Yes	417.56	561.2	18.84	54.9	21.8	10270	118810	132598	No
PEDF	DTDTGALLFIGK	Yes	417.56	577.4	18.84	54.9	15.8	11929	142253	169729	No
PEDF	ELLDTVTAPQK	Yes	607.84	372.2	12.50	79.4	38.2	1756990	196476	258025	No
PEDF	ELLDTVTAPQK	Yes	607.84	544.3	12.50	79.4	29.2	554696	75290	73789	No
PEDF	ELLDTVTAPQK	Yes	607.84	859.5	12.50	79.4	29.2	462839	65310	72966	No
PEDF	ELLDTVTAPQK	Yes	607.84	972.5	12.50	79.4	29.2	188955	23100	32983	No
PEDF	LQSLFDSPDFSK	Yes	692.34	329.2	17.88	90.3	33	397596	1234166	1527847	No
PEDF	LQSLFDSPDFSK	Yes	692.34	593.3	17.88	90.3	42	367525	1227194	1519981	No
PEDF	LQSLFDSPDFSK	Yes	692.34	795.4	17.88	90.3	33	249855	816699	1001342	No
PEDF	LQSLFDSPDFSK	Yes	692.34	942.4	17.88	90.3	33	216281	731379	878393	No
PEDF	LSYEGEVTK	Yes	513.26	533.3	9.08	67.2	25.1	319573	687484	889962	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
PEDF	LSYEGEVTK	Yes	513.26	662.3	9.08	67.2	25.1	289821	568465	748021	No
PEDF	LSYEGEVTK	Yes	513.26	825.4	9.08	67.2	25.1	669677	1408785	1867390	No
PEDF	LSYEGEVTK	Yes	513.26	912.4	9.08	67.2	25.1	322195	646303	777990	No
PEDF	TVQAVLTVPK	Yes	528.33	557.4	13.16	69.2	25.7	131486	740145	850267	No
PEDF	TVQAVLTVPK	Yes	528.33	656.4	13.16	69.2	25.7	74854	453188	471248	No
PEDF	TVQAVLTVPK	Yes	528.33	727.5	13.16	69.2	25.7	204094	997642	1255095	No
PEDF	TVQAVLTVPK	Yes	528.33	855.5	13.16	69.2	25.7	227455	1386036	1625205	No
PERM	AVSNEIVR	Yes	444.25	387.3	8.41	58.3	28	16180	ND	ND	No
PERM	AVSNEIVR	Yes	444.25	516.3	8.41	58.3	31	12593	ND	ND	No
PERM	AVSNEIVR	Yes	444.25	630.4	8.41	58.3	28	14028	ND	ND	No
PERM	AVSNEIVR	Yes	444.25	717.4	8.41	58.3	22	110523	ND	ND	No
PERM	FPTDQLTPDQER	Yes	723.85	461.2	11.81	94.4	37.3	21022	ND	ND	No
PERM	FPTDQLTPDQER	Yes	723.85	644.3	11.81	94.4	43.3	112526	ND	ND	No
PERM	FPTDQLTPDQER	Yes	723.85	745.3	11.81	94.4	43.3	63232	ND	ND	No
PERM	FPTDQLTPDQER	Yes	723.85	858.4	11.81	94.4	43.3	32448	ND	ND	No
PERM	IANVFTNAFR	Yes	576.81	608.3	18.47	75.4	27.9	37737	ND	ND	No
PERM	IANVFTNAFR	Yes	576.81	755.4	18.47	75.4	27.9	76732	ND	ND	No
PERM	IANVFTNAFR	Yes	576.81	854.5	18.47	75.4	36.9	11535	ND	ND	No
PERM	IANVFTNAFR	Yes	576.81	968.5	18.47	75.4	27.9	17327	ND	ND	No
PERM	VFFASWR	Yes	456.74	361.2	18.11	59.9	31.6	13623	ND	ND	No
PERM	VFFASWR	Yes	456.74	519.3	18.11	59.9	22.6	70069	ND	ND	No
PERM	VFFASWR	Yes	456.74	666.3	18.11	59.9	22.6	170500	ND	ND	No
PERM	VFFASWR	Yes	456.74	813.4	18.11	59.9	31.6	26055	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PERM	VVLEGGIDPILR	Yes	640.88	312.2	17.89	83.7	30.7	228040	ND	ND	No
PERM	VVLEGGIDPILR	Yes	640.88	613.4	17.89	83.7	30.7	154669	ND	ND	No
PERM	VVLEGGIDPILR	Yes	640.88	840.5	17.89	83.7	30.7	395655	ND	ND	No
PERM	VVLEGGIDPILR	Yes	640.88	969.5	17.89	83.7	30.7	155222	ND	ND	No
PERP1	LSLPLLLLLLGAWAIPGGLGDR	Yes	753.46	671.3	24.79	98.2	33	12823	ND	ND	No
PERP1	LSLPLLLLLLGAWAIPGGLGDR	Yes	753.46	784.4	24.79	98.2	39	4320	ND	ND	No
PERP1	LSLPLLLLLLGAWAIPGGLGDR	Yes	753.46	855.5	24.79	98.2	33	3046	ND	ND	No
PERP1	LSLPLLLLLLGAWAIPGGLGDR	Yes	753.46	863.6	24.79	98.2	39	ND	ND	ND	No
PERP1	NWQDYGVR	Yes	519.24	429.2	11.95	68	31.3	4976	ND	ND	No
PERP1	NWQDYGVR	Yes	519.24	494.3	11.95	68	34.3	37992	ND	ND	No
PERP1	NWQDYGVR	Yes	519.24	609.3	11.95	68	28.3	19972	ND	ND	No
PERP1	NWQDYGVR	Yes	519.24	737.4	11.95	68	25.3	25334	ND	ND	No
PGAM1	ALPFWNEEIVPQIK	Yes	842.5	1069.6	24.60	100	42.6	ND	28379	21397	No
PGAM1	ALPFWNEEIVPQIK	Yes	842.5	485.3	24.60	100	42.6	ND	28143	26612	No
PGAM1	ALPFWNEEIVPQIK	Yes	842.5	584.4	24.60	100	42.6	ND	16179	13220	No
PGAM1	ALPFWNEEIVPQIK	Yes	842.5	750.4	24.60	100	42.6	ND	ND	ND	No
PGAM1	AMEAVAAQGK	Yes	488.2	403.2	9.60	100	27	ND	13582	19536	No
PGAM1	AMEAVAAQGK	Yes	488.2	474.3	9.60	100	27	ND	4146	4002	No
PGAM1	AMEAVAAQGK	Yes	488.2	644.3	9.60	100	27	ND	6004	11099	No
PGAM1	AMEAVAAQGK	Yes	488.2	773.4	9.60	100	27	ND	7541	10827	No
PGAM1	FSGWYDADLSPAGHEEAK	Yes	660.6	419.7	17.40	100	34.2	ND	ND	3992	No
PGAM1	FSGWYDADLSPAGHEEAK	Yes	660.6	613.3	17.40	100	34.2	ND	41338	39525	No
PGAM1	FSGWYDADLSPAGHEEAK	Yes	660.6	838.4	17.40	100	34.2	ND	6760	9931	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
PGAM1	FSGWYDADLSPAGHEEAK	Yes	990.4	1038.5	17.40	100	49.1	ND	53872	56447	No
PGAM1	FSGWYDADLSPAGHEEAK	Yes	990.4	1153.6	17.40	100	49.1	ND	ND	ND	No
PGAM1	FSGWYDADLSPAGHEEAK	Yes	990.4	838.4	17.40	100	49.1	ND	ND	ND	No
PGAM1	FSGWYDADLSPAGHEEAK	Yes	990.4	925.4	17.40	100	49.1	ND	3349	3362	No
PGAM1	HGESAWNLENR	Yes	656.8	1175.5	10.06	100	34.4	ND	ND	ND	No
PGAM1	HGESAWNLENR	Yes	656.8	289.2	10.06	100	40.4	ND	ND	ND	No
PGAM1	HGESAWNLENR	Yes	656.8	831.4	10.06	100	34.4	ND	ND	ND	No
PGAM1	HGESAWNLENR	Yes	656.8	989.5	10.06	100	40.4	ND	ND	ND	No
PGAM1	NLKPIKPMQFLGDEETVR	Yes	705.7	633.3	26.20	100	36.5	ND	ND	ND	No
PGAM1	NLKPIKPMQFLGDEETVR	Yes	705.7	748.3	26.20	100	36.5	ND	ND	ND	No
PGAM1	NLKPIKPMQFLGDEETVR	Yes	705.7	805.4	26.20	100	36.5	ND	ND	ND	No
PGAM1	NLKPIKPMQFLGDEETVR	Yes	705.7	918.5	26.20	100	36.5	ND	ND	ND	No
PLAC1	No peptide										
PLACL	IHTYVYEFIYLVR	No									
PLACL	LDPSPFIADFQTTAEELGLLSSSPNLL	No									
PLACL	VVSEETLLFQTELYFTPR	No									
PLIN2	DAVTTTVTGAK	Yes	532.29	576.3	8.47	69.7	28.9	260657	ND	ND	No
PLIN2	DAVTTTVTGAK	Yes	532.29	677.4	8.47	69.7	25.9	438190	ND	ND	No
PLIN2	DAVTTTVTGAK	Yes	532.29	778.4	8.47	69.7	25.9	1401979	ND	ND	No
PLIN2	DAVTTTVTGAK	Yes	532.29	877.5	8.47	69.7	25.9	166067	ND	ND	No
PLIN2	EVSDSLLTSSK	Yes	583.3	422.2	11.39	76.2	28.2	441447	ND	ND	No
PLIN2	EVSDSLLTSSK	Yes	583.3	535.3	11.39	76.2	28.2	301728	ND	ND	No
PLIN2	EVSDSLLTSSK	Yes	583.3	735.4	11.39	76.2	28.2	157351	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PLIN2	EVSDSLLTSSK	Yes	583.3	937.5	11.39	76.2	28.2	231181	ND	ND	No
PLIN2	LPILNQPSTQIVANAK	Yes	853.99	324.2	15.59	111.2	46.1	56414	ND	ND	No
PLIN2	LPILNQPSTQIVANAK	Yes	853.99	403.2	15.59	111.2	43.1	17620	ND	ND	No
PLIN2	LPILNQPSTQIVANAK	Yes	853.99	551.4	15.59	111.2	43.1	9157	ND	ND	No
PLIN2	LPILNQPSTQIVANAK	Yes	853.99	679.4	15.59	111.2	43.1	16886	ND	ND	No
PLIN2	SELLVEQYLPLTEEELEK	Yes	1081.56	330.2	23.37	140.5	59.1	29784	ND	ND	No
PLIN2	SELLVEQYLPLTEEELEK	Yes	1081.56	443.3	23.37	140.5	50.1	16138	ND	ND	No
PLIN2	SELLVEQYLPLTEEELEK	Yes	1081.56	542.3	23.37	140.5	47.1	10806	ND	ND	No
PLIN2	SELLVEQYLPLTEEELEK	Yes	1081.56	962.5	23.37	140.5	47.1	5724	ND	ND	No
PLIN2	SVVSGSINTVLGSR	Yes	688.38	319.2	16.02	89.8	32.8	16370	ND	ND	No
PLIN2	SVVSGSINTVLGSR	Yes	688.38	432.3	16.02	89.8	32.8	15171	ND	ND	No
PLIN2	SVVSGSINTVLGSR	Yes	688.38	746.4	16.02	89.8	41.8	14498	ND	ND	No
PLIN2	SVVSGSINTVLGSR	Yes	688.38	859.5	16.02	89.8	41.8	3762	ND	ND	No
PLIN3	DTVATQLSEAVDATR	Yes	526.27	462.2	16.76	68.9	24.4	21584	ND	ND	No
PLIN3	DTVATQLSEAVDATR	Yes	526.27	561.3	16.76	68.9	24.4	13956	ND	ND	No
PLIN3	DTVATQLSEAVDATR	Yes	526.27	761.4	16.76	68.9	33.4	5076	ND	ND	No
PLIN3	DTVATQLSEAVDATR	Yes	526.27	848.4	16.76	68.9	33.4	4521	ND	ND	No
PLIN3	IATSLDGFDVASVQQQR	Yes	917.97	431.2	16.40	119.4	48.9	8139	ND	ND	No
PLIN3	IATSLDGFDVASVQQQR	Yes	917.97	559.3	16.40	119.4	42.9	19026	ND	ND	No
PLIN3	IATSLDGFDVASVQQQR	Yes	917.97	745.4	16.40	119.4	39.9	20059	ND	ND	No
PLIN3	IATSLDGFDVASVQQQR	Yes	917.97	816.4	16.40	119.4	42.9	23953	ND	ND	No
PLIN3	LEENLPILQQPTEK	Yes	826.45	474.3	16.47	107.6	47.9	121563	ND	ND	No
PLIN3	LEENLPILQQPTEK	Yes	826.45	486.2	16.47	107.6	38.9	51652	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PLIN3	LEENLPILQQPTEK	Yes	826.45	599.3	16.47	107.6	35.9	107061	ND	ND	No
PLIN3	LEENLPILQQPTEK	Yes	826.45	730.4	16.47	107.6	38.9	26625	ND	ND	No
PLIN3	SEEWADNHLPLTDAELAR	Yes	689.66	346.1	16.95	90	29.7	45976	ND	ND	No
PLIN3	SEEWADNHLPLTDAELAR	Yes	689.66	559.3	16.95	90	41.7	40894	ND	ND	No
PLIN3	SEEWADNHLPLTDAELAR	Yes	689.66	775.4	16.95	90	29.7	15104	ND	ND	No
PLIN3	SEEWADNHLPLTDAELAR	Yes	689.66	985.5	16.95	90	41.7	47412	ND	ND	No
PLIN3	TLTAAAVSGAQPILSK	Yes	764.44	999.6	14.32	99.6	36.1	53601	ND	ND	No
PLIN3	TLTAAAVSGAQPILSK	Yes	764.44	557.4	14.32	99.6	45.1	201537	ND	ND	No
PLIN3	TLTAAAVSGAQPILSK	Yes	764.44	813.5	14.32	99.6	36.1	74745	ND	ND	No
PLIN3	TLTAAAVSGAQPILSK	Yes	764.44	900.5	14.32	99.6	36.1	103522	ND	ND	No
PLOD1	AQVEEFLAQHGSEYQSVK	Yes	684	299.2	14.47	89.2	29.4	49127	ND	ND	No
PLOD1	AQVEEFLAQHGSEYQSVK	Yes	684	333.2	14.47	89.2	38.4	20133	ND	ND	No
PLOD1	AQVEEFLAQHGSEYQSVK	Yes	684	624.3	14.47	89.2	41.4	7557	ND	ND	No
PLOD1	AQVEEFLAQHGSEYQSVK	Yes	684	897.4	14.47	89.2	38.4	13781	ND	ND	No
PLOD1	IFQNLDGALDEVVLK	Yes	837.46	458.3	22.05	109	48.3	31437	ND	ND	No
PLOD1	IFQNLDGALDEVVLK	Yes	837.46	503.3	22.05	109	39.3	45552	ND	ND	No
PLOD1	IFQNLDGALDEVVLK	Yes	837.46	815.5	22.05	109	39.3	48511	ND	ND	No
PLOD1	IFQNLDGALDEVVLK	Yes	837.46	943.5	22.05	109	39.3	50095	ND	ND	No
PLOD1	LQLNYLGNYIPR	No									
PLOD1	LTHYHEGLPTTR	Yes	475.58	377.2	8.37	62.3	30.8	34804	ND	ND	No
PLOD1	LTHYHEGLPTTR	Yes	475.58	644.4	8.37	62.3	30.8	11420	ND	ND	No
PLOD1	LTHYHEGLPTTR	Yes	475.58	838.4	8.37	62.3	21.8	4445	ND	ND	No
PLOD1	LTHYHEGLPTTR	Yes	475.58	910.5	8.37	62.3	18.8	2184	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PLOD1	NLAYDTLPVLIHGNGPTK	Yes	641.68	299.2	18.37	83.8	27.3	218140	ND	ND	No
PLOD1	NLAYDTLPVLIHGNGPTK	Yes	641.68	573.3	18.37	83.8	39.3	70120	ND	ND	No
PLOD1	NLAYDTLPVLIHGNGPTK	Yes	641.68	710.4	18.37	83.8	39.3	72542	ND	ND	No
PLOD1	NLAYDTLPVLIHGNGPTK	Yes	641.68	823.4	18.37	83.8	39.3	33657	ND	ND	No
PLOD2	IVGPEENLSQAEAR	Yes	756.89	375.2	11.39	98.6	41.8	19496	ND	ND	No
PLOD2	IVGPEENLSQAEAR	Yes	756.89	574.3	11.39	98.6	44.8	15836	ND	ND	No
PLOD2	IVGPEENLSQAEAR	Yes	756.89	661.3	11.39	98.6	44.8	59996	ND	ND	No
PLOD2	IVGPEENLSQAEAR	Yes	756.89	888.5	11.39	98.6	44.8	28623	ND	ND	No
PLOD2	IVQQWNLQDNDDDQLFYTK	No									
PLOD2	LTHLHEGLPVK	Yes	415.24	343.2	9.62	54.6	24.7	258869	ND	ND	No
PLOD2	LTHLHEGLPVK	Yes	415.24	513.3	9.62	54.6	21.7	57036	ND	ND	No
PLOD2	LTHLHEGLPVK	Yes	415.24	779.4	9.62	54.6	21.7	62603	ND	ND	No
PLOD2	LTHLHEGLPVK	Yes	415.24	901.5	9.62	54.6	27.7	ND	ND	ND	No
PLOD2	LWSNFWGALSPDGYYAR	Yes	1001.98	629.3	24.48	130.3	55.6	22841	ND	ND	No
PLOD2	LWSNFWGALSPDGYYAR	Yes	1001.98	648.3	24.48	130.3	43.6	8062	ND	ND	No
PLOD2	LWSNFWGALSPDGYYAR	Yes	1001.98	841.4	24.48	130.3	43.6	22988	ND	ND	No
PLOD2	LWSNFWGALSPDGYYAR	Yes	1001.98	928.4	24.48	130.3	43.6	18234	ND	ND	No
PLOD2	SEDYVDIVQGNR	Yes	697.83	332.1	13.30	91	39.2	71789	ND	ND	No
PLOD2	SEDYVDIVQGNR	Yes	697.83	573.3	13.30	91	33.2	29577	ND	ND	No
PLOD2	SEDYVDIVQGNR	Yes	697.83	801.4	13.30	91	36.2	57702	ND	ND	No
PLOD2	SEDYVDIVQGNR	Yes	697.83	900.5	13.30	91	42.2	12415	ND	ND	No
PLSL	IGNFSTDIK	Yes	497.76	563.3	12.16	65.2	24.4	183136	ND	ND	No
PLSL	IGNFSTDIK	Yes	497.76	710.4	12.16	65.2	24.4	68433	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PLSL	IGNFSTDIK	Yes	497.76	824.4	12.16	65.2	24.4	83963	ND	ND	No
PLSL	IGNFSTDIK	Yes	497.76	881.4	12.16	65.2	24.4	143929	ND	ND	No
PLSL	ISFDEFIK	Yes	499.76	536.3	19.34	65.5	27.5	48520	1511	3326	No
PLSL	ISFDEFIK	Yes	499.76	651.3	19.34	65.5	24.5	72681	6326	2791	No
PLSL	ISFDEFIK	Yes	499.76	798.4	19.34	65.5	24.5	407983	28276	23189	No
PLSL	ISFDEFIK	Yes	499.76	885.4	19.34	65.5	24.5	330425	12882	14980	No
PLSL	VDTDGNGYISFNELNDLFK	Yes	1081.01	636.3	24.35	140.5	59.1	8889	ND	ND	No
PLSL	VDTDGNGYISFNELNDLFK	Yes	1081.01	822.3	24.35	140.5	47.1	7966	ND	ND	No
PLSL	VDTDGNGYISFNELNDLFK	Yes	1081.01	935.4	24.35	140.5	47.1	5312	ND	ND	No
PLSL	VDTDGNGYISFNELNDLFK	Yes	1081.01	992.5	24.35	140.5	50.1	7452	ND	ND	No
PLSL	VPVDWNR	No									
PLSL	YPALHKPENQDIDWGALEGETR	Yes	847.08	591.3	16.08	110.3	40.8	1349	ND	ND	No
PLSL	YPALHKPENQDIDWGALEGETR	Yes	847.08	704.4	16.08	110.3	37.8	3755	ND	ND	No
PLSL	YPALHKPENQDIDWGALEGETR	Yes	847.08	710.4	16.08	110.3	43.8	1090	ND	ND	No
PLSL	YPALHKPENQDIDWGALEGETR	Yes	847.08	775.4	16.08	110.3	46.8	ND	ND	ND	No
PLUNC	LDITAEILAVR	Yes	607.36	700.4	21.19	79.3	29.2	6923	ND	ND	No
PLUNC	LDITAEILAVR	Yes	607.36	771.5	21.19	79.3	29.2	11867	ND	ND	No
PLUNC	LDITAEILAVR	Yes	607.36	872.5	21.19	79.3	29.2	20708	ND	ND	No
PLUNC	LDITAEILAVR	Yes	607.36	985.6	21.19	79.3	32.2	ND	ND	ND	Yes (Based on Manual Review)
PLUNC	LQVNTPLVGASLLR	Yes	740.95	341.2	19.57	96.6	35.1	43538	ND	ND	No
PLUNC	LQVNTPLVGASLLR	Yes	740.95	556.3	19.57	96.6	32.1	42005	ND	ND	No
PLUNC	LQVNTPLVGASLLR	Yes	740.95	616.4	19.57	96.6	41.1	48631	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PLUNC	LQVNTPLVGASLLR	Yes	740.95	925.6	19.57	96.6	38.1	90980	ND	ND	No
PLUNC	LYVTIPLGIK	Yes	558.86	277.2	20.23	73.1	24.1	1257022	34633	30268	Yes (Based on Transition Ratios)
PLUNC	LYVTIPLGIK	Yes	558.86	527.4	20.23	73.1	36.1	879721	11303	6515	No
PLUNC	LYVTIPLGIK	Yes	558.86	741.5	20.23	73.1	27.1	517880	7349	4470	No
PLUNC	LYVTIPLGIK	Yes	558.86	840.6	20.23	73.1	27.1	798614	9812	4058	No
PLUNC	VTDPQLLELGLVQSPDGHR	Yes	692.04	369.2	18.45	90.3	41.8	39971	ND	ND	No
PLUNC	VTDPQLLELGLVQSPDGHR	Yes	692.04	581.3	18.45	90.3	41.8	26502	ND	ND	No
PLUNC	VTDPQLLELGLVQSPDGHR	Yes	692.04	668.3	18.45	90.3	41.8	20636	ND	ND	No
PLUNC	VTDPQLLELGLVQSPDGHR	Yes	692.04	796.4	18.45	90.3	35.8	21192	ND	ND	No
PLUNC	VTSVIPGLNNIIDIK	Yes	798.47	999.6	22.79	104	34.6	4901	ND	ND	No
PLUNC	VTSVIPGLNNIIDIK	Yes	798.47	288.2	22.79	104	46.6	21350	ND	ND	No
PLUNC	VTSVIPGLNNIIDIK	Yes	798.47	387.2	22.79	104	37.6	40384	ND	ND	No
PLUNC	VTSVIPGLNNIIDIK	Yes	798.47	500.3	22.79	104	34.6	42409	ND	ND	No
PLXB3	ELPVPIYVTQGEAQR	Yes	567.31	374.2	16.84	74.2	35.5	125582	ND	ND	No
PLXB3	ELPVPIYVTQGEAQR	Yes	567.31	688.3	16.84	74.2	35.5	20131	ND	ND	No
PLXB3	ELPVPIYVTQGEAQR	Yes	567.31	789.4	16.84	74.2	26.5	42072	ND	ND	No
PLXB3	ELPVPIYVTQGEAQR	Yes	567.31	888.5	16.84	74.2	32.5	8028	ND	ND	No
PLXB3	GPSGAEEATVEYGVTSR	Yes	855.4	519.3	11.28	111.3	49.1	19508	ND	ND	No
PLXB3	GPSGAEEATVEYGVTSR	Yes	855.4	682.4	11.28	111.3	49.1	20559	ND	ND	No
PLXB3	GPSGAEEATVEYGVTSR	Yes	855.4	699.3	11.28	111.3	40.1	7735	ND	ND	No
PLXB3	GPSGAEEATVEYGVTSR	Yes	855.4	811.4	11.28	111.3	40.1	23528	ND	ND	No
PLXB3	GPVDAVTGK	Yes	422.23	305.2	8.60	55.5	30.1	809606	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PLXB3	GPVDAVTGK	Yes	422.23	475.3	8.60	55.5	24.1	196652	ND	ND	No
PLXB3	GPVDAVTGK	Yes	422.23	590.3	8.60	55.5	21.1	781169	ND	ND	No
PLXB3	GPVDAVTGK	Yes	422.23	689.4	8.60	55.5	21.1	350145	ND	ND	No
PLXB3	QLAGSQPFSSEGLGR	No									
PLXB3	SQPPGISSQHFTYQDPVLLSLSPR	Yes	885.46	559.3	20.00	115.2	51.7	9042	ND	ND	No
PLXB3	SQPPGISSQHFTYQDPVLLSLSPR	Yes	885.46	672.4	20.00	115.2	42.7	7634	ND	ND	No
PLXB3	SQPPGISSQHFTYQDPVLLSLSPR	Yes	885.46	785.5	20.00	115.2	51.7	6935	ND	ND	No
PLXB3	SQPPGISSQHFTYQDPVLLSLSPR	Yes	885.46	981.6	20.00	115.2	51.7	14191	ND	ND	No
PLXC1	FWVNILK	Yes	460.274	334.156	19.37	100	22.8	ND	ND	ND	No
PLXC1	FWVNILK	Yes	460.274	487.3	19.37	100	25.8	ND	ND	ND	No
PLXC1	FWVNILK	Yes	460.274	586.393	19.37	100	22.8	ND	ND	ND	No
PLXC1	FWVNILK	Yes	460.274	772.5	19.37	100	25.8	ND	ND	ND	No
PLXC1	LNTIGHYEISNGSTIK	Yes	582.973	619.341	11.74	100	27.3	ND	78642	51870	No
PLXC1	LNTIGHYEISNGSTIK	Yes	582.973	706.374	11.74	100	33.3	ND	ND	4463	No
PLXC1	LNTIGHYEISNGSTIK	Yes	582.973	817.4	11.74	100	30.2	ND	ND	ND	No
PLXC1	LNTIGHYEISNGSTIK	Yes	582.973	819.5	11.74	100	30.2	ND	ND	ND	No
PLXC1	LNTIGHYEISNGSTIK	Yes	874	1111.6	11.74	100	44	ND	ND	ND	No
PLXC1	LNTIGHYEISNGSTIK	Yes	874	706.4	11.74	100	44	ND	ND	ND	No
PLXC1	LNTIGHYEISNGSTIK	Yes	874	948.5	11.74	100	44	ND	ND	ND	No
PLXC1	NPQFVFDIK	Yes	554.3	260.2	19.50	100	29.9	ND	ND	ND	No
PLXC1	NPQFVFDIK	Yes	554.3	497.3	19.50	100	29.9	ND	ND	ND	No
PLXC1	NPQFVFDIK	Yes	554.3	522.3	19.50	100	29.9	ND	ND	ND	No
PLXC1	NPQFVFDIK	Yes	554.3	768.4	19.50	100	29.9	ND	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
POSTN	GFEPGVTNILK	Yes	587.83	334.1	16.56	76.8	25.4	324313	ND	ND	No
POSTN	GFEPGVTNILK	Yes	587.83	744.5	16.56	76.8	37.4	83588	ND	ND	No
POSTN	GFEPGVTNILK	Yes	587.83	841.5	16.56	76.8	28.4	403607	ND	ND	No
POSTN	GFEPGVTNILK	Yes	587.83	970.6	16.56	76.8	28.4	15107	ND	ND	No
POSTN	IIDGVPVEITEK	Yes	656.87	399.2	15.07	85.7	31.4	99834	ND	ND	No
POSTN	IIDGVPVEITEK	Yes	656.87	498.3	15.07	85.7	28.4	231637	ND	ND	No
POSTN	IIDGVPVEITEK	Yes	656.87	815.5	15.07	85.7	31.4	505541	ND	ND	No
POSTN	IIDGVPVEITEK	Yes	656.87	971.5	15.07	85.7	40.4	15408	ND	ND	No
POSTN	IIHGNQIATNGVVHVIDR	Yes	652.7	364.2	13.14	85.2	33.8	7454	ND	ND	No
POSTN	IIHGNQIATNGVVHVIDR	Yes	652.7	502.3	13.14	85.2	36.8	6706	ND	ND	No
POSTN	IIHGNQIATNGVVHVIDR	Yes	652.7	738.4	13.14	85.2	33.8	5578	2007	ND	No
POSTN	IIHGNQIATNGVVHVIDR	Yes	652.7	847.5	13.14	85.2	33.8	1948	ND	ND	No
POSTN	LLYPADTPVGNDQLLEILNK	Yes	742.74	261.2	23.13	96.8	41.4	56393	ND	ND	No
POSTN	LLYPADTPVGNDQLLEILNK	Yes	742.74	616.4	23.13	96.8	32.4	33407	ND	ND	No
POSTN	LLYPADTPVGNDQLLEILNK	Yes	742.74	774.4	23.13	96.8	32.4	23106	ND	ND	No
POSTN	LLYPADTPVGNDQLLEILNK	Yes	742.74	842.5	23.13	96.8	35.4	25420	ND	ND	No
POSTN	VLTQIGTSIQDFIEAEDDLSSFR	No									
PPAL	DPYQEEEWPQGFGQLTK	Yes	1026.47	546.3	18.53	133.4	53.7	20226	ND	ND	No
PPAL	DPYQEEEWPQGFGQLTK	Yes	1026.47	633.3	18.53	133.4	47.7	16600	ND	ND	No
PPAL	DPYQEEEWPQGFGQLTK	Yes	1026.47	891.3	18.53	133.4	47.7	22850	ND	ND	No
PPAL	DPYQEEEWPQGFGQLTK	Yes	1026.47	975.5	18.53	133.4	47.7	54225	ND	ND	No
PPAL	FLFGIYQQAEK	Yes	672.35	261.2	19.73	87.7	29.1	907541	ND	ND	No
PPAL	FLFGIYQQAEK	Yes	672.35	603.3	19.73	87.7	29.1	114404	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PPAL	FLFGIYQQAEK	Yes	672.35	766.4	19.73	87.7	32.1	448857	ND	ND	No
PPAL	FLFGIYQQAEK	Yes	672.35	936.5	19.73	87.7	32.1	267851	ND	ND	No
PPAL	FVTLLYR	Yes	456.27	338.2	16.82	59.9	19.6	38696	ND	ND	No
PPAL	FVTLLYR	Yes	456.27	564.4	16.82	59.9	22.6	48800	ND	ND	No
PPAL	FVTLLYR	Yes	456.27	665.4	16.82	59.9	22.6	290264	ND	ND	No
PPAL	FVTLLYR	Yes	456.27	764.5	16.82	59.9	31.6	22123	ND	ND	No
PPAL	HVADGEDHA	Yes	475.7	528.2	5.36	62.4	29.4	37415	ND	ND	No
PPAL	HVADGEDHA	Yes	475.7	714.3	5.36	62.4	23.4	89949	ND	ND	No
PPAL	HVADGEDHA	Yes	475.7	724.3	5.36	62.4	26.4	41875	ND	ND	No
PPAL	HVADGEDHA	Yes	475.7	813.3	5.36	62.4	23.4	29580	ND	ND	No
PPAL	LTEPVVPK	Yes	441.77	343.2	10.22	58	30.9	132269	ND	ND	No
PPAL	LTEPVVPK	Yes	441.77	539.4	10.22	58	21.9	300416	ND	ND	No
PPAL	LTEPVVPK	Yes	441.77	668.4	10.22	58	21.9	237137	ND	ND	No
PPAL	LTEPVVPK	Yes	441.77	769.4	10.22	58	21.9	138062	ND	ND	No
PPBT	ANEGTVGVSAATER	Yes	681.34	634.3	8.17	88.9	32.5	31298	ND	ND	No
PPBT	ANEGTVGVSAATER	Yes	681.34	733.4	8.17	88.9	32.5	8835	ND	ND	No
PPBT	ANEGTVGVSAATER	Yes	681.34	790.4	8.17	88.9	32.5	61787	ND	ND	No
PPBT	ANEGTVGVSAATER	Yes	681.34	889.5	8.17	88.9	32.5	15618	ND	ND	No
PPBT	DQAQETLK	Yes	466.74	361.2	6.29	61.2	32	123889	ND	ND	No
PPBT	DQAQETLK	Yes	466.74	490.3	6.29	61.2	23	75097	ND	ND	No
PPBT	DQAQETLK	Yes	466.74	618.3	6.29	61.2	23	114894	ND	ND	No
PPBT	DQAQETLK	Yes	466.74	689.4	6.29	61.2	20	356340	ND	ND	No
PPBT	HETHGGEDVAVFSK	Yes	504.91	381.2	9.31	66.1	32.3	64382	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
PPBT	HETHGGEDVAVFSK	Yes	504.91	480.3	9.31	66.1	29.3	17424	ND	ND	No
PPBT	HETHGGEDVAVFSK	Yes	504.91	551.3	9.31	66.1	26.3	34602	ND	ND	No
PPBT	HETHGGEDVAVFSK	Yes	504.91	650.4	9.31	66.1	26.3	11166	ND	ND	No
PPBT	LDGLDLVDTWK	Yes	637.84	434.2	20.73	83.3	39.6	69928	ND	ND	No
PPBT	LDGLDLVDTWK	Yes	637.84	549.3	20.73	83.3	30.6	82624	ND	ND	No
PPBT	LDGLDLVDTWK	Yes	637.84	761.4	20.73	83.3	30.6	62217	ND	ND	No
PPBT	LDGLDLVDTWK	Yes	637.84	876.4	20.73	83.3	30.6	151694	ND	ND	No
PPBT	YFLHQSHEER	Yes	449.21	311.1	7.82	58.9	23.5	12003	ND	ND	No
PPBT	YFLHQSHEER	Yes	449.21	570.3	7.82	58.9	29.5	3782	ND	ND	No
PPBT	YFLHQSHEER	Yes	449.21	657.3	7.82	58.9	29.5	7495	ND	ND	No
PPBT	YFLHQSHEER	Yes	449.21	785.4	7.82	58.9	29.5	11764	ND	ND	No
PPIB	FPDENFK	Yes	448.71	537.3	11.04	58.9	28.2	ND	ND	ND	No
PPIB	FPDENFK	Yes	448.71	603.2	11.04	58.9	25.2	16363	ND	ND	No
PPIB	FPDENFK	Yes	448.71	652.3	11.04	58.9	25.2	ND	ND	ND	No
PPIB	FPDENFK	Yes	448.71	749.3	11.04	58.9	22.2	ND	ND	ND	No
PPIB	IEVEKPFAIAK	Yes	415.58	331.2	13.47	54.6	24.7	24279	ND	ND	No
PPIB	IEVEKPFAIAK	Yes	415.58	646.4	13.47	54.6	21.7	66870	ND	ND	No
PPIB	IEVEKPFAIAK	Yes	415.58	774.5	13.47	54.6	18.7	13166	ND	ND	No
PPIB	IEVEKPFAIAK	Yes	415.58	903.5	13.47	54.6	27.7	ND	ND	ND	No
PPIB	TVDNFVALATGEK	Yes	682.86	430.2	17.66	89.1	29.5	19753	ND	ND	No
PPIB	TVDNFVALATGEK	Yes	682.86	577.3	17.66	89.1	32.5	41987	ND	ND	No
PPIB	TVDNFVALATGEK	Yes	682.86	788.5	17.66	89.1	32.5	85171	ND	ND	No
PPIB	TVDNFVALATGEK	Yes	682.86	935.5	17.66	89.1	32.5	16719	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PPIB	VIFGLFGK	Yes	440.77	351.2	21.03	57.9	27.9	191828	3553	5492	No
PPIB	VIFGLFGK	Yes	440.77	521.3	21.03	57.9	21.9	82929	ND	ND	No
PPIB	VIFGLFGK	Yes	440.77	668.4	21.03	57.9	21.9	493439	8187	3865	No
PPIB	VIFGLFGK	Yes	440.77	781.5	21.03	57.9	21.9	48307	ND	ND	No
PPIB	VYFDLR	Yes	406.72	263.1	15.07	53.5	20.4	114362	17538	15604	No
PPIB	VYFDLR	Yes	406.72	288.2	15.07	53.5	29.4	375616	106116	99482	Yes (Based on Transition Ratios)
PPIB	VYFDLR	Yes	406.72	550.3	15.07	53.5	20.4	182617	12041	3981	Yes (Based on Transition Ratios)
PPIB	VYFDLR	Yes	406.72	713.4	15.07	53.5	20.4	33985	4712	2849	No
PRDX1	ADEGISFR	Yes	447.72	409.2	12.95	58.8	22.2	3701027	ND	ND	No
PRDX1	ADEGISFR	Yes	447.72	522.3	12.95	58.8	31.2	652531	ND	ND	No
PRDX1	ADEGISFR	Yes	447.72	579.3	12.95	58.8	22.2	3080780	ND	ND	No
PRDX1	ADEGISFR	Yes	447.72	708.4	12.95	58.8	22.2	2003432	ND	ND	No
PRDX1	ATAVMPDGQFK	Yes	582.79	691.3	13.05	76.2	25.1	2294568	ND	ND	No
PRDX1	ATAVMPDGQFK	Yes	582.79	822.4	13.05	76.2	28.1	1466078	ND	ND	No
PRDX1	ATAVMPDGQFK	Yes	582.79	921.5	13.05	76.2	28.1	338255	ND	ND	No
PRDX1	ATAVMPDGQFK	Yes	582.79	992.5	13.05	76.2	28.1	243882	ND	ND	No
PRDX1	DISLSDYK	Yes	470.74	310.2	13.83	61.7	32.2	1002950	ND	ND	No
PRDX1	DISLSDYK	Yes	470.74	512.2	13.83	61.7	32.2	411632	ND	ND	No
PRDX1	DISLSDYK	Yes	470.74	625.3	13.83	61.7	20.2	292890	ND	ND	No
PRDX1	DISLSDYK	Yes	470.74	712.4	13.83	61.7	23.2	3091300	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PRDX1	GLFIIDDK	Yes	460.76	377.2	19.23	60.4	31.8	1500328	ND	ND	No
PRDX1	GLFIIDDK	Yes	460.76	490.3	19.23	60.4	22.8	4342656	ND	ND	No
PRDX1	GLFIIDDK	Yes	460.76	603.3	19.23	60.4	22.8	3694805	ND	ND	No
PRDX1	GLFIIDDK	Yes	460.76	750.4	19.23	60.4	22.8	5186862	ND	ND	No
PRDX1	IGHPAPNFK	Yes	327.52	294.2	9.63	43.3	23.3	132510	16466	13802	No
PRDX1	IGHPAPNFK	Yes	327.52	505.3	9.63	43.3	23.3	464807	28679	21394	No
PRDX1	IGHPAPNFK	Yes	327.52	576.3	9.63	43.3	23.3	70900	4280	3124	No
PRDX1	IGHPAPNFK	Yes	327.52	673.4	9.63	43.3	14.3	248474	12334	11693	No
PRDX1	LVQAFQFTDK	Yes	598.82	341.2	17.24	78.2	28.8	2501033	ND	ND	No
PRDX1	LVQAFQFTDK	Yes	598.82	785.4	17.24	78.2	28.8	1624977	ND	ND	No
PRDX1	LVQAFQFTDK	Yes	598.82	856.4	17.24	78.2	28.8	2372000	ND	ND	No
PRDX1	LVQAFQFTDK	Yes	598.82	984.5	17.24	78.2	28.8	2567310	ND	ND	No
PRDX1	QGGLGPMNIPLVSDPK	Yes	811.93	356.2	20.30	105.7	35.2	61858	ND	ND	No
PRDX1	QGGLGPMNIPLVSDPK	Yes	811.93	446.2	20.30	105.7	38.2	83998	ND	ND	No
PRDX1	QGGLGPMNIPLVSDPK	Yes	811.93	545.3	20.30	105.7	44.2	29740	ND	ND	No
PRDX1	QGGLGPMNIPLVSDPK	Yes	811.93	658.4	20.30	105.7	38.2	7730	ND	ND	No
PRDX1	QITVNDLPVGR	Yes	606.34	428.3	15.49	79.2	29.2	127667	508208	448173	No
PRDX1	QITVNDLPVGR	Yes	606.34	770.4	15.49	79.2	35.2	78489	296072	261143	No
PRDX1	QITVNDLPVGR	Yes	606.34	869.5	15.49	79.2	32.2	34766	112074	120150	No
PRDX1	QITVNDLPVGR	Yes	606.34	970.5	15.49	79.2	29.2	48375	237220	193548	No
PRDX1	SVDETLR	Yes	410.21	288.2	8.82	53.9	29.5	195411	ND	ND	No
PRDX1	SVDETLR	Yes	410.21	389.3	8.82	53.9	29.5	802324	12313	8666	No
PRDX1	SVDETLR	Yes	410.21	518.3	8.82	53.9	29.5	1103612	10364	10942	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
PRDX1	SVDETLR	Yes	410.21	633.3	8.82	53.9	20.5	7404432	68155	77770	No
PRDX1	TIAQDYGVLK	Yes	554.31	579.4	14.78	72.5	35.9	798348	4550	7874	No
PRDX1	TIAQDYGVLK	Yes	554.31	694.4	14.78	72.5	35.9	400510	ND	ND	No
PRDX1	TIAQDYGVLK	Yes	554.31	822.4	14.78	72.5	26.9	567772	4908	3884	No
PRDX1	TIAQDYGVLK	Yes	554.31	893.5	14.78	72.5	26.9	3574901	27475	20315	No
PRDX4	DYGVYLEDSGHTLR	Yes	812.88	336.1	14.10	105.9	44.3	70861	ND	ND	No
PRDX4	DYGVYLEDSGHTLR	Yes	812.88	435.2	14.10	105.9	38.3	21839	ND	ND	No
PRDX4	DYGVYLEDSGHTLR	Yes	812.88	785.4	14.10	105.9	47.3	12808	ND	ND	No
PRDX4	DYGVYLEDSGHTLR	Yes	812.88	914.4	14.10	105.9	38.3	11577	ND	ND	No
PRDX4	IPLLSDLTHQISK	Yes	488.95	612.3	19.91	64.1	25.5	46897	ND	ND	No
PRDX4	IPLLSDLTHQISK	Yes	488.95	713.4	19.91	64.1	31.5	46450	ND	ND	No
PRDX4	IPLLSDLTHQISK	Yes	488.95	826.5	19.91	64.1	28.5	25816	ND	ND	No
PRDX4	IPLLSDLTHQISK	Yes	488.95	941.5	19.91	64.1	31.5	5655	ND	ND	No
PRDX4	ISKPAPYWEGTAVIDGEFK	Yes	703.36	595.3	18.43	91.7	42.4	22471	ND	ND	No
PRDX4	ISKPAPYWEGTAVIDGEFK	Yes	703.36	757.4	18.43	91.7	30.4	11421	ND	ND	No
PRDX4	ISKPAPYWEGTAVIDGEFK	Yes	703.36	807.4	18.43	91.7	30.4	31258	ND	ND	No
PRDX4	ISKPAPYWEGTAVIDGEFK	Yes	703.36	878.5	18.43	91.7	33.4	14455	ND	ND	No
PRDX4	QITLNDLPVGR	Yes	613.35	428.3	16.08	80.1	29.5	133612	ND	ND	No
PRDX4	QITLNDLPVGR	Yes	613.35	541.3	16.08	80.1	38.5	100623	ND	ND	No
PRDX4	QITLNDLPVGR	Yes	613.35	770.4	16.08	80.1	38.5	55159	ND	ND	No
PRDX4	QITLNDLPVGR	Yes	613.35	984.5	16.08	80.1	29.5	39840	ND	ND	No
PRDX4	VSVADHSLHLSK	Yes	431.57	484.3	9.86	56.7	25.6	14129	ND	ND	No
PRDX4	VSVADHSLHLSK	Yes	431.57	597.4	9.86	56.7	19.6	155578	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PRDX4	VSVADHSLHLSK	Yes	431.57	684.4	9.86	56.7	28.6	14908	ND	ND	No
PRDX4	VSVADHSLHLSK	Yes	431.57	821.5	9.86	56.7	28.6	6677	ND	ND	No
PROF1	DSPSVWAAVPGK	Yes	607.3	301.2	16.90	100	32.2	ND	ND	ND	No
PROF1	DSPSVWAAVPGK	Yes	607.3	400.3	16.90	100	32.2	ND	ND	ND	No
PROF1	DSPSVWAAVPGK	Yes	607.3	542.3	16.90	100	32.2	ND	ND	ND	No
PROF1	DSPSVWAAVPGK	Yes	607.3	728.4	16.90	100	32.2	ND	ND	ND	No
PROF1	SSFYVNGLTLGGQK	Yes	735.9	389.2	18.80	100	37.9	ND	ND	ND	No
PROF1	SSFYVNGLTLGGQK	Yes	735.9	773.5	18.80	100	37.9	ND	ND	ND	No
PROF1	SSFYVNGLTLGGQK	Yes	735.9	887.5	18.80	100	37.9	ND	ND	ND	No
PROF1	SSFYVNGLTLGGQK	Yes	735.9	986.6	18.80	100	37.9	ND	ND	ND	No
PROF1	STGGAPTFNVTVTK	Yes	690.361	1006.56	11.98	100	32.9	ND	9893	22358	No
PROF1	STGGAPTFNVTVTK	Yes	690.361	374.2	11.98	100	35.9	ND	15264	14282	No
PROF1	STGGAPTFNVTVTK	Yes	690.361	448.3	11.98	100	35.9	ND	6462	ND	No
PROF1	STGGAPTFNVTVTK	Yes	690.361	503.782	11.98	100	35.9	ND	24463	22889	No
PROF1	TFVNITPAEVGVLVGK	Yes	822.471	1069.63	20.28	100	35.7	ND	ND	ND	No
PROF1	TFVNITPAEVGVLVGK	Yes	822.471	416.3	20.28	100	41.7	ND	ND	ND	No
PROF1	TFVNITPAEVGVLVGK	Yes	822.471	575.3	20.28	100	41.7	ND	ND	ND	No
PROF1	TFVNITPAEVGVLVGK	Yes	822.471	968.578	20.28	100	35.7	ND	ND	ND	No
PRP31	IEEYISK	No									
PRP31	IYEYVESR	Yes	529.76	490.3	9.93	69.3	25.8	20716	ND	ND	No
PRP31	IYEYVESR	Yes	529.76	653.3	9.93	69.3	25.8	33632	ND	ND	No
PRP31	IYEYVESR	Yes	529.76	782.4	9.93	69.3	25.8	86637	ND	ND	No
PRP31	IYEYVESR	Yes	529.76	945.4	9.93	69.3	28.8	18826	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
PRP31	QTQVNEATK	Yes	509.76	562.3	5.53	66.8	27.9	73958	ND	ND	No
PRP31	QTQVNEATK	Yes	509.76	661.4	5.53	66.8	27.9	37533	ND	ND	No
PRP31	QTQVNEATK	Yes	509.76	789.4	5.53	66.8	24.9	26323	ND	ND	No
PRP31	QTQVNEATK	Yes	509.76	890.5	5.53	66.8	24.9	5684	ND	ND	No
PRP31	VDSFHESTEGK	Yes	618.28	521.3	6.65	80.8	38.7	21457	ND	ND	No
PRP31	VDSFHESTEGK	Yes	618.28	650.3	6.65	80.8	38.7	21053	ND	ND	No
PRP31	VDSFHESTEGK	Yes	618.28	715.3	6.65	80.8	38.7	7600	ND	ND	No
PRP31	VDSFHESTEGK	Yes	618.28	787.4	6.65	80.8	35.7	29351	ND	ND	No
PRP31	VIVDANNLTVEIENELNIIHK	No									
PRS6A	AMEVDERPTEQYSDIGGLDK	Yes	1127	602.4	16.10	100	55.1	ND	ND	ND	No
PRS6A	AMEVDERPTEQYSDIGGLDK	Yes	1127	789.9	16.10	100	55.1	ND	ND	ND	No
PRS6A	AMEVDERPTEQYSDIGGLDK	Yes	1127	831.4	16.10	100	55.1	ND	ND	ND	No
PRS6A	AMEVDERPTEQYSDIGGLDK	Yes	1127	854.4	16.10	100	55.1	ND	ND	ND	No
PRS6A	AMEVDERPTEQYSDIGGLDK	Yes	751.7	1026	16.10	100	38.8	ND	45571	29298	No
PRS6A	AMEVDERPTEQYSDIGGLDK	Yes	751.7	804.4	16.10	100	38.8	ND	ND	ND	No
PRS6A	AMEVDERPTEQYSDIGGLDK	Yes	751.7	854.4	16.10	100	38.8	ND	ND	4788	No
PRS6A	AMEVDERPTEQYSDIGGLDK	Yes	751.7	961.5	16.10	100	38.8	ND	75283	35017	No
PRS6A	GVLMYGPPGTGK	Yes	588.8	556.3	15.40	100	31.4	ND	ND	ND	No
PRS6A	GVLMYGPPGTGK	Yes	588.8	613.3	15.40	100	31.4	ND	ND	ND	No
PRS6A	GVLMYGPPGTGK	Yes	588.8	776.4	15.40	100	31.4	ND	ND	ND	No
PRS6A	GVLMYGPPGTGK	Yes	588.8	907.4	15.40	100	31.4	ND	ND	ND	No
PRS6A	LAGPQLVQMFIGDGAK	Yes	822.9	1065.5	25.50	100	41.7	ND	ND	ND	No
PRS6A	LAGPQLVQMFIGDGAK	Yes	822.9	702.4	25.50	100	41.7	ND	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PRS6A	LAGPQLVQMFIGDGAK	Yes	822.9	838.4	25.50	100	41.7	ND	55736	44857	No
PRS6A	LAGPQLVQMFIGDGAK	Yes	822.9	966.5	25.50	100	41.7	ND	16190	16601	No
PRS6A	QIQELVEAIVLPMNHK	Yes	621.3	313.7	24.10	100	32.2	ND	35061	17523	No
PRS6A	QIQELVEAIVLPMNHK	Yes	621.3	626.3	24.10	100	32.2	ND	35100	14838	No
PRS6A	QIQELVEAIVLPMNHK	Yes	621.3	739.4	24.10	100	32.2	ND	33602	16891	No
PRS6A	QIQELVEAIVLPMNHK	Yes	621.3	838.5	24.10	100	32.2	ND	15616	8028	No
PRS6A	QIQELVEAIVLPMNHK	Yes	931.5	1022.6	24.10	100	46.5	ND	ND	ND	No
PRS6A	QIQELVEAIVLPMNHK	Yes	931.5	739.4	24.10	100	46.5	ND	ND	ND	No
PRS6A	QIQELVEAIVLPMNHK	Yes	931.5	838.5	24.10	100	46.5	ND	ND	ND	No
PRS6A	QIQELVEAIVLPMNHK	Yes	931.5	951.5	24.10	100	46.5	ND	ND	ND	No
PRS6A	VDILDPALLR	Yes	562.8	328.2	18.82	100	30.3	ND	13790	7143	No
PRS6A	VDILDPALLR	Yes	562.8	569.4	18.82	100	36.3	ND	37667	9857	No
PRS6A	VDILDPALLR	Yes	562.8	684.4	18.82	100	30.3	ND	31287	13854	No
PRS6A	VDILDPALLR	Yes	562.8	797.5	18.82	100	27.3	ND	41349	17299	No
PSCA	AVGLLTVISK	Yes	500.82	347.2	18.26	65.6	33.5	82471	ND	ND	No
PSCA	AVGLLTVISK	Yes	500.82	547.3	18.26	65.6	24.5	77656	ND	ND	No
PSCA	AVGLLTVISK	Yes	500.82	660.4	18.26	65.6	24.5	122632	ND	ND	No
PSCA	AVGLLTVISK	Yes	500.82	830.5	18.26	65.6	24.5	286806	ND	ND	No
PTGIS	AGYLTLYGIEALPR	Yes	512.95	272.2	22.85	67.2	23.7	156593	ND	ND	No
PTGIS	AGYLTLYGIEALPR	Yes	512.95	456.3	22.85	67.2	26.7	379281	ND	ND	No
PTGIS	AGYLTLYGIEALPR	Yes	512.95	585.3	22.85	67.2	23.7	518928	ND	ND	No
PTGIS	AGYLTLYGIEALPR	Yes	512.95	755.4	22.85	67.2	29.7	139317	ND	ND	No
PTGIS	DPEIYTDPEVFK	Yes	726.85	342.1	17.29	94.8	43.5	1501781	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PTGIS	DPEIYTDPEVFK	Yes	726.85	619.3	17.29	94.8	43.5	508525	ND	ND	No
PTGIS	DPEIYTDPEVFK	Yes	726.85	835.4	17.29	94.8	34.5	246757	ND	ND	No
PTGIS	DPEIYTDPEVFK	Yes	726.85	998.5	17.29	94.8	31.5	497005	ND	ND	No
PTGIS	EVVVDLAMPMADGR	Yes	751.87	646.3	19.93	98	35.6	655707	ND	ND	No
PTGIS	EVVVDLAMPMADGR	Yes	751.87	777.3	19.93	98	35.6	334644	ND	ND	No
PTGIS	EVVVDLAMPMADGR	Yes	751.87	848.4	19.93	98	35.6	360759	ND	ND	No
PTGIS	EVVVDLAMPMADGR	Yes	751.87	961.5	19.93	98	41.6	120473	ND	ND	No
PTGIS	GELESILWQAEQPVSQTTTLPQK	Yes	861.78	372.2	22.51	112.2	41.5	203105	ND	ND	No
PTGIS	GELESILWQAEQPVSQTTTLPQK	Yes	861.78	485.3	22.51	112.2	41.5	28516	ND	ND	No
PTGIS	GELESILWQAEQPVSQTTTLPQK	Yes	861.78	742.4	22.51	112.2	44.5	18098	ND	ND	No
PTGIS	GELESILWQAEQPVSQTTTLPQK	Yes	861.78	788.5	22.51	112.2	47.5	31883	ND	ND	No
PTGIS	HGDIFTILVGGR	Yes	642.86	310.1	22.99	83.9	39.8	527727	ND	ND	No
PTGIS	HGDIFTILVGGR	Yes	642.86	423.2	22.99	83.9	36.8	252665	ND	ND	No
PTGIS	HGDIFTILVGGR	Yes	642.86	715.4	22.99	83.9	36.8	131406	ND	ND	No
PTGIS	HGDIFTILVGGR	Yes	642.86	862.5	22.99	83.9	36.8	277938	ND	ND	No
PTGIS	IFDVQLPHYSPSDEK	Yes	592.29	276.2	18.64	77.4	36.8	484721	ND	ND	No
PTGIS	IFDVQLPHYSPSDEK	Yes	592.29	376.2	18.64	77.4	30.8	338854	ND	ND	No
PTGIS	IFDVQLPHYSPSDEK	Yes	592.29	662.3	18.64	77.4	36.8	331765	ND	ND	No
PTGIS	IFDVQLPHYSPSDEK	Yes	592.29	825.4	18.64	77.4	33.8	291884	ND	ND	No
PTGIS	LLLFPFLSPQR	Yes	665.9	340.3	25.29	86.9	34.8	2202922	ND	ND	No
PTGIS	LLLFPFLSPQR	Yes	665.9	600.3	25.29	86.9	40.8	474763	ND	ND	No
PTGIS	LLLFPFLSPQR	Yes	665.9	747.4	25.29	86.9	40.8	349550	ND	ND	No
PTGIS	LLLFPFLSPQR	Yes	665.9	991.5	25.29	86.9	34.8	408407	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PTGIS	VHSADVFHTFR	No									
PTGIS	VLDSTPVLDSVLSESLR	Yes	915.5	328.2	24.11	119.1	48.8	125364	ND	ND	No
PTGIS	VLDSTPVLDSVLSESLR	Yes	915.5	516.3	24.11	119.1	39.8	132134	ND	ND	No
PTGIS	VLDSTPVLDSVLSESLR	Yes	915.5	591.3	24.11	119.1	39.8	58863	ND	ND	No
PTGIS	VLDSTPVLDSVLSESLR	Yes	915.5	890.5	24.11	119.1	42.8	35814	ND	ND	No
PTGIS	YGFGLMQPEHDVPVR	Yes	582.29	371.2	18.36	76.1	36.2	173552	ND	ND	No
PTGIS	YGFGLMQPEHDVPVR	Yes	582.29	470.3	18.36	76.1	36.2	196226	ND	ND	No
PTGIS	YGFGLMQPEHDVPVR	Yes	582.29	722.4	18.36	76.1	36.2	52001	ND	ND	No
PTGIS	YGFGLMQPEHDVPVR	Yes	582.29	948.5	18.36	76.1	27.2	114080	ND	ND	No
PTPA	FGSLLPIHPVTSG	Yes	662.87	292.1	18.64	86.5	34.7	93586	ND	ND	No
PTPA	FGSLLPIHPVTSG	Yes	662.87	597.3	18.64	86.5	40.7	29405	ND	ND	No
PTPA	FGSLLPIHPVTSG	Yes	662.87	807.4	18.64	86.5	31.7	199555	ND	ND	No
PTPA	FGSLLPIHPVTSG	Yes	662.87	920.5	18.64	86.5	31.7	35169	ND	ND	No
PTPA	LDEEAENLVATVVPTHLAAAVPEVAVYLK	No									
PTPA	TGPFAEHSNQLWNISAVPSWSK	Yes	819.4	604.3	20.62	106.7	45.3	38204	ND	ND	No
PTPA	TGPFAEHSNQLWNISAVPSWSK	Yes	819.4	774.4	20.62	106.7	36.3	10483	ND	ND	No
PTPA	TGPFAEHSNQLWNISAVPSWSK	Yes	819.4	861.4	20.62	106.7	36.3	30780	ND	ND	No
PTPA	TGPFAEHSNQLWNISAVPSWSK	Yes	819.4	974.5	20.62	106.7	36.3	4767	ND	ND	No
PTPA	VDDQIAIVFK	Yes	574.32	294.2	17.40	75.1	30.8	20366	ND	ND	No
PTPA	VDDQIAIVFK	Yes	574.32	393.3	17.40	75.1	24.8	15685	ND	ND	No
PTPA	VDDQIAIVFK	Yes	574.32	690.5	17.40	75.1	27.8	12476	ND	1621	No
PTPA	VDDQIAIVFK	Yes	574.32	933.5	17.40	75.1	27.8	9720	ND	ND	No
PTPA	WIDETPPVDQPSR	Yes	770.38	487.3	12.43	100.4	45.4	40752	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PTPA	WIDETPPVDQPSR	Yes	770.38	645.3	12.43	100.4	33.4	27965	ND	ND	No
PTPA	WIDETPPVDQPSR	Yes	770.38	895.5	12.43	100.4	36.4	29750	ND	ND	No
PTPA	WIDETPPVDQPSR	Yes	770.38	996.5	12.43	100.4	36.4	4746	ND	ND	No
PTPRC	DLQYSTDYTFK	Yes	690.82	294.2	14.26	90.1	41.9	84108	ND	ND	No
PTPRC	DLQYSTDYTFK	Yes	690.82	357.2	14.26	90.1	29.9	161971	ND	ND	No
PTPRC	DLQYSTDYTFK	Yes	690.82	395.2	14.26	90.1	41.9	43075	ND	ND	No
PTPRC	DLQYSTDYTFK	Yes	690.82	861.4	14.26	90.1	32.9	78102	ND	ND	No
PTPRC	SEAAHQGVITWNPPQR	Yes	597.64	400.2	12.79	78.1	37	23172	ND	ND	No
PTPRC	SEAAHQGVITWNPPQR	Yes	597.64	497.3	12.79	78.1	28	67926	ND	ND	No
PTPRC	SEAAHQGVITWNPPQR	Yes	597.64	780.4	12.79	78.1	37	15611	ND	ND	No
PTPRC	SEAAHQGVITWNPPQR	Yes	597.64	994.5	12.79	78.1	25	6303	ND	ND	No
PTPRC	TLILDVPPGVEK	Yes	640.88	328.2	16.42	83.7	27.7	315717	ND	ND	No
PTPRC	TLILDVPPGVEK	Yes	640.88	725.4	16.42	83.7	30.7	106646	ND	ND	No
PTPRC	TLILDVPPGVEK	Yes	640.88	840.4	16.42	83.7	30.7	222926	ND	ND	No
PTPRC	TLILDVPPGVEK	Yes	640.88	953.5	16.42	83.7	30.7	142920	ND	ND	No
PTPRC	YDLQNLKPYTK	Yes	461.58	279.1	12.92	60.5	21.1	193901	ND	ND	No
PTPRC	YDLQNLKPYTK	Yes	461.58	508.3	12.92	60.5	30.1	328966	ND	ND	No
PTPRC	YDLQNLKPYTK	Yes	461.58	636.4	12.92	60.5	27.1	37715	ND	ND	No
PTPRC	YDLQNLKPYTK	Yes	461.58	863.5	12.92	60.5	24.1	29296	ND	ND	No
PTPRC	YVDILPYDYNR	Yes	715.85	378.2	17.38	93.3	34	161115	ND	ND	No
PTPRC	YVDILPYDYNR	Yes	715.85	491.3	17.38	93.3	34	109277	ND	ND	No
PTPRC	YVDILPYDYNR	Yes	715.85	827.4	17.38	93.3	34	279264	ND	ND	No
PTPRC	YVDILPYDYNR	Yes	715.85	940.5	17.38	93.3	31	48676	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
PTPRJ	AGSPTAPVHDESLVGPVDPSSGQQSR	Yes	859.08	662.3	12.08	111.8	50.4	2220	ND	ND	No
PTPRJ	AGSPTAPVHDESLVGPVDPSSGQQSR	Yes	859.08	749.4	12.08	111.8	47.4	2096	486	ND	No
PTPRJ	AGSPTAPVHDESLVGPVDPSSGQQSR	Yes	859.08	961.4	12.08	111.8	38.4	4263	ND	ND	No
PTPRJ	AVSISPTNVILTWK	Yes	764.94	258.1	21.31	99.7	36.2	12528	30868	32783	No
PTPRJ	AVSISPTNVILTWK	Yes	764.94	434.2	21.31	99.7	36.2	5005	9961	12748	No
PTPRJ	AVSISPTNVILTWK	Yes	764.94	458.3	21.31	99.7	33.2	10454	23820	22010	No
PTPRJ	AVSISPTNVILTWK	Yes	764.94	547.3	21.31	99.7	42.2	5949	13603	9396	No
PTPRJ	TPSSTGPSPVFDIK	Yes	716.87	260.2	14.98	93.5	34	333148	26596	33358	No
PTPRJ	TPSSTGPSPVFDIK	Yes	716.87	522.3	14.98	93.5	43	136301	12500	13826	No
PTPRJ	TPSSTGPSPVFDIK	Yes	716.87	902.5	14.98	93.5	40	147716	9215	10517	No
PTPRJ	TPSSTGPSPVFDIK	Yes	716.87	959.5	14.98	93.5	37	179272	10592	12066	No
PTPRJ	VITEPIPVSDLR	Yes	669.89	288.2	15.87	87.4	41	123416	110071	116804	No
PTPRJ	VITEPIPVSDLR	Yes	669.89	314.2	15.87	87.4	35	69889	52537	67558	No
PTPRJ	VITEPIPVSDLR	Yes	669.89	443.3	15.87	87.4	29	71970	61358	56714	No
PTPRJ	VITEPIPVSDLR	Yes	669.89	896.5	15.87	87.4	32	180212	153508	162361	No
PTPRJ	VLLESIGSHEELTQDSR	Yes	638.33	262.2	14.51	83.3	39.1	161418	118246	151314	Yes (Based on Transition Ratios)
PTPRJ	VLLESIGSHEELTQDSR	Yes	638.33	606.3	14.51	83.3	39.1	201524	29712	31102	No
PTPRJ	VLLESIGSHEELTQDSR	Yes	638.33	719.4	14.51	83.3	39.1	83592	12931	22498	No
PTPRJ	VLLESIGSHEELTQDSR	Yes	638.33	848.4	14.51	83.3	33.1	ND	11877	5526	Yes (Based on Manual Review)
PVR	EGPPSEHSGISR	Yes	626.8	519.3	6.20	81.9	36.1	7517	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
PVR	EGPPSEHSGISR	Yes	626.8	656.3	6.20	81.9	39.1	9148	ND	ND	No
PVR	EGPPSEHSGISR	Yes	626.8	872.4	6.20	81.9	39.1	5370	ND	ND	No
PVR	EGPPSEHSGISR	Yes	626.8	969.5	6.20	81.9	39.1	11179	ND	ND	No
PVR	ENSSSQDPQTEGTR	Yes	768.33	333.2	5.45	100.1	33.3	15133	ND	ND	No
PVR	ENSSSQDPQTEGTR	Yes	768.33	563.3	5.45	100.1	42.3	9419	ND	ND	No
PVR	ENSSSQDPQTEGTR	Yes	768.33	788.4	5.45	100.1	42.3	60537	ND	ND	No
PVR	ENSSSQDPQTEGTR	Yes	768.33	903.4	5.45	100.1	39.3	13459	ND	ND	No
PVR	QAELTVQVK	Yes	508.29	473.3	13.28	66.6	24.9	3998	ND	ND	No
PVR	QAELTVQVK	Yes	508.29	574.4	13.28	66.6	24.9	47277	ND	ND	No
PVR	QAELTVQVK	Yes	508.29	687.4	13.28	66.6	24.9	17273	ND	ND	No
PVR	QAELTVQVK	Yes	508.29	816.5	13.28	66.6	33.9	2581	ND	ND	No
PVR	SVDIWLR	Yes	444.75	302.1	16.87	58.4	22.1	22809	96590	97613	No
PVR	SVDIWLR	Yes	444.75	474.3	16.87	58.4	22.1	18205	117062	104481	No
PVR	SVDIWLR	Yes	444.75	587.4	16.87	58.4	31.1	13053	61747	76450	No
PVR	SVDIWLR	Yes	444.75	702.4	16.87	58.4	22.1	54572	283778	342198	No
PVR	VLAKPQNTAEVQK	Yes	475.94	374.2	6.81	62.4	27.8	34361	15637	21662	No
PVR	VLAKPQNTAEVQK	Yes	475.94	503.3	6.81	62.4	21.8	22727	12199	14154	No
PVR	VLAKPQNTAEVQK	Yes	475.94	574.3	6.81	62.4	21.8	43193	16786	17291	No
PVR	VLAKPQNTAEVQK	Yes	475.94	789.4	6.81	62.4	27.8	31934	13608	20565	No
RAB32	DNINIEEAAR	Yes	572.78	317.2	10.78	74.9	33.7	19604	ND	ND	No
RAB32	DNINIEEAAR	Yes	572.78	457.2	10.78	74.9	27.7	17583	ND	ND	No
RAB32	DNINIEEAAR	Yes	572.78	688.4	10.78	74.9	27.7	26678	ND	ND	No
RAB32	DNINIEEAAR	Yes	572.78	802.4	10.78	74.9	27.7	56526	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
RAB32	ILVNHQSFPNEENDVDK	Yes	666.66	262.1	11.33	87	37.5	ND	ND	ND	No
RAB32	ILVNHQSFPNEENDVDK	Yes	666.66	719.3	11.33	87	31.5	ND	ND	ND	No
RAB32	ILVNHQSFPNEENDVDK	Yes	666.66	939.5	11.33	87	28.5	ND	ND	ND	No
RAB32	ILVNHQSFPNEENDVDK	Yes	666.66	962.4	11.33	87	31.5	ND	ND	ND	No
RAB32	LDQETLR	No									
RAB32	VHLPNGSPIPAVLLANK	Yes	580.68	558.4	18.62	75.9	36.2	79050	ND	ND	No
RAB32	VHLPNGSPIPAVLLANK	Yes	580.68	705.4	18.62	75.9	27.2	137728	ND	ND	No
RAB32	VHLPNGSPIPAVLLANK	Yes	580.68	825.5	18.62	75.9	27.2	404908	ND	ND	No
RAB32	VHLPNGSPIPAVLLANK	Yes	580.68	915.5	18.62	75.9	27.2	83964	ND	ND	No
RAB32	VLVIGELGVGK	Yes	542.34	312.2	17.62	71	26.4	283213	ND	ND	No
RAB32	VLVIGELGVGK	Yes	542.34	659.4	17.62	71	26.4	245151	ND	ND	No
RAB32	VLVIGELGVGK	Yes	542.34	772.5	17.62	71	26.4	210012	ND	ND	No
RAB32	VLVIGELGVGK	Yes	542.34	871.5	17.62	71	26.4	155956	ND	ND	No
RAGE	AELNQSEEPEAGESSTGGP	Yes	944.91	691.3	9.23	122.9	47.1	1479	ND	ND	No
RAGE	AELNQSEEPEAGESSTGGP	Yes	944.91	762.3	9.23	122.9	41.1	2781	ND	ND	No
RAGE	AELNQSEEPEAGESSTGGP	Yes	944.91	901.4	9.23	122.9	41.1	2446	ND	ND	No
RAGE	AELNQSEEPEAGESSTGGP	Yes	944.91	988.4	9.23	122.9	44.1	4492	ND	ND	No
RAGE	IGEPLVLK	Yes	434.78	300.2	13.70	57.1	21.6	642182	ND	1139	No
RAGE	IGEPLVLK	Yes	434.78	569.4	13.70	57.1	21.6	740035	ND	3021	No
RAGE	IGEPLVLK	Yes	434.78	698.4	13.70	57.1	21.6	194909	ND	3371	No
RAGE	IGEPLVLK	Yes	434.78	755.5	13.70	57.1	21.6	1012378	2600	6308	No
RAGE	VLPNGSLFLPAVGIQDEGIFR	Yes	1121.62	621.3	24.48	145.7	60.9	26881	ND	ND	No
RAGE	VLPNGSLFLPAVGIQDEGIFR	Yes	1121.62	681.4	24.48	145.7	48.9	12004	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
RAGE	VLPNGSLFLPAVGIQDEGIFR	Yes	1121.62	828.5	24.48	145.7	48.9	29372	ND	ND	No
RAGE	VLPNGSLFLPAVGIQDEGIFR	Yes	1121.62	941.5	24.48	145.7	48.9	32952	ND	ND	No
RAGE	VLSPQGGGPWDSVAR	Yes	763.39	547.3	14.71	99.5	42.1	21829	ND	ND	No
RAGE	VLSPQGGGPWDSVAR	Yes	763.39	830.4	14.71	99.5	45.1	21005	ND	ND	No
RAGE	VLSPQGGGPWDSVAR	Yes	763.39	887.4	14.71	99.5	45.1	11778	ND	ND	No
RAGE	VLSPQGGGPWDSVAR	Yes	763.39	944.5	14.71	99.5	39.1	10928	ND	ND	No
RAGE	VYQIPGKPEIVDSASELTAGVPNK	Yes	838.11	358.2	16.95	109.1	40.3	31793	ND	ND	No
RAGE	VYQIPGKPEIVDSASELTAGVPNK	Yes	838.11	391.2	16.95	109.1	40.3	25875	ND	ND	No
RAGE	VYQIPGKPEIVDSASELTAGVPNK	Yes	838.11	514.3	16.95	109.1	49.3	3469	ND	ND	No
RAGE	VYQIPGKPEIVDSASELTAGVPNK	Yes	838.11	686.4	16.95	109.1	40.3	5536	ND	ND	No
RAN	FNVWDTAGQEK	Yes	647.81	262.1	14.74	84.6	31	858762	5638	3588	No
RAN	FNVWDTAGQEK	Yes	647.81	461.2	14.74	84.6	40	71918	ND	ND	No
RAN	FNVWDTAGQEK	Yes	647.81	748.3	14.74	84.6	40	123355	ND	ND	No
RAN	FNVWDTAGQEK	Yes	647.81	934.4	14.74	84.6	31	153257	ND	ND	No
RAN	LVLVGDGGTGK	Yes	508.29	326.2	11.32	66.6	24.9	416446	ND	ND	No
RAN	LVLVGDGGTGK	Yes	508.29	591.3	11.32	66.6	24.9	562567	ND	ND	No
RAN	LVLVGDGGTGK	Yes	508.29	690.3	11.32	66.6	24.9	241811	ND	ND	No
RAN	LVLVGDGGTGK	Yes	508.29	803.4	11.32	66.6	24.9	426148	ND	ND	No
RAN	NVPNWHR	Yes	308.16	498.3	8.37	40.8	19.3	7198	ND	ND	No
RAN	NVPNWHR	Yes	308.16	612.3	8.37	40.8	16.3	3642	ND	ND	No
RAP2B	ASVDELFAEIVR	Yes	674.86	373.2	24.20	88.1	32.2	14181	ND	ND	No
RAP2B	ASVDELFAEIVR	Yes	674.86	587.4	24.20	88.1	32.2	37846	ND	ND	No
RAP2B	ASVDELFAEIVR	Yes	674.86	734.4	24.20	88.1	32.2	51901	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
RAP2B	ASVDELFAEIVR	Yes	674.86	847.5	24.20	88.1	32.2	22881	ND	ND	No
RAP2B	EVSYGEGK	Yes	434.71	333.2	6.12	57.1	18.6	48293	ND	ND	No
RAP2B	EVSYGEGK	Yes	434.71	390.2	6.12	57.1	24.6	693650	ND	ND	No
RAP2B	EVSYGEGK	Yes	434.71	553.3	6.12	57.1	21.6	214059	ND	ND	No
RAP2B	EVSYGEGK	Yes	434.71	640.3	6.12	57.1	21.6	472268	ND	ND	No
RAP2B	SALTVQFVTGSFIEK	No									
RAP2B	VDLEGER	Yes	409.21	361.2	7.88	53.8	29.5	51707	ND	ND	No
RAP2B	VDLEGER	Yes	409.21	490.2	7.88	53.8	29.5	18844	ND	ND	No
RAP2B	VDLEGER	Yes	409.21	603.3	7.88	53.8	20.5	63894	ND	ND	No
RAP2B	VDLEGER	Yes	409.21	718.3	7.88	53.8	20.5	39225	ND	ND	No
RAP2B	VVVLGSGGVGK	Yes	324.53	360.2	9.84	42.9	17.1	ND	ND	ND	No
RAP2B	VVVLGSGGVGK	Yes	324.53	417.2	9.84	42.9	20.1	ND	ND	ND	No
RAP2B	VVVLGSGGVGK	Yes	324.53	561.3	9.84	42.9	20.1	751	ND	ND	No
RAP2B	VVVLGSGGVGK	Yes	324.53	674.4	9.84	42.9	23.1	ND	ND	ND	No
RAP2C	SALTVQFVTGTFIEK	No									
RAP2C	VDLEPER	No									
RAP2C	VPLILVGNK	Yes	476.81	530.3	15.42	62.5	26.5	126877	ND	ND	No
RAP2C	VPLILVGNK	Yes	476.81	643.4	15.42	62.5	26.5	147551	ND	ND	No
RAP2C	VPLILVGNK	Yes	476.81	756.5	15.42	62.5	23.5	88717	ND	ND	No
RAP2C	VPLILVGNK	Yes	476.81	853.6	15.42	62.5	32.5	15714	ND	ND	No
RAP2C	VVVLGSGGVGK	Yes	324.53	360.2	9.84	42.9	17.1	ND	ND	ND	No
RAP2C	VVVLGSGGVGK	Yes	324.53	417.2	9.84	42.9	20.1	ND	ND	ND	No
RAP2C	VVVLGSGGVGK	Yes	324.53	561.3	9.84	42.9	20.1	751	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
RAP2C	VVVLGSGGVGK	Yes	324.53	674.4	9.84	42.9	23.1	ND	ND	ND	No
RCN3	AGDGDGWVSLAELR	Yes	723.35	416.1	19.87	94.3	34.3	28885	ND	ND	No
RCN3	AGDGDGWVSLAELR	Yes	723.35	488.3	19.87	94.3	34.3	26051	ND	ND	No
RCN3	AGDGDGWVSLAELR	Yes	723.35	688.4	19.87	94.3	34.3	65108	ND	ND	No
RCN3	AGDGDGWVSLAELR	Yes	723.35	787.5	19.87	94.3	34.3	59833	ND	ND	No
RCN3	AWIAHTQQR	Yes	555.79	258.1	7.95	72.7	30	ND	ND	ND	No
RCN3	AWIAHTQQR	Yes	555.79	371.2	7.95	72.7	27	ND	ND	ND	No
RCN3	AWIAHTQQR	Yes	555.79	532.3	7.95	72.7	33	ND	ND	ND	No
RCN3	AWIAHTQQR	Yes	555.79	853.5	7.95	72.7	36	ND	ND	ND	No
RCN3	DIVIAETLEDLDR	Yes	751.39	328.2	22.08	97.9	32.6	14427	ND	ND	No
RCN3	DIVIAETLEDLDR	Yes	751.39	647.3	22.08	97.9	35.6	5210	ND	ND	No
RCN3	DIVIAETLEDLDR	Yes	751.39	861.4	22.08	97.9	35.6	3650	ND	ND	No
RCN3	DIVIAETLEDLDR	Yes	751.39	990.5	22.08	97.9	35.6	3831	ND	ND	No
RCN3	EFDQLTPEESQAR	Yes	775.36	374.2	11.64	101	45.6	30224	ND	ND	No
RCN3	EFDQLTPEESQAR	Yes	775.36	734.3	11.64	101	36.6	6019	ND	ND	No
RCN3	EFDQLTPEESQAR	Yes	775.36	816.4	11.64	101	36.6	69648	ND	ND	No
RCN3	EFDQLTPEESQAR	Yes	775.36	917.4	11.64	101	45.6	24932	ND	ND	No
RCN3	VGWEELR	Yes	444.73	417.2	13.21	58.4	22.1	2057	ND	ND	No
RCN3	VGWEELR	Yes	444.73	546.3	13.21	58.4	19.1	ND	ND	ND	No
RCN3	VGWEELR	Yes	444.73	732.4	13.21	58.4	25.1	ND	ND	ND	No
RCN3	VGWEELR	Yes	444.73	789.4	13.21	58.4	31.1	ND	ND	ND	No
RL24	VFQFLNAK	Yes	483.77	445.3	16.67	63.4	32.8	174791	ND	ND	No
RL24	VFQFLNAK	Yes	483.77	592.3	16.67	63.4	23.8	275187	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
RL24	VFQFLNAK	Yes	483.77	720.4	16.67	63.4	23.8	327998	ND	ND	No
RL24	VFQFLNAK	Yes	483.77	867.5	16.67	63.4	23.8	67580	ND	ND	No
S10A1	DVDAVDK	Yes	381.19	262.1	6.01	50.2	28.3	528766	14896	17878	Yes (Based on Transition Ratios)
S10A1	DVDAVDK	Yes	381.19	330.1	6.01	50.2	19.3	67402	ND	ND	No
S10A1	DVDAVDK	Yes	381.19	432.2	6.01	50.2	19.3	147420	ND	ND	No
S10A1	DVDAVDK	Yes	381.19	547.3	6.01	50.2	19.3	1361694	322694	278264	Yes (Based on Transition Ratios)
S10A1	ELLQTELSGFLDAQK	Yes	846.45	461.2	22.61	110.2	36.7	12426	ND	ND	No
S10A1	ELLQTELSGFLDAQK	Yes	846.45	721.4	22.61	110.2	36.7	3990	ND	ND	No
S10A1	ELLQTELSGFLDAQK	Yes	846.45	778.4	22.61	110.2	39.7	18561	ND	ND	No
S10A1	ELLQTELSGFLDAQK	Yes	846.45	978.5	22.61	110.2	39.7	13013	ND	ND	No
S10A6	DQEVNFQEYVTFLGALALIYNEALK	No									
S10A6	ELTIGSK	Yes	374.22	291.2	8.73	49.3	19	ND	24997	27801	Yes (Based on Manual Review)
S10A6	ELTIGSK	Yes	374.22	404.3	8.73	49.3	19	205261	3676	6124	No
S10A6	ELTIGSK	Yes	374.22	505.3	8.73	49.3	19	251227	5278	9418	No
S10A6	ELTIGSK	Yes	374.22	618.4	8.73	49.3	22	10567	ND	ND	No
S10A6	LQDAEIAR	Yes	458.25	359.2	8.02	60.1	31.7	ND	10713	18949	Yes (Based on Manual Review)
S10A6	LQDAEIAR	Yes	458.25	559.3	8.02	60.1	31.7	29745	23029	16082	No
S10A6	LQDAEIAR	Yes	458.25	674.3	8.02	60.1	22.7	80482	45910	62354	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
S10A6	LQDAEIAR	Yes	458.25	802.4	8.02	60.1	31.7	9118	5266	4497	No
S10A7	No peptide										
SAA	DPNHFRPAGLPEK	Yes	739.38	373.2	9.96	96.4	41	56757	ND	ND	No
SAA	DPNHFRPAGLPEK	Yes	739.38	464.2	9.96	96.4	44	4421	ND	ND	No
SAA	DPNHFRPAGLPEK	Yes	739.38	543.3	9.96	96.4	38	2963	ND	ND	No
SAA	DPNHFRPAGLPEK	Yes	739.38	867.5	9.96	96.4	41	2291	ND	ND	No
SAA	EANYIGSDK	Yes	498.74	406.2	7.45	65.3	24.4	959911	ND	ND	No
SAA	EANYIGSDK	Yes	498.74	519.3	7.45	65.3	24.4	351713	ND	ND	No
SAA	EANYIGSDK	Yes	498.74	682.3	7.45	65.3	24.4	84700	ND	ND	No
SAA	EANYIGSDK	Yes	498.74	796.4	7.45	65.3	24.4	112529	ND	ND	No
SAA	FFGHGAEDSLADQAANEWGR	Yes	1089.49	418.2	16.92	141.5	53.4	4927	ND	ND	No
SAA	FFGHGAEDSLADQAANEWGR	Yes	1089.49	489.2	16.92	141.5	53.4	4675	ND	ND	No
SAA	FFGHGAEDSLADQAANEWGR	Yes	1089.49	661.3	16.92	141.5	59.4	ND	ND	ND	No
SAA	FFGHGAEDSLADQAANEWGR	Yes	1089.49	931.4	16.92	141.5	56.4	ND	ND	ND	No
SAA	SFFSFLGEAFDGAR	Yes	775.87	303.2	24.69	101.1	45.6	ND	11314	ND	Yes (Based on Manual Review)
SAA	SFFSFLGEAFDGAR	Yes	775.87	636.3	24.69	101.1	36.6	ND	ND	ND	Yes (Based on Manual Review)
SAA	SFFSFLGEAFDGAR	Yes	775.87	822.4	24.69	101.1	33.6	148875	16482	ND	No
SAA	SFFSFLGEAFDGAR	Yes	775.87	935.5	24.69	101.1	33.6	45584	7530	6834	No
SCF	FSNISEGLSNYSIIDK	Yes	893.95	349.2	17.92	116.3	44.8	60571	ND	ND	No
SCF	FSNISEGLSNYSIIDK	Yes	893.95	375.2	17.92	116.3	38.8	24301	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
SCF	FSNISEGLSNYSIIDK	Yes	893.95	462.2	17.92	116.3	38.8	17281	ND	ND	No
SCF	FSNISEGLSNYSIIDK	Yes	893.95	939.5	17.92	116.3	41.8	16469	ND	ND	No
SCF	LFTPEEFFR	Yes	593.3	261.2	22.31	77.5	28.6	73410	ND	ND	No
SCF	LFTPEEFFR	Yes	593.3	362.2	22.31	77.5	25.6	48497	ND	ND	No
SCF	LFTPEEFFR	Yes	593.3	824.4	22.31	77.5	28.6	81177	ND	ND	No
SCF	LFTPEEFFR	Yes	593.3	925.4	22.31	77.5	28.6	28216	ND	ND	No
SCF	LVANLPK	Yes	377.74	357.3	10.46	49.7	28.1	145411	ND	ND	No
SCF	LVANLPK	Yes	377.74	471.3	10.46	49.7	19.1	54580	ND	ND	No
SCF	LVANLPK	Yes	377.74	542.3	10.46	49.7	19.1	1228873	ND	ND	No
SCF	LVANLPK	Yes	377.74	641.4	10.46	49.7	19.1	210875	ND	ND	No
SDC1	DTQLLTAIPTSPEPTGLEATAASTSTLPAGEGPK	No									
SDC1	EGEAVVLPEVEPGLTAR	Yes	883.47	387.2	17.02	115	41.4	51603	ND	ND	No
SDC1	EGEAVVLPEVEPGLTAR	Yes	883.47	486.2	17.02	115	41.4	82652	ND	ND	No
SDC1	EGEAVVLPEVEPGLTAR	Yes	883.47	585.3	17.02	115	38.4	105119	ND	ND	No
SDC1	EGEAVVLPEVEPGLTAR	Yes	883.47	698.4	17.02	115	38.4	125757	ND	ND	No
SDC1	EQEATPRPR	No									
SDC1	ETTQLPTTHLASTTTATTAQEPATSHPHR	No									
SDC1	QANGGAYQKPTK	Yes	631.83	345.2	5.43	82.5	33.3	15593	ND	ND	No
SDC1	QANGGAYQKPTK	Yes	631.83	473.3	5.43	82.5	39.3	5862	ND	ND	No
SDC1	QANGGAYQKPTK	Yes	631.83	764.4	5.43	82.5	39.3	4242	ND	ND	No
SDC1	QANGGAYQKPTK	Yes	631.83	949.5	5.43	82.5	30.3	2685	ND	ND	No
SEM3G	DILQLIGFANLPR	Yes	735.43	570.3	24.69	95.9	34.9	13429	ND	ND	No
SEM3G	DILQLIGFANLPR	Yes	735.43	583.3	24.69	95.9	31.9	26884	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
SEM3G	DILQLIGFANLPR	Yes	735.43	774.4	24.69	95.9	31.9	55757	ND	ND	No
SEM3G	DILQLIGFANLPR	Yes	735.43	887.5	24.69	95.9	34.9	24186	ND	ND	No
SEM3G	DYPDEVLQFAR	Yes	676.83	521.3	18.18	88.3	35.3	73122	ND	ND	No
SEM3G	DYPDEVLQFAR	Yes	676.83	634.4	18.18	88.3	35.3	105183	ND	ND	No
SEM3G	DYPDEVLQFAR	Yes	676.83	733.4	18.18	88.3	38.3	62824	ND	ND	No
SEM3G	DYPDEVLQFAR	Yes	676.83	977.5	18.18	88.3	41.3	60392	ND	ND	No
SEM3G	EVLWPPQPGQR	Yes	653.85	457.3	15.69	85.3	40.3	7847	ND	ND	No
SEM3G	EVLWPPQPGQR	Yes	653.85	682.4	15.69	85.3	40.3	4405	ND	ND	No
SEM3G	EVLWPPQPGQR	Yes	653.85	779.4	15.69	85.3	31.3	23474	ND	ND	No
SEM3G	EVLWPPQPGQR	Yes	653.85	965.5	15.69	85.3	31.3	1420	ND	ND	No
SEM3G	LFLGGLDALYSLR	Yes	719.41	375.2	24.59	93.8	31.2	144365	6636	6922	No
SEM3G	LFLGGLDALYSLR	Yes	719.41	538.3	24.59	93.8	34.2	131258	17970	5471	No
SEM3G	LFLGGLDALYSLR	Yes	719.41	651.4	24.59	93.8	34.2	ND	ND	ND	Yes (Based on Manual Review)
SEM3G	LFLGGLDALYSLR	Yes	719.41	837.4	24.59	93.8	34.2	214355	24277	25910	No
SEM3G	VIALQAGGSAEPEEVVLEELQVFK	Yes	852.46	294.2	24.59	111	38	20072	ND	ND	No
SEM3G	VIALQAGGSAEPEEVVLEELQVFK	Yes	852.46	763.4	24.59	111	38	13805	ND	ND	No
SEM3G	VIALQAGGSAEPEEVVLEELQVFK	Yes	852.46	892.5	24.59	111	41	15384	ND	ND	No
SEM3G	VIALQAGGSAEPEEVVLEELQVFK	Yes	852.46	997.5	24.59	111	41	12632	ND	ND	No
SEPR	LAYVYQNNIYLK	Yes	751.41	260.2	16.00	97.9	35.6	6421	ND	ND	No
SEPR	LAYVYQNNIYLK	Yes	751.41	348.2	16.00	97.9	35.6	22566	ND	ND	No
SEPR	LAYVYQNNIYLK	Yes	751.41	423.3	16.00	97.9	35.6	5825	ND	ND	No
SEPR	LAYVYQNNIYLK	Yes	751.41	892.5	16.00	97.9	35.6	2276	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
SEPR	NVDYLLIHGTADDNVHFQNSAQIAK	No									
SEPR	QFVVYLESDYSK	Yes	689.83	397.2	14.91	90	41.9	17314	ND	ND	No
SEPR	QFVVYLESDYSK	Yes	689.83	599.3	14.91	90	32.9	13219	ND	ND	No
SEPR	QFVVYLESDYSK	Yes	689.83	728.3	14.91	90	32.9	20818	ND	ND	No
SEPR	QFVVYLESDYSK	Yes	689.83	841.4	14.91	90	29.9	10426	ND	ND	No
SEPR	SVFAVNWISYLASK	No									
SEPR	TQEHIEESR	Yes	564.77	520.2	5.62	73.9	33.3	2630	ND	ND	No
SEPR	TQEHIEESR	Yes	564.77	633.3	5.62	73.9	36.3	3506	ND	ND	No
SEPR	TQEHIEESR	Yes	564.77	770.4	5.62	73.9	33.3	3068	ND	ND	No
SEPR	TQEHIEESR	Yes	564.77	899.4	5.62	73.9	27.3	2053	ND	ND	No
SERPH	AVLSAEQLR	Yes	493.79	545.3	11.41	64.7	24.2	68233	ND	ND	No
SERPH	AVLSAEQLR	Yes	493.79	616.3	11.41	64.7	24.2	102913	ND	1077	No
SERPH	AVLSAEQLR	Yes	493.79	703.4	11.41	64.7	24.2	227242	ND	ND	No
SERPH	AVLSAEQLR	Yes	493.79	816.5	11.41	64.7	24.2	184073	ND	ND	No
SERPH	DEEVHAGLGELLR	Yes	479.92	401.3	16.64	62.9	25	118601	ND	ND	No
SERPH	DEEVHAGLGELLR	Yes	479.92	587.4	16.64	62.9	22	108940	ND	ND	No
SERPH	DEEVHAGLGELLR	Yes	479.92	757.5	16.64	62.9	31	103628	ND	ND	No
SERPH	DEEVHAGLGELLR	Yes	479.92	828.5	16.64	62.9	31	108592	ND	ND	No
SERPH	DQAVENILVSPVVVASSLGLVSLGGK	Yes	851.15	374.2	23.92	110.8	47	11523	ND	9547	No
SERPH	DQAVENILVSPVVVASSLGLVSLGGK	Yes	851.15	657.3	23.92	110.8	47	4351	ND	5348	No
SERPH	DQAVENILVSPVVVASSLGLVSLGGK	Yes	851.15	673.4	23.92	110.8	41	5133	ND	7478	No
SERPH	DQAVENILVSPVVVASSLGLVSLGGK	Yes	851.15	730.4	23.92	110.8	44	13071	ND	6341	No
SERPH	DTQSGSLLFIGR	Yes	647.34	492.3	17.85	84.5	31	97460	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
SERPH	DTQSGSLLFIGR	Yes	647.34	605.4	17.85	84.5	34	66640	ND	ND	No
SERPH	DTQSGSLLFIGR	Yes	647.34	805.5	17.85	84.5	34	30443	ND	ND	No
SERPH	DTQSGSLLFIGR	Yes	647.34	862.5	17.85	84.5	40	54942	ND	ND	No
SERPH	GVVEVTHDLQK	Yes	408.89	503.3	10.37	53.7	21.4	15922	ND	ND	No
SERPH	GVVEVTHDLQK	Yes	408.89	640.3	10.37	53.7	21.4	21168	ND	ND	No
SERPH	GVVEVTHDLQK	Yes	408.89	741.4	10.37	53.7	21.4	30420	ND	ND	No
SERPH	GVVEVTHDLQK	Yes	408.89	840.5	10.37	53.7	27.4	4748	ND	ND	No
SFPA2	GPPGLPAHLDEELQATLHDFR	Yes	771.73	322.2	23.25	100.6	39.9	57460	ND	ND	No
SFPA2	GPPGLPAHLDEELQATLHDFR	Yes	771.73	422.2	23.25	100.6	36.9	37974	ND	ND	No
SFPA2	GPPGLPAHLDEELQATLHDFR	Yes	771.73	574.3	23.25	100.6	36.9	15512	ND	ND	No
SFPA2	GPPGLPAHLDEELQATLHDFR	Yes	771.73	859.4	23.25	100.6	42.9	19392	ND	ND	No
SFPA2	HQILQTR	Yes	448.26	266.1	7.08	58.8	25.2	34686	1288	2524	No
SFPA2	HQILQTR	Yes	448.26	517.3	7.08	58.8	25.2	11846	ND	ND	No
SFPA2	HQILQTR	Yes	448.26	630.4	7.08	58.8	25.2	31337	1284	4356	No
SFPA2	HQILQTR	Yes	448.26	758.5	7.08	58.8	25.2	ND	1989	3294	Yes (Based on Manual Review)
SFPA2	YSDGTPVNYTNWYR	Yes	868.39	338.2	16.13	113	43.7	11969	ND	ND	No
SFPA2	YSDGTPVNYTNWYR	Yes	868.39	366.1	16.13	113	40.7	7192	ND	ND	No
SFPA2	YSDGTPVNYTNWYR	Yes	868.39	739.4	16.13	113	40.7	12602	ND	ND	No
SFPA2	YSDGTPVNYTNWYR	Yes	868.39	902.4	16.13	113	37.7	5659	ND	ND	No
SFTA1	GPPGLPAHLDEELQATLHDFR	Yes	771.73	322.2	23.25	100.6	39.9	57460	ND	ND	No
SFTA1	GPPGLPAHLDEELQATLHDFR	Yes	771.73	422.2	23.25	100.6	36.9	37974	ND	ND	No
SFTA1	GPPGLPAHLDEELQATLHDFR	Yes	771.73	574.3	23.25	100.6	36.9	15512	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
SFTA1	GPPGLPAHLDEELQATLHDFR	Yes	771.73	859.4	23.25	100.6	42.9	19392	ND	ND	No
SFTA1	HQILQTR	Yes	448.26	266.1	7.08	58.8	25.2	34686	1288	2524	No
SFTA1	HQILQTR	Yes	448.26	517.3	7.08	58.8	25.2	11846	ND	ND	No
SFTA1	HQILQTR	Yes	448.26	630.4	7.08	58.8	25.2	31337	1284	4356	No
SFTA1	HQILQTR	Yes	448.26	758.5	7.08	58.8	25.2	ND	1989	3294	Yes (Based on Manual Review)
SFTA1	YSDGTPVNYTNWYR	Yes	868.39	338.2	16.13	113	43.7	11969	ND	ND	No
SFTA1	YSDGTPVNYTNWYR	Yes	868.39	366.1	16.13	113	40.7	7192	ND	ND	No
SFTA1	YSDGTPVNYTNWYR	Yes	868.39	739.4	16.13	113	40.7	12602	ND	ND	No
SFTA1	YSDGTPVNYTNWYR	Yes	868.39	902.4	16.13	113	37.7	5659	ND	ND	No
SG3A2	VPLPVDK	Yes	384.24	262.1	9.63	50.6	28.4	275093	ND	ND	No
SG3A2	VPLPVDK	Yes	384.24	458.3	9.63	50.6	25.4	501455	ND	ND	No
SG3A2	VPLPVDK	Yes	384.24	571.3	9.63	50.6	19.4	76171	ND	ND	No
SG3A2	VPLPVDK	Yes	384.24	668.4	9.63	50.6	19.4	87385	ND	ND	No
SGPL1	AGYPLEHPFDFR	No									
SGPL1	ALPSQGLSSSAVLEK	Yes	743.91	389.2	13.29	97	44.2	49971	ND	ND	No
SGPL1	ALPSQGLSSSAVLEK	Yes	743.91	820.4	13.29	97	44.2	63025	ND	ND	No
SGPL1	ALPSQGLSSSAVLEK	Yes	743.91	933.5	13.29	97	44.2	8920	ND	ND	No
SGPL1	ALPSQGLSSSAVLEK	Yes	743.91	990.5	13.29	97	35.2	19727	ND	ND	No
SGPL1	DFDIYR	No									
SGPL1	GIFVFGNPQLSVIALGSR	No									
SGPL1	TPEIVAPQSAHAAFNK	Yes	560.96	328.2	11.69	73.4	26.2	149023	ND	ND	No
SGPL1	TPEIVAPQSAHAAFNK	Yes	560.96	441.2	11.69	73.4	26.2	72289	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
SGPL1	TPEIVAPQSAHAAFNK	Yes	560.96	687.4	11.69	73.4	32.2	37928	ND	ND	No
SGPL1	TPEIVAPQSAHAAFNK	Yes	560.96	845.4	11.69	73.4	35.2	35212	ND	ND	No
SIAL	AYEDEYSYFK	Yes	657.78	544.3	14.00	85.9	40.4	102772	ND	ND	No
SIAL	AYEDEYSYFK	Yes	657.78	707.3	14.00	85.9	31.4	58308	ND	ND	No
SIAL	AYEDEYSYFK	Yes	657.78	836.4	14.00	85.9	31.4	49778	ND	ND	No
SIAL	AYEDEYSYFK	Yes	657.78	951.4	14.00	85.9	31.4	131440	ND	ND	No
SIAL	GQGYDGYDGQNYYHHQ	Yes	951.38	284.1	9.57	123.7	50.4	ND	ND	ND	No
SIAL	GQGYDGYDGQNYYHHQ	Yes	951.38	421.2	9.57	123.7	47.4	ND	ND	ND	No
SIAL	GQGYDGYDGQNYYHHQ	Yes	951.38	584.3	9.57	123.7	53.4	ND	ND	ND	No
SIAL	GQGYDGYDGQNYYHHQ	Yes	951.38	861.4	9.57	123.7	47.4	ND	ND	ND	No
SIAL	IEDSEENGVFK	Yes	633.8	358.2	10.57	82.8	30.4	35270	ND	ND	No
SIAL	IEDSEENGVFK	Yes	633.8	693.4	10.57	82.8	27.4	12215	ND	ND	No
SIAL	IEDSEENGVFK	Yes	633.8	822.4	10.57	82.8	30.4	9168	ND	ND	No
SIAL	IEDSEENGVFK	Yes	633.8	874.3	10.57	82.8	30.4	3520	ND	ND	No
SIAL	TTSPPFGK	Yes	417.72	387.2	8.48	54.9	20.9	44759	ND	ND	No
SIAL	TTSPPFGK	Yes	417.72	448.3	8.48	54.9	26.9	246252	ND	ND	No
SIAL	TTSPPFGK	Yes	417.72	545.3	8.48	54.9	20.9	299686	ND	ND	No
SIAL	TTSPPFGK	Yes	417.72	632.3	8.48	54.9	20.9	547713	ND	ND	No
SIAL	TTTSPNGGFEPTTPPQVYR	Yes	1025.5	338.2	12.99	133.3	44.6	6244	ND	ND	No
SIAL	TTTSPNGGFEPTTPPQVYR	Yes	1025.5	602.3	12.99	133.3	56.6	7636	ND	ND	No
SIAL	TTTSPNGGFEPTTPPQVYR	Yes	1025.5	759.4	12.99	133.3	47.6	20935	ND	ND	No
SIAL	TTTSPNGGFEPTTPPQVYR	Yes	1025.5	992.4	12.99	133.3	47.6	3002	ND	ND	No
SLPI	SSGLFPFLVLLALGTLAPWAVEGSGK	No									

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
SMD3	NQGSGAGR	No									
SMD3	VAQLEQVYIR	No									
SMS	NFFWK	Yes	371.19	333.2	17.26	48.9	18.8	27733	4228	8383	No
SMS	NFFWK	Yes	371.19	409.2	17.26	48.9	18.8	8846	ND	ND	No
SMS	NFFWK	Yes	371.19	480.3	17.26	48.9	18.8	116706	16729	10016	No
SMS	NFFWK	Yes	371.19	627.3	17.26	48.9	18.8	21709	10288	4234	No
SODM	AIWNVINWENVTER	No									
SODM	FNGGGHINHSIFWTNLSPNGGGEPK	Yes	879.76	433.2	16.74	114.5	51.4	1171	ND	ND	No
SODM	FNGGGHINHSIFWTNLSPNGGGEPK	Yes	879.76	544.3	16.74	114.5	45.4	2358	ND	ND	No
SODM	FNGGGHINHSIFWTNLSPNGGGEPK	Yes	879.76	755.4	16.74	114.5	39.4	3251	ND	ND	No
SODM	FNGGGHINHSIFWTNLSPNGGGEPK	Yes	879.76	842.4	16.74	114.5	42.4	4754	ND	ND	No
SODM	GDVTAQIALQPALK	Yes	712.91	428.3	15.00	93	33.9	81532	7739	2940	No
SODM	GDVTAQIALQPALK	Yes	712.91	669.4	15.00	93	33.9	23355	5523	1834	No
SODM	GDVTAQIALQPALK	Yes	712.91	740.5	15.00	93	33.9	58585	8465	7802	No
SODM	GDVTAQIALQPALK	Yes	712.91	853.6	15.00	93	33.9	28422	1075	1361	No
SODM	LTAASVGVQGSGWGWLGFNK	No									
SODM	NVRPDYLK	Yes	335.52	260.2	8.57	44.3	17.7	70512	ND	6466	No
SODM	NVRPDYLK	Yes	335.52	423.3	8.57	44.3	17.7	44798	ND	3806	No
SODM	NVRPDYLK	Yes	335.52	538.3	8.57	44.3	23.7	36248	ND	1726	No
SODM	NVRPDYLK	Yes	335.52	635.3	8.57	44.3	11.7	15838	ND	ND	No
SORL	ENQEVILEEVR	Yes	679.352	532.273	13.43	100	29.4	ND	13820	11459	No
SORL	ENQEVILEEVR	Yes	679.352	645.4	13.43	100	35.4	ND	ND	8233	No
SORL	ENQEVILEEVR	Yes	679.352	758.4	13.43	100	35.4	ND	11793	3221	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
SORL	ENQEVILEEVR	Yes	679.352	857.51	13.43	100	38.4	ND	8544	7627	No
SORL	ESAPGLIIATGSVGK	Yes	700.4	556.8	17.40	100	36.3	ND	ND	ND	No
SORL	ESAPGLIIATGSVGK	Yes	700.4	619.3	17.40	100	36.3	ND	ND	ND	No
SORL	ESAPGLIIATGSVGK	Yes	700.4	732.4	17.40	100	36.3	ND	ND	ND	No
SORL	ESAPGLIIATGSVGK	Yes	700.4	845.5	17.40	100	36.3	ND	ND	ND	No
SORL	LHGGSAPLPQDR	Yes	416.6	258.1	7.27	100	21.7	ND	ND	ND	No
SORL	LHGGSAPLPQDR	Yes	416.6	515.3	7.27	100	21.7	ND	ND	ND	No
SORL	LHGGSAPLPQDR	Yes	416.6	523.3	7.27	100	21.7	ND	ND	ND	No
SORL	LHGGSAPLPQDR	Yes	416.6	733.4	7.27	100	21.7	ND	ND	ND	No
SORL	LHGGSAPLPQDR	Yes	624.329	251.151	7.27	100	36	ND	85623	147821	No
SORL	LHGGSAPLPQDR	Yes	624.329	567.8	7.27	100	33	ND	ND	ND	No
SORL	LHGGSAPLPQDR	Yes	624.329	725.4	7.27	100	33	ND	ND	ND	No
SORL	LHGGSAPLPQDR	Yes	624.329	997.507	7.27	100	36	ND	14853	23090	No
SPB3	GLVLSGVLHK	Yes	341.55	284.2	14.72	45.1	24	192929	ND	ND	No
SPB3	GLVLSGVLHK	Yes	341.55	553.3	14.72	45.1	18	62664	ND	ND	No
SPB3	GLVLSGVLHK	Yes	341.55	640.4	14.72	45.1	15	204170	ND	ND	No
SPB3	GLVLSGVLHK	Yes	341.55	753.5	14.72	45.1	24	ND	ND	ND	No
SPB3	NLIPEGNIGSNTTLVLVNAIYFK	No									
SPB3	QYTSFHFASLEDVQAK	Yes	624.3	346.2	17.05	81.5	38.4	8551	ND	ND	No
SPB3	QYTSFHFASLEDVQAK	Yes	624.3	445.3	17.05	81.5	38.4	16391	ND	ND	No
SPB3	QYTSFHFASLEDVQAK	Yes	624.3	560.3	17.05	81.5	29.4	9678	ND	ND	No
SPB3	QYTSFHFASLEDVQAK	Yes	624.3	689.3	17.05	81.5	29.4	13037	ND	ND	No
SPB3	VDLHLPR	Yes	283.84	385.3	12.13	37.6	18	ND	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
SPB3	VDLHLPR	Yes	283.84	465.2	12.13	37.6	12	4124	ND	ND	No
SPB3	VDLHLPR	Yes	283.84	522.3	12.13	37.6	18	35766	ND	ND	No
SPB3	VDLHLPR	Yes	283.84	635.4	12.13	37.6	12	ND	ND	ND	No
SPB3	VLEIPYK	Yes	431.26	407.2	13.67	56.6	30.5	590572	4254	3421	No
SPB3	VLEIPYK	Yes	431.26	520.3	13.67	56.6	21.5	75406	ND	ND	No
SPB3	VLEIPYK	Yes	431.26	649.4	13.67	56.6	21.5	369423	ND	ND	No
SPB3	VLEIPYK	Yes	431.26	762.4	13.67	56.6	21.5	96046	ND	ND	No
SPB5	DELNADHPFIYIIR	Yes	572.63	358.2	19.89	74.9	23.8	24816	ND	ND	No
SPB5	DELNADHPFIYIIR	Yes	572.63	401.3	19.89	74.9	35.8	13409	ND	ND	No
SPB5	DELNADHPFIYIIR	Yes	572.63	795.3	19.89	74.9	23.8	2662	ND	ND	No
SPB5	DELNADHPFIYIIR	Yes	572.63	921.6	19.89	74.9	35.8	49769	ND	ND	No
SPB5	DLTDGHFENILADNSVNDQTK	No									
SPB5	DVEDESTGLEK	Yes	611.28	446.3	8.45	79.9	38.4	64116	ND	ND	No
SPB5	DVEDESTGLEK	Yes	611.28	547.3	8.45	79.9	38.4	37035	ND	ND	No
SPB5	DVEDESTGLEK	Yes	611.28	763.4	8.45	79.9	29.4	49081	ND	ND	No
SPB5	DVEDESTGLEK	Yes	611.28	878.4	8.45	79.9	29.4	85051	ND	ND	No
SPB5	DVPFGFQTVTSDVNK	Yes	827.41	261.2	17.80	107.7	47.9	74574	ND	5664	No
SPB5	DVPFGFQTVTSDVNK	Yes	827.41	360.2	17.80	107.7	44.9	38625	ND	2681	No
SPB5	DVPFGFQTVTSDVNK	Yes	827.41	762.4	17.80	107.7	44.9	24254	ND	3051	No
SPB5	DVPFGFQTVTSDVNK	Yes	827.41	863.4	17.80	107.7	44.9	40087	ND	5728	No
SPB5	ILVVNAAYFVGK	No									
SPON2	AFIPPAPVLPSR	Yes	632.87	571.4	15.59	82.6	27.3	1733	ND	ND	No
SPON2	AFIPPAPVLPSR	Yes	632.87	668.4	15.59	82.6	27.3	3393	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
SPON2	AFIPPAPVLPSR	Yes	632.87	836.5	15.59	82.6	33.3	4536	ND	ND	No
SPON2	AFIPPAPVLPSR	Yes	632.87	933.6	15.59	82.6	30.3	4096	ND	ND	No
SPON2	ALPPIAR	No									
SPON2	WSQTAFPK	Yes	482.75	391.2	11.79	63.3	32.7	107595	ND	ND	No
SPON2	WSQTAFPK	Yes	482.75	563.3	11.79	63.3	23.7	88376	ND	ND	No
SPON2	WSQTAFPK	Yes	482.75	691.4	11.79	63.3	23.7	81074	ND	ND	No
SPON2	WSQTAFPK	Yes	482.75	778.4	11.79	63.3	23.7	133951	ND	ND	No
SPON2	YSITFTGK	Yes	458.74	251.1	12.91	60.2	22.7	1267465	ND	ND	No
SPON2	YSITFTGK	Yes	458.74	553.3	12.91	60.2	22.7	796157	10847	7398	No
SPON2	YSITFTGK	Yes	458.74	666.4	12.91	60.2	22.7	857802	8054	4641	No
SPON2	YSITFTGK	Yes	458.74	753.4	12.91	60.2	22.7	651450	40124	55070	Yes (Based on Transition Ratios)
SPRC	DEDNNLLTEK	Yes	595.78	377.2	10.66	77.9	28.7	74665	ND	965	No
SPRC	DEDNNLLTEK	Yes	595.78	490.3	10.66	77.9	25.7	31424	ND	ND	No
SPRC	DEDNNLLTEK	Yes	595.78	717.4	10.66	77.9	37.7	9062	ND	ND	No
SPRC	DEDNNLLTEK	Yes	595.78	946.5	10.66	77.9	28.7	20671	ND	ND	No
SPRC	NVLVTLYER	Yes	369.55	304.2	16.24	48.7	13.4	4899	ND	ND	No
SPRC	NVLVTLYER	Yes	369.55	327.2	16.24	48.7	22.4	2525	ND	ND	No
SPRC	NVLVTLYER	Yes	369.55	467.2	16.24	48.7	16.4	25054	ND	ND	No
SPRC	NVLVTLYER	Yes	369.55	580.3	16.24	48.7	25.4	3220	ND	ND	No
SRC	EVLDQVER	Yes	494.26	403.2	9.60	64.8	24.2	67838	ND	ND	No
SRC	EVLDQVER	Yes	494.26	531.3	9.60	64.8	33.2	99156	ND	ND	No
SRC	EVLDQVER	Yes	494.26	646.3	9.60	64.8	24.2	95990	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
SRC	EVLDQVER	Yes	494.26	759.4	9.60	64.8	24.2	103615	ND	ND	No
SRC	GPSAAFAPAAAEPK	Yes	642.83	683.4	10.86	83.9	30.8	275364	ND	ND	No
SRC	GPSAAFAPAAAEPK	Yes	642.83	754.4	10.86	83.9	30.8	174979	ND	ND	No
SRC	GPSAAFAPAAAEPK	Yes	642.83	901.5	10.86	83.9	30.8	101520	ND	ND	No
SRC	GPSAAFAPAAAEPK	Yes	642.83	972.5	10.86	83.9	30.8	67505	ND	ND	No
SRC	LFGGFNSSDTVTSPQR	Yes	856.92	400.2	14.88	111.5	40.2	256788	3693	ND	No
SRC	LFGGFNSSDTVTSPQR	Yes	856.92	487.3	14.88	111.5	43.2	188542	6824	ND	No
SRC	LFGGFNSSDTVTSPQR	Yes	856.92	588.3	14.88	111.5	43.2	228174	2986	ND	No
SRC	LFGGFNSSDTVTSPQR	Yes	856.92	990.5	14.88	111.5	49.2	78889	1127	ND	No
SRC	LLLNAENPR	Yes	520.3	386.2	11.72	68.1	34.4	55595	ND	ND	No
SRC	LLLNAENPR	Yes	520.3	586.3	11.72	68.1	34.4	87145	ND	ND	No
SRC	LLLNAENPR	Yes	520.3	700.3	11.72	68.1	25.4	180581	ND	ND	No
SRC	LLLNAENPR	Yes	520.3	813.4	11.72	68.1	25.4	199431	ND	ND	No
SRC	TQFNSLQQLVAYYSK	Yes	895.46	397.2	23.05	116.5	38.9	15360	ND	ND	No
SRC	TQFNSLQQLVAYYSK	Yes	895.46	560.3	23.05	116.5	47.9	7150	ND	ND	No
SRC	TQFNSLQQLVAYYSK	Yes	895.46	631.3	23.05	116.5	38.9	12878	ND	ND	No
SRC	TQFNSLQQLVAYYSK	Yes	895.46	730.4	23.05	116.5	44.9	4813	ND	ND	No
SSRD	GTWNGPWVSTEVLAAAIGLVIYYLAFSAK	No									
SSRD	NNEDISIIPPLFTVSVDHR	Yes	722.71	312.2	23.70	94.2	43.4	127785	ND	ND	No
SSRD	NNEDISIIPPLFTVSVDHR	Yes	722.71	358.1	23.70	94.2	31.4	27695	ND	ND	No
SSRD	NNEDISIIPPLFTVSVDHR	Yes	722.71	473.2	23.70	94.2	31.4	33156	ND	ND	No
SSRD	NNEDISIIPPLFTVSVDHR	Yes	722.71	586.2	23.70	94.2	31.4	22009	ND	ND	No
SSRD	QFPVTR	No									

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
SSRD	SAHAGTYEVR	Yes	545.77	296.1	6.45	71.4	32.5	33645	ND	ND	No
SSRD	SAHAGTYEVR	Yes	545.77	367.2	6.45	71.4	26.5	12326	ND	ND	No
SSRD	SAHAGTYEVR	Yes	545.77	724.4	6.45	71.4	29.5	18140	ND	ND	No
SSRD	SAHAGTYEVR	Yes	545.77	795.4	6.45	71.4	29.5	24761	ND	ND	No
SSRD	YQVSWSLDHK	Yes	631.81	292.1	13.54	82.5	33.3	196929	ND	ND	No
SSRD	YQVSWSLDHK	Yes	631.81	599.3	13.54	82.5	36.3	19994	ND	ND	No
SSRD	YQVSWSLDHK	Yes	631.81	872.4	13.54	82.5	39.3	22060	ND	ND	No
SSRD	YQVSWSLDHK	Yes	631.81	971.5	13.54	82.5	30.3	30157	ND	ND	No
STAT1	FNQAQSGNIQSTVMLDK	Yes	941	1205.6	16.20	100	46.9	ND	ND	ND	No
STAT1	FNQAQSGNIQSTVMLDK	Yes	941	793.4	16.20	100	46.9	ND	ND	ND	No
STAT1	FNQAQSGNIQSTVMLDK	Yes	941	921.5	16.20	100	46.9	ND	ND	ND	No
STAT1	LLGPNASPDGLIPWTR	Yes	854	1054.6	22.40	100	43.1	ND	ND	ND	No
STAT1	LLGPNASPDGLIPWTR	Yes	854	1141.6	22.40	100	43.1	ND	ND	ND	No
STAT1	LLGPNASPDGLIPWTR	Yes	854	559.3	22.40	100	43.1	ND	ND	ND	No
STAT1	LLGPNASPDGLIPWTR	Yes	854	842.5	22.40	100	43.1	ND	ND	ND	No
STAT1	TELISVSEVHPSR	Yes	727.386	359.204	11.69	100	43.5	ND	ND	9962	No
STAT1	TELISVSEVHPSR	Yes	727.386	496.3	11.69	100	37.5	ND	ND	3023	No
STAT1	TELISVSEVHPSR	Yes	727.386	811.406	11.69	100	37.5	ND	ND	7034	No
STAT1	TELISVSEVHPSR	Yes	727.386	997.5	11.69	100	37.5	ND	ND	ND	No
STAT1	VMAAENIPENPLK	Yes	713.4	1053.6	16.90	100	36.9	ND	ND	ND	No
STAT1	VMAAENIPENPLK	Yes	713.4	697.4	16.90	100	36.9	ND	ND	ND	No
STAT1	VMAAENIPENPLK	Yes	713.4	810.5	16.90	100	36.9	ND	ND	ND	No
STAT1	VMAAENIPENPLK	Yes	713.4	924.5	16.90	100	36.9	ND	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
STAT1	YTYEHDPITK	Yes	422.872	265.119	8.34	100	22.1	ND	ND	26674	No
STAT1	YTYEHDPITK	Yes	422.872	355.7	8.34	100	22.1	ND	ND	22889	No
STAT1	YTYEHDPITK	Yes	422.872	458.298	8.34	100	25.1	ND	ND	44991	No
STAT1	YTYEHDPITK	Yes	422.872	710.4	8.34	100	22.1	ND	ND	ND	No
STAT1	YTYEHDPITK	Yes	633.8	458.3	8.34	100	33.4	ND	ND	ND	No
STAT1	YTYEHDPITK	Yes	633.8	501.7	8.34	100	33.4	ND	ND	ND	No
STAT1	YTYEHDPITK	Yes	633.8	710.4	8.34	100	33.4	ND	ND	ND	No
STAT1	YTYEHDPITK	Yes	633.8	809.3	8.34	100	33.4	ND	ND	ND	No
STAT3	AILSTKPPGTFLLR	Yes	505.31	401.3	17.61	66.2	32.3	16798	ND	ND	No
STAT3	AILSTKPPGTFLLR	Yes	505.31	548.4	17.61	66.2	32.3	9191	ND	ND	No
STAT3	AILSTKPPGTFLLR	Yes	505.31	803.5	17.61	66.2	32.3	79119	ND	ND	No
STAT3	AILSTKPPGTFLLR	Yes	505.31	900.5	17.61	66.2	26.3	120448	ND	ND	No
STAT3	ESHATLVFHNLLGEIDQQYSR	Yes	819.74	354.1	21.70	106.7	36.4	5115	ND	ND	No
STAT3	ESHATLVFHNLLGEIDQQYSR	Yes	819.74	681.3	21.70	106.7	48.4	12385	ND	ND	No
STAT3	ESHATLVFHNLLGEIDQQYSR	Yes	819.74	738.4	21.70	106.7	45.4	4895	ND	ND	No
STAT3	ESHATLVFHNLLGEIDQQYSR	Yes	819.74	796.4	21.70	106.7	42.4	8369	ND	ND	No
STAT3	LENWITSLAESQLQTR	Yes	944.99	543.3	23.08	122.9	41.1	2449	ND	ND	No
STAT3	LENWITSLAESQLQTR	Yes	944.99	656.3	23.08	122.9	41.1	3089	ND	ND	No
STAT3	LENWITSLAESQLQTR	Yes	944.99	732.4	23.08	122.9	41.1	2394	ND	ND	No
STAT3	LENWITSLAESQLQTR	Yes	944.99	861.4	23.08	122.9	50.1	2404	ND	ND	No
STAT3	LLQTAATAAQQGGQANHPTAAVVTEK	No									
STAT3	VVENLQDDFDFNYK	Yes	873.4	310.2	18.22	113.7	40.9	5089	ND	ND	No
STAT3	VVENLQDDFDFNYK	Yes	873.4	442.2	18.22	113.7	40.9	4231	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
STAT3	VVENLQDDFDFNYK	Yes	873.4	555.3	18.22	113.7	37.9	7882	ND	ND	No
STAT3	VVENLQDDFDFNYK	Yes	873.4	948.4	18.22	113.7	40.9	2960	ND	ND	No
STC1	SFLYSAAK	Yes	443.74	376.2	16.19	58.2	31	6755	ND	ND	No
STC1	SFLYSAAK	Yes	443.74	511.3	16.19	58.2	22	1580	ND	ND	No
STC1	SFLYSAAK	Yes	443.74	539.3	16.19	58.2	22	9348	2870	1324	Yes (Based on Transition Ratios)
STC1	SFLYSAAK	Yes	443.74	652.4	16.19	58.2	22	7845	36546	28241	Yes (Based on Transition Ratios)
STC1	VAAQNSAEVVR	Yes	572.31	274.2	7.19	74.8	24.7	5563	ND	ND	No
STC1	VAAQNSAEVVR	Yes	572.31	502.3	7.19	74.8	36.7	8166	ND	ND	No
STC1	VAAQNSAEVVR	Yes	572.31	660.4	7.19	74.8	30.7	17051	ND	ND	No
STC1	VAAQNSAEVVR	Yes	572.31	774.4	7.19	74.8	33.7	36124	ND	ND	No
STT3A	ENDYYTPTGEFR	Yes	746.32	359.1	12.79	97.3	38.3	53810	ND	ND	No
STT3A	ENDYYTPTGEFR	Yes	746.32	706.4	12.79	97.3	35.3	107523	ND	ND	No
STT3A	ENDYYTPTGEFR	Yes	746.32	807.4	12.79	97.3	35.3	80985	ND	ND	No
STT3A	ENDYYTPTGEFR	Yes	746.32	970.5	12.79	97.3	35.3	33542	ND	ND	No
STT3A	FESVIHEFDPYFNYR	Yes	654.97	277.1	21.37	85.5	28	202848	ND	ND	No
STT3A	FESVIHEFDPYFNYR	Yes	654.97	599.3	21.37	85.5	31	114503	ND	ND	No
STT3A	FESVIHEFDPYFNYR	Yes	654.97	762.4	21.37	85.5	40	35428	ND	ND	No
STT3A	FESVIHEFDPYFNYR	Yes	654.97	859.4	21.37	85.5	40	191228	ND	ND	No
STT3A	FLAEEGFYK	Yes	552.27	643.3	14.77	72.2	29.8	247485	ND	ND	No
STT3A	FLAEEGFYK	Yes	552.27	772.4	14.77	72.2	26.8	252763	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
STT3A	FLAEEGFYK	Yes	552.27	843.4	14.77	72.2	26.8	1415684	ND	ND	No
STT3A	FLAEEGFYK	Yes	552.27	956.5	14.77	72.2	26.8	103326	ND	ND	No
STT3A	FYSLLDPSYAK	Yes	652.33	565.3	18.39	85.2	40.2	1933745	13200	4635	No
STT3A	FYSLLDPSYAK	Yes	652.33	680.3	18.39	85.2	31.2	424964	ND	1430	No
STT3A	FYSLLDPSYAK	Yes	652.33	793.4	18.39	85.2	31.2	497872	ND	11074	Yes (Based on Transition Ratios)
STT3A	FYSLLDPSYAK	Yes	652.33	993.5	18.39	85.2	31.2	691753	ND	ND	No
STT3A	IIFDDFR	Yes	463.24	322.2	17.41	60.8	31.9	229319	13403	9048	No
STT3A	IIFDDFR	Yes	463.24	552.2	17.41	60.8	22.9	17303	ND	ND	No
STT3A	IIFDDFR	Yes	463.24	699.3	17.41	60.8	22.9	144370	ND	ND	No
STT3A	IIFDDFR	Yes	463.24	812.4	17.41	60.8	22.9	14846	ND	ND	No
TAGL	AAEDYGVIK	Yes	483.25	579.4	10.00	63.3	26.8	67577	ND	ND	No
TAGL	AAEDYGVIK	Yes	483.25	694.4	10.00	63.3	23.8	75872	ND	ND	No
TAGL	AAEDYGVIK	Yes	483.25	823.4	10.00	63.3	23.8	140912	ND	ND	No
TAGL	AAEDYGVIK	Yes	483.25	894.5	10.00	63.3	23.8	19445	ND	ND	No
TAGL	LGFQVWLK	Yes	495.79	673.4	20.80	65	21.3	41548	ND	ND	No
TAGL	LGFQVWLK	Yes	495.79	731.4	20.80	65	24.3	16006	ND	ND	No
TAGL	LGFQVWLK	Yes	495.79	820.5	20.80	65	24.3	83479	ND	ND	No
TAGL	LGFQVWLK	Yes	495.79	877.5	20.80	65	24.3	145144	ND	ND	No
TAGL	LVNSLYPDGSKPVK	Yes	506.28	414.2	11.09	66.3	26.4	196067	ND	ND	No
TAGL	LVNSLYPDGSKPVK	Yes	506.28	615.4	11.09	66.3	29.4	48165	ND	ND	No
TAGL	LVNSLYPDGSKPVK	Yes	506.28	827.5	11.09	66.3	26.4	153727	ND	ND	No
TAGL	LVNSLYPDGSKPVK	Yes	506.28	990.5	11.09	66.3	23.4	15492	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
TAGL	NDGHYR	Yes	381.17	338.2	5.26	50.2	25.3	16914	ND	ND	No
TAGL	NDGHYR	Yes	381.17	475.2	5.26	50.2	25.3	5756	ND	ND	No
TAGL	NDGHYR	Yes	381.17	532.3	5.26	50.2	22.3	13168	ND	ND	No
TAGL	NDGHYR	Yes	381.17	647.3	5.26	50.2	22.3	5354	ND	ND	No
TAGL	NGVILSK	Yes	365.73	271.1	8.42	48.2	18.6	122488	ND	ND	No
TAGL	NGVILSK	Yes	365.73	460.3	8.42	48.2	18.6	175691	ND	ND	No
TAGL	NGVILSK	Yes	365.73	559.4	8.42	48.2	18.6	31175	ND	ND	No
TAGL	NGVILSK	Yes	365.73	616.4	8.42	48.2	18.6	46640	ND	ND	No
TARA	AGSEVISR	Yes	409.72	375.2	6.56	53.9	20.5	32598	ND	ND	No
TARA	AGSEVISR	Yes	409.72	474.3	6.56	53.9	23.5	30271	ND	ND	No
TARA	AGSEVISR	Yes	409.72	603.3	6.56	53.9	17.5	7174	ND	ND	No
TARA	AGSEVISR	Yes	409.72	690.4	6.56	53.9	20.5	8089	ND	ND	No
TARA	ASSTQQEISR	Yes	553.78	475.2	5.95	72.4	23.9	6103	ND	ND	No
TARA	ASSTQQEISR	Yes	553.78	504.3	5.95	72.4	23.9	5882	ND	ND	No
TARA	ASSTQQEISR	Yes	553.78	632.3	5.95	72.4	32.9	21676	ND	ND	No
TARA	ASSTQQEISR	Yes	553.78	760.4	5.95	72.4	26.9	10685	ND	ND	No
TARA	LQGEAPQSALR	Yes	585.32	359.2	8.82	76.5	34.3	38307	ND	ND	No
TARA	LQGEAPQSALR	Yes	585.32	671.4	8.82	76.5	34.3	1732	ND	ND	No
TARA	LQGEAPQSALR	Yes	585.32	928.5	8.82	76.5	28.3	2644	ND	ND	No
TARA	LSEEIDQLR	Yes	551.79	531.3	12.23	72.2	29.8	72095	ND	ND	No
TARA	LSEEIDQLR	Yes	551.79	773.4	12.23	72.2	29.8	35568	ND	ND	No
TARA	LSEEIDQLR	Yes	551.79	902.5	12.23	72.2	26.8	24032	ND	ND	No
TARA	LSEEIDQLR	Yes	551.79	989.5	12.23	72.2	32.8	25091	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
TARA	YQDVYVELSHIK	Yes	498.59	407.2	16.37	65.3	29	30136	ND	ND	No
TARA	YQDVYVELSHIK	Yes	498.59	597.4	16.37	65.3	23	25786	ND	ND	No
TARA	YQDVYVELSHIK	Yes	498.59	726.4	16.37	65.3	26	34912	ND	ND	No
TARA	YQDVYVELSHIK	Yes	498.59	825.5	16.37	65.3	23	11214	ND	ND	No
TBA1B	AVFVDLEPTVIDEVR	Yes	851.456	1057.55	19.86	100	37	ND	ND	ND	No
TBA1B	AVFVDLEPTVIDEVR	Yes	851.456	1170.6	19.86	100	43	ND	ND	ND	No
TBA1B	AVFVDLEPTVIDEVR	Yes	851.456	631.3	19.86	100	43	ND	ND	ND	No
TBA1B	AVFVDLEPTVIDEVR	Yes	851.456	928.51	19.86	100	46	ND	ND	ND	No
TBA1B	EIIDLVLDR	Yes	543.313	403.2	18.62	100	29.4	ND	ND	ND	No
TBA1B	EIIDLVLDR	Yes	543.313	502.299	18.62	100	23.4	ND	ND	ND	No
TBA1B	EIIDLVLDR	Yes	543.313	730.41	18.62	100	26.4	ND	ND	ND	No
TBA1B	EIIDLVLDR	Yes	543.313	843.5	18.62	100	29.4	ND	ND	ND	No
TBB2A	AILVDLEPGTMDSVR	Yes	808.42	298.2	20.02	105.3	41.1	215017	12251	13536	No
TBB2A	AILVDLEPGTMDSVR	Yes	808.42	754.4	20.02	105.3	35.1	107749	ND	3732	No
TBB2A	AILVDLEPGTMDSVR	Yes	808.42	862.4	20.02	105.3	38.1	416366	14445	15123	No
TBB2A	AILVDLEPGTMDSVR	Yes	808.42	991.5	20.02	105.3	35.1	78984	ND	ND	No
TBB2A	EVDEQMLNVQNK	Yes	723.85	389.2	13.05	94.4	31.3	1249923	ND	ND	No
TBB2A	EVDEQMLNVQNK	Yes	723.85	488.3	13.05	94.4	34.3	710517	ND	ND	No
TBB2A	EVDEQMLNVQNK	Yes	723.85	602.3	13.05	94.4	34.3	1503983	ND	ND	No
TBB2A	EVDEQMLNVQNK	Yes	723.85	846.5	13.05	94.4	34.3	1151947	ND	ND	No
TBB2A	FPGQLNADLR	Yes	565.8	288.2	15.30	74	33.4	10439534	ND	ND	No
TBB2A	FPGQLNADLR	Yes	565.8	701.4	15.30	74	36.4	1306410	ND	ND	No
TBB2A	FPGQLNADLR	Yes	565.8	843.4	15.30	74	27.4	1317171	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
TBB2A	FPGQLNADLR	Yes	565.8	886.5	15.30	74	33.4	3202550	ND	ND	No
TBB2A	GHYTEGAELVDSVLDVVR	Yes	979.99	358.2	24.86	127.4	54.6	116201	ND	ND	No
TBB2A	GHYTEGAELVDSVLDVVR	Yes	979.99	588.2	24.86	127.4	48.6	34030	ND	ND	No
TBB2A	GHYTEGAELVDSVLDVVR	Yes	979.99	845.3	24.86	127.4	42.6	17082	ND	ND	No
TBB2A	GHYTEGAELVDSVLDVVR	Yes	979.99	902.5	24.86	127.4	45.6	21921	ND	ND	No
TBB2A	ISEQFTAMFR	Yes	615.3	453.2	19.95	80.4	35.6	104452	ND	ND	No
TBB2A	ISEQFTAMFR	Yes	615.3	524.3	19.95	80.4	32.6	170251	ND	ND	No
TBB2A	ISEQFTAMFR	Yes	615.3	772.4	19.95	80.4	35.6	288014	ND	ND	No
TBB2A	ISEQFTAMFR	Yes	615.3	900.4	19.95	80.4	29.6	98583	ND	ND	No
TBB2A	LAVNMVPFPR	Yes	572.32	516.3	19.63	74.8	27.7	3192860	ND	ND	No
TBB2A	LAVNMVPFPR	Yes	572.32	615.4	19.63	74.8	36.7	728533	ND	ND	No
TBB2A	LAVNMVPFPR	Yes	572.32	860.4	19.63	74.8	30.7	1014914	ND	ND	No
TBB2A	LAVNMVPFPR	Yes	572.32	959.5	19.63	74.8	27.7	283699	ND	ND	No
TBB2A	LHFFMPGFAPLTSR	Yes	540.95	363.2	24.02	70.8	34.1	108471	ND	ND	No
TBB2A	LHFFMPGFAPLTSR	Yes	540.95	573.3	24.02	70.8	25.1	599921	ND	ND	No
TBB2A	LHFFMPGFAPLTSR	Yes	540.95	676.3	24.02	70.8	28.1	97316	ND	ND	No
TBB2A	LHFFMPGFAPLTSR	Yes	540.95	830.4	24.02	70.8	25.1	111968	ND	ND	No
TBB2A	MSATFIGNSTAIQELFK	No									
TBB2A	NSSYFVEWIPNNVK	Yes	848.92	571.3	21.68	110.5	48.9	1305800	ND	ND	No
TBB2A	NSSYFVEWIPNNVK	Yes	848.92	684.4	21.68	110.5	36.9	256555	ND	ND	No
TBB2A	NSSYFVEWIPNNVK	Yes	848.92	870.5	21.68	110.5	39.9	260320	ND	ND	No
TBB2A	NSSYFVEWIPNNVK	Yes	848.92	999.5	21.68	110.5	39.9	207943	ND	ND	No
TBB2A	SGPFGQIFRPDNFVFGQSGAGNNWAK	Yes	933.45	574.3	23.78	121.4	48.2	ND	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
TBB2A	SGPFGQIFRPDNFVFGQSGAGNNWAK	Yes	933.45	687.3	23.78	121.4	54.2	ND	ND	ND	No
TBB2A	SGPFGQIFRPDNFVFGQSGAGNNWAK	Yes	933.45	817.4	23.78	121.4	45.2	ND	ND	ND	No
TBB2A	SGPFGQIFRPDNFVFGQSGAGNNWAK	Yes	933.45	904.4	23.78	121.4	51.2	ND	ND	ND	No
TBB3	ALTVPELTQQMFDAK	Yes	846.4	654.3	23.40	100	42.7	ND	ND	ND	No
TBB3	ALTVPELTQQMFDAK	Yes	846.4	703.9	23.40	100	42.7	ND	ND	ND	No
TBB3	ALTVPELTQQMFDAK	Yes	846.4	968.5	23.40	100	42.7	ND	ND	ND	No
TBB3	EVDEQMLAIQSK	Yes	695.8	475.3	15.60	100	36.1	ND	ND	ND	No
TBB3	EVDEQMLAIQSK	Yes	695.8	546.3	15.60	100	36.1	ND	ND	ND	No
TBB3	EVDEQMLAIQSK	Yes	695.8	659.4	15.60	100	36.1	ND	ND	ND	No
TBB3	EVDEQMLAIQSK	Yes	695.8	790.5	15.60	100	36.1	ND	ND	ND	No
TBB3	ISVYYNEASSHK	Yes	466.562	201.124	8.88	100	21.3	ND	38473	44339	No
TBB3	ISVYYNEASSHK	Yes	466.562	458.236	8.88	100	27.3	ND	958929	535335	No
TBB3	ISVYYNEASSHK	Yes	466.562	529.3	8.88	100	24.3	ND	28811	16234	No
TBB3	ISVYYNEASSHK	Yes	466.562	935.4	8.88	100	24.3	ND	ND	ND	No
TBB3	ISVYYNEASSHK	Yes	699.3	1098.5	8.88	100	36.3	ND	ND	ND	No
TBB3	ISVYYNEASSHK	Yes	699.3	599.3	8.88	100	36.3	ND	ND	ND	No
TBB3	ISVYYNEASSHK	Yes	699.3	772.4	8.88	100	36.3	ND	ND	ND	No
TBB3	ISVYYNEASSHK	Yes	699.3	935.4	8.88	100	36.3	ND	ND	ND	No
TBB3	MSSTFIGNSTAIQELFK	Yes	937.5	1036.6	25.00	100	46.7	ND	ND	14544	No
TBB3	MSSTFIGNSTAIQELFK	Yes	937.5	1207.6	25.00	100	46.7	ND	ND	27100	No
TBB3	MSSTFIGNSTAIQELFK	Yes	937.5	536.3	25.00	100	46.7	ND	ND	43607	No
TBB3	MSSTFIGNSTAIQELFK	Yes	937.5	664.4	25.00	100	46.7	ND	ND	104439	No
TBB3	YLTVATVFR	Yes	535.306	277.2	17.21	100	29.1	ND	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
TBB3	YLTVATVFR	Yes	535.306	593.3	17.21	100	29.1	ND	2832	3421	No
TBB3	YLTVATVFR	Yes	535.306	692.41	17.21	100	26.1	ND	91889	83241	No
TBB3	YLTVATVFR	Yes	535.306	793.457	17.21	100	26.1	ND	39628	19768	No
TBB5	AILVDLEPGTMDSVR	Yes	808.42	298.2	20.02	105.3	41.1	215017	12251	13536	No
TBB5	AILVDLEPGTMDSVR	Yes	808.42	754.4	20.02	105.3	35.1	107749	ND	3732	No
TBB5	AILVDLEPGTMDSVR	Yes	808.42	862.4	20.02	105.3	38.1	416366	14445	15123	No
TBB5	AILVDLEPGTMDSVR	Yes	808.42	991.5	20.02	105.3	35.1	78984	ND	ND	No
TBB5	FPGQLNADLR	Yes	565.8	288.2	15.30	74	33.4	10439534	ND	ND	No
TBB5	FPGQLNADLR	Yes	565.8	701.4	15.30	74	36.4	1306410	ND	ND	No
TBB5	FPGQLNADLR	Yes	565.8	843.4	15.30	74	27.4	1317171	ND	ND	No
TBB5	FPGQLNADLR	Yes	565.8	886.5	15.30	74	33.4	3202550	ND	ND	No
TBB5	GHYTEGAELVDSVLDVVR	Yes	979.99	358.2	24.86	127.4	54.6	116201	ND	ND	No
TBB5	GHYTEGAELVDSVLDVVR	Yes	979.99	588.2	24.86	127.4	48.6	34030	ND	ND	No
TBB5	GHYTEGAELVDSVLDVVR	Yes	979.99	845.3	24.86	127.4	42.6	17082	ND	ND	No
TBB5	GHYTEGAELVDSVLDVVR	Yes	979.99	902.5	24.86	127.4	45.6	21921	ND	ND	No
TBB5	IMNTFSVVPSPK	No									
TBB5	ISEQFTAMFR	Yes	615.3	453.2	19.95	80.4	35.6	104452	ND	ND	No
TBB5	ISEQFTAMFR	Yes	615.3	524.3	19.95	80.4	32.6	170251	ND	ND	No
TBB5	ISEQFTAMFR	Yes	615.3	772.4	19.95	80.4	35.6	288014	ND	ND	No
TBB5	ISEQFTAMFR	Yes	615.3	900.4	19.95	80.4	29.6	98583	ND	ND	No
TBB5	LAVNMVPFPR	Yes	572.32	516.3	19.63	74.8	27.7	3192860	ND	ND	No
TBB5	LAVNMVPFPR	Yes	572.32	615.4	19.63	74.8	36.7	728533	ND	ND	No
TBB5	LAVNMVPFPR	Yes	572.32	860.4	19.63	74.8	30.7	1014914	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
TBB5	LAVNMVPFPR	Yes	572.32	959.5	19.63	74.8	27.7	283699	ND	ND	No
TBB5	LHFFMPGFAPLTSR	Yes	540.95	363.2	24.02	70.8	34.1	108471	ND	ND	No
TBB5	LHFFMPGFAPLTSR	Yes	540.95	573.3	24.02	70.8	25.1	599921	ND	ND	No
TBB5	LHFFMPGFAPLTSR	Yes	540.95	676.3	24.02	70.8	28.1	97316	ND	ND	No
TBB5	LHFFMPGFAPLTSR	Yes	540.95	830.4	24.02	70.8	25.1	111968	ND	ND	No
TBB5	MAVTFIGNSTAIQELFK	No									
TBB5	NSSYFVEWIPNNVK	Yes	848.92	571.3	21.68	110.5	48.9	1305800	ND	ND	No
TBB5	NSSYFVEWIPNNVK	Yes	848.92	684.4	21.68	110.5	36.9	256555	ND	ND	No
TBB5	NSSYFVEWIPNNVK	Yes	848.92	870.5	21.68	110.5	39.9	260320	ND	ND	No
TBB5	NSSYFVEWIPNNVK	Yes	848.92	999.5	21.68	110.5	39.9	207943	ND	ND	No
TBB5	YLTVAAVFR	Yes	520.3	492.3	20.85	68.1	25.4	384016	ND	ND	No
TBB5	YLTVAAVFR	Yes	520.3	563.3	20.85	68.1	28.4	1135831	ND	ND	No
TBB5	YLTVAAVFR	Yes	520.3	662.4	20.85	68.1	25.4	460826	ND	ND	No
TBB5	YLTVAAVFR	Yes	520.3	763.4	20.85	68.1	25.4	1568096	ND	ND	No
TCPA	FATEAAITILR	Yes	603.35	502.3	17.76	78.8	26	28642	ND	ND	No
TCPA	FATEAAITILR	Yes	603.35	686.5	17.76	78.8	29	27488	ND	ND	No
TCPA	FATEAAITILR	Yes	603.35	757.5	17.76	78.8	38	41795	ND	ND	No
TCPA	FATEAAITILR	Yes	603.35	987.6	17.76	78.8	29	10869	ND	ND	No
TCPA	IHPTSVISGYR	Yes	615.34	251.2	14.09	80.4	29.6	197929	335561	171316	No
TCPA	IHPTSVISGYR	Yes	615.34	781.4	14.09	80.4	29.6	ND	ND	ND	No
TCPA	IHPTSVISGYR	Yes	615.34	892.5	14.09	80.4	29.6	ND	ND	ND	No
TCPA	IHPTSVISGYR	Yes	615.34	979.5	14.09	80.4	29.6	44113	86797	46592	No
TCPA	LGVQVVITDPEK	No									

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
TCPA	SSLGPVGLDK	Yes	486.77	432.2	11.67	63.8	32.9	553086	ND	ND	No
TCPA	SSLGPVGLDK	Yes	486.77	628.4	11.67	63.8	23.9	501469	ND	ND	No
TCPA	SSLGPVGLDK	Yes	486.77	685.4	11.67	63.8	23.9	1048739	ND	ND	No
TCPA	SSLGPVGLDK	Yes	486.77	798.5	11.67	63.8	23.9	367030	ND	ND	No
TCPA	YINENLIVNTDELGR	No									
TCPD	AYILNLVK	Yes	467.29	359.3	17.78	61.3	29.1	13366	ND	ND	No
TCPD	AYILNLVK	Yes	467.29	586.4	17.78	61.3	23.1	69764	ND	ND	No
TCPD	AYILNLVK	Yes	467.29	699.5	17.78	61.3	23.1	99354	ND	ND	No
TCPD	AYILNLVK	Yes	467.29	862.5	17.78	61.3	23.1	4239	ND	ND	No
TCPD	GDVTITNDGATILK	No									
TCPD	GIHPTIISESFQK	Yes	728.89	275.2	14.02	95	43.6	4958	ND	ND	No
TCPD	GIHPTIISESFQK	Yes	728.89	308.2	14.02	95	37.6	48360	ND	ND	No
TCPD	GIHPTIISESFQK	Yes	728.89	509.3	14.02	95	43.6	6900	ND	ND	No
TCPD	GIHPTIISESFQK	Yes	728.89	838.4	14.02	95	43.6	2569	ND	ND	No
TCPD	IDDVVNTR	Yes	466.25	489.3	8.42	61.1	20	27850	ND	ND	No
TCPD	IDDVVNTR	Yes	466.25	588.3	8.42	61.1	32	19884	ND	ND	No
TCPD	IDDVVNTR	Yes	466.25	703.4	8.42	61.1	23	34778	ND	ND	No
TCPD	IDDVVNTR	Yes	466.25	818.4	8.42	61.1	23	27380	ND	ND	No
TCPD	VIDPATATSVDLR	Yes	453.25	288.2	13.80	59.5	29.7	135452	ND	ND	No
TCPD	VIDPATATSVDLR	Yes	453.25	502.3	13.80	59.5	20.7	14680	ND	ND	No
TCPD	VIDPATATSVDLR	Yes	453.25	589.3	13.80	59.5	17.7	19088	ND	ND	No
TCPD	VIDPATATSVDLR	Yes	453.25	690.4	13.80	59.5	20.7	14065	ND	ND	No
TCPQ	AVDDGVNTFK	Yes	533.26	509.3	10.08	69.8	35	97505	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
TCPQ	AVDDGVNTFK	Yes	533.26	665.4	10.08	69.8	26	66984	ND	ND	No
TCPQ	AVDDGVNTFK	Yes	533.26	780.4	10.08	69.8	26	59999	ND	ND	No
TCPQ	AVDDGVNTFK	Yes	533.26	895.4	10.08	69.8	26	189903	ND	ND	No
TCPQ	DIDEVSSLLR	Yes	573.8	344.1	17.79	75	27.7	213624	ND	ND	No
TCPQ	DIDEVSSLLR	Yes	573.8	674.4	17.79	75	27.7	144309	ND	ND	No
TCPQ	DIDEVSSLLR	Yes	573.8	803.5	17.79	75	30.7	99887	ND	ND	No
TCPQ	DIDEVSSLLR	Yes	573.8	918.5	17.79	75	27.7	209111	ND	ND	No
TCPQ	LATNAAVTVLR	Yes	564.84	587.4	13.05	73.9	36.4	22973	ND	ND	No
TCPQ	LATNAAVTVLR	Yes	564.84	658.4	13.05	73.9	27.4	26785	ND	ND	No
TCPQ	LATNAAVTVLR	Yes	564.84	729.5	13.05	73.9	36.4	12680	ND	ND	No
TCPQ	LATNAAVTVLR	Yes	564.84	843.5	13.05	73.9	27.4	6195	ND	ND	No
TCPQ	LYAVHQEGNK	Yes	386.87	318.2	6.79	50.9	23.3	49687	ND	ND	No
TCPQ	LYAVHQEGNK	Yes	386.87	348.2	6.79	50.9	26.3	23699	ND	ND	No
TCPQ	LYAVHQEGNK	Yes	386.87	575.3	6.79	50.9	20.3	45643	ND	ND	No
TCPQ	LYAVHQEGNK	Yes	386.87	811.4	6.79	50.9	26.3	1085	ND	ND	No
TCPQ	NVGLDIEAEVPAVK	Yes	727.4	271.1	17.46	94.8	34.5	68541	10688	9515	Yes (Based on Transition Ratios)
TCPQ	NVGLDIEAEVPAVK	Yes	727.4	414.3	17.46	94.8	40.5	146741	64907	82059	No
TCPQ	NVGLDIEAEVPAVK	Yes	727.4	842.5	17.46	94.8	34.5	39982	23604	37627	No
TCPQ	NVGLDIEAEVPAVK	Yes	727.4	955.5	17.46	94.8	34.5	10964	2516	5326	No
TCPZ	ALQFLEEVK	Yes	538.8	504.3	19.33	70.5	26.2	1287068	ND	ND	No
TCPZ	ALQFLEEVK	Yes	538.8	617.4	19.33	70.5	26.2	1418294	ND	ND	No
TCPZ	ALQFLEEVK	Yes	538.8	764.4	19.33	70.5	26.2	3395708	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
TCPZ	ALQFLEEVK	Yes	538.8	892.5	19.33	70.5	26.2	2214371	ND	ND	No
TCPZ	AQAALAVNISAAR	Yes	628.36	730.4	14.61	82.1	30.1	466648	ND	ND	No
TCPZ	AQAALAVNISAAR	Yes	628.36	801.5	14.61	82.1	30.1	821451	ND	ND	No
TCPZ	AQAALAVNISAAR	Yes	628.36	914.5	14.61	82.1	33.1	369300	ND	ND	No
TCPZ	AQAALAVNISAAR	Yes	628.36	985.6	14.61	82.1	33.1	228924	ND	ND	No
TCPZ	AQLGVQAFADALLIIPK	Yes	884.52	313.2	25.23	115.1	41.4	ND	ND	ND	No
TCPZ	AQLGVQAFADALLIIPK	Yes	884.52	597.3	25.23	115.1	38.4	ND	ND	ND	No
TCPZ	AQLGVQAFADALLIIPK	Yes	884.52	668.4	25.23	115.1	41.4	ND	ND	ND	No
TCPZ	AQLGVQAFADALLIIPK	Yes	884.52	953.6	25.23	115.1	41.4	ND	ND	ND	No
TCPZ	GIDPFSLDALSK	Yes	631.84	286.1	21.71	82.5	27.3	2840246	ND	ND	No
TCPZ	GIDPFSLDALSK	Yes	631.84	733.4	21.71	82.5	39.3	1338376	ND	ND	No
TCPZ	GIDPFSLDALSK	Yes	631.84	880.5	21.71	82.5	39.3	686786	ND	ND	No
TCPZ	GIDPFSLDALSK	Yes	631.84	977.5	21.71	82.5	27.3	1332319	ND	ND	No
TCPZ	GLVLDHGAR	Yes	313.18	440.2	10.19	41.4	22.5	1804958	ND	ND	No
TCPZ	GLVLDHGAR	Yes	313.18	555.3	10.19	41.4	19.5	2085697	ND	ND	No
TCPZ	GLVLDHGAR	Yes	313.18	668.3	10.19	41.4	22.5	6618	ND	ND	No
TCPZ	QADLYISEGLHPR	Yes	500.26	272.2	15.44	65.5	29.1	467756	ND	ND	No
TCPZ	QADLYISEGLHPR	Yes	500.26	409.2	15.44	65.5	32.1	151277	ND	ND	No
TCPZ	QADLYISEGLHPR	Yes	500.26	708.4	15.44	65.5	29.1	132568	ND	ND	No
TCPZ	QADLYISEGLHPR	Yes	500.26	795.4	15.44	65.5	29.1	585195	ND	ND	No
TCPZ	TEVNSGFFYK	Yes	596.29	661.3	16.18	77.9	28.7	334620	ND	ND	No
TCPZ	TEVNSGFFYK	Yes	596.29	748.4	16.18	77.9	28.7	624244	ND	ND	No
TCPZ	TEVNSGFFYK	Yes	596.29	862.4	16.18	77.9	28.7	1592373	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
TCPZ	TEVNSGFFYK	Yes	596.29	961.5	16.18	77.9	28.7	1594788	ND	ND	No
TCPZ	VATAQDDITGDGTTSNVLIIGELLK	No									
TCPZ	VHAELADVLTEAVVDSILAIK	Yes	736.08	331.2	25.04	96	38.1	ND	ND	ND	No
TCPZ	VHAELADVLTEAVVDSILAIK	Yes	736.08	759.5	25.04	96	35.1	ND	ND	ND	No
TCPZ	VHAELADVLTEAVVDSILAIK	Yes	736.08	858.5	25.04	96	38.1	ND	ND	ND	No
TCPZ	VHAELADVLTEAVVDSILAIK	Yes	736.08	957.6	25.04	96	32.1	ND	ND	ND	No
TCPZ	VLAQNSGFDLQETLVK	Yes	881.47	460.3	19.20	114.7	50.3	42219	ND	ND	No
TCPZ	VLAQNSGFDLQETLVK	Yes	881.47	589.4	19.20	114.7	47.3	26547	ND	ND	No
TCPZ	VLAQNSGFDLQETLVK	Yes	881.47	717.4	19.20	114.7	50.3	25754	ND	ND	No
TCPZ	VLAQNSGFDLQETLVK	Yes	881.47	945.5	19.20	114.7	50.3	26754	ND	ND	No
TDRD3	HFNVNTDYQNPVR	Yes	535.26	371.2	11.27	70	24.8	25367	ND	ND	No
TDRD3	HFNVNTDYQNPVR	Yes	535.26	485.3	11.27	70	24.8	34956	ND	ND	No
TDRD3	HFNVNTDYQNPVR	Yes	535.26	498.2	11.27	70	33.8	12808	ND	ND	No
TDRD3	HFNVNTDYQNPVR	Yes	535.26	613.3	11.27	70	24.8	9120	ND	ND	No
TDRD3	SEDEEDLGNARPSAPSTLFDFLESK	Yes	918.76	332.1	23.36	119.5	44.4	8520	27267	22933	No
TDRD3	SEDEEDLGNARPSAPSTLFDFLESK	Yes	918.76	461.2	23.36	119.5	44.4	4408	10764	ND	No
TDRD3	SEDEEDLGNARPSAPSTLFDFLESK	Yes	918.76	705.2	23.36	119.5	44.4	3731	ND	9938	No
TDRD3	SEDEEDLGNARPSAPSTLFDFLESK	Yes	918.76	885.4	23.36	119.5	50.4	3157	10043	12682	No
TDRD3	SNIGTEGGPPPFVPFGQK	Yes	914.97	332.2	17.44	119	48.8	38221	ND	ND	No
TDRD3	SNIGTEGGPPPFVPFGQK	Yes	914.97	576.3	17.44	119	42.8	266334	ND	ND	No
TDRD3	SNIGTEGGPPPFVPFGQK	Yes	914.97	602.3	17.44	119	42.8	13572	ND	ND	No
TDRD3	SNIGTEGGPPPFVPFGQK	Yes	914.97	716.3	17.44	119	39.8	23476	ND	ND	No
TDRD3	SVLEGSGLPR	Yes	338.86	272.2	10.91	44.7	17.8	1027	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
TDRD3	SVLEGSGLPR	Yes	338.86	300.2	10.91	44.7	14.8	2565	ND	ND	No
TDRD3	SVLEGSGLPR	Yes	338.86	442.3	10.91	44.7	14.8	ND	ND	ND	No
TDRD3	SVLEGSGLPR	Yes	338.86	586.3	10.91	44.7	11.8	ND	ND	ND	No
TDRD3	TAAIAEVAK	Yes	437.26	517.3	8.58	57.4	21.7	149124	ND	ND	No
TDRD3	TAAIAEVAK	Yes	437.26	630.4	8.58	57.4	21.7	89489	ND	ND	No
TDRD3	TAAIAEVAK	Yes	437.26	701.4	8.58	57.4	21.7	282892	ND	ND	No
TDRD3	TAAIAEVAK	Yes	437.26	772.5	8.58	57.4	21.7	28546	ND	ND	No
TENA	AVDIPGLEAATPYR	Yes	491.6	435.2	17.12	64.4	22.6	29687	ND	5261	No
TENA	AVDIPGLEAATPYR	Yes	491.6	536.3	17.12	64.4	22.6	26807	ND	6948	No
TENA	AVDIPGLEAATPYR	Yes	491.6	607.3	17.12	64.4	22.6	18456	ND	1582	No
TENA	AVDIPGLEAATPYR	Yes	491.6	678.4	17.12	64.4	31.6	18339	ND	1568	No
TENA	GLEPGQEYNVLLTAEK	Yes	880.96	448.2	17.44	114.6	50.3	85558	9831	12872	No
TENA	GLEPGQEYNVLLTAEK	Yes	880.96	561.3	17.44	114.6	50.3	42445	6143	13988	No
TENA	GLEPGQEYNVLLTAEK	Yes	880.96	582.3	17.44	114.6	41.3	11901	ND	ND	No
TENA	GLEPGQEYNVLLTAEK	Yes	880.96	674.4	17.44	114.6	50.3	43788	ND	8609	No
TENA	TAHISGLPPSTDFIVYLSGLAPSIR	Yes	871.47	472.3	24.58	113.4	39	52609	10121	11526	No
TENA	TAHISGLPPSTDFIVYLSGLAPSIR	Yes	871.47	680.4	24.58	113.4	51	22206	3170	5391	No
TENA	TAHISGLPPSTDFIVYLSGLAPSIR	Yes	871.47	713.4	24.58	113.4	42	25260	6062	9159	No
TENA	TAHISGLPPSTDFIVYLSGLAPSIR	Yes	871.47	800.5	24.58	113.4	39	34316	7009	6605	No
TENA	TVSGNTVEYALTDLEPATEYTLR	Yes	848.42	552.3	22.04	110.4	43.8	2874	8598	2966	No
TENA	TVSGNTVEYALTDLEPATEYTLR	Yes	848.42	782.4	22.04	110.4	37.8	ND	ND	ND	Yes (Based on Manual Review)
TENA	TVSGNTVEYALTDLEPATEYTLR	Yes	848.42	950.5	22.04	110.4	40.8	18295	39889	41543	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
TENA	TVSGNTVEYALTDLEPATEYTLR	Yes	848.42	951.4	22.04	110.4	37.8	4002	9202	12912	No
TENA	YAPISGGDHAEVDVPK	Yes	552.27	332.2	11.11	72.2	25.7	12662	ND	ND	No
TENA	YAPISGGDHAEVDVPK	Yes	552.27	343.2	11.11	72.2	31.7	54253	ND	ND	No
TENA	YAPISGGDHAEVDVPK	Yes	552.27	686.4	11.11	72.2	34.7	5413	ND	ND	No
TENA	YAPISGGDHAEVDVPK	Yes	552.27	757.4	11.11	72.2	34.7	9262	ND	ND	No
TENX	DAQGQPQAVPVSGDLR	Yes	819.42	372.2	11.04	106.7	44.6	43116	23755	24599	No
TENX	DAQGQPQAVPVSGDLR	Yes	819.42	500.2	11.04	106.7	35.6	62767	31297	33797	No
TENX	DAQGQPQAVPVSGDLR	Yes	819.42	743.4	11.04	106.7	38.6	110974	34940	50256	No
TENX	DAQGQPQAVPVSGDLR	Yes	819.42	895.4	11.04	106.7	38.6	17664	6818	5108	No
TENX	GFEESEPLTGFLTTVPDGPTQLR	No									
TENX	VPGHEDGVTISGLEPDHK	Yes	629.65	496.3	11.93	82.2	38.7	41209	ND	ND	No
TENX	VPGHEDGVTISGLEPDHK	Yes	629.65	795.4	11.93	82.2	29.7	24337	ND	ND	No
TENX	VPGHEDGVTISGLEPDHK	Yes	629.65	882.4	11.93	82.2	32.7	20569	ND	ND	No
TENX	VPGHEDGVTISGLEPDHK	Yes	629.65	892.4	11.93	82.2	32.7	9729	ND	ND	No
TENX	VSYQLADGGEPQSVQVDGQAR	Yes	1102.53	431.2	12.39	143.2	60	8504	11556	4316	No
TENX	VSYQLADGGEPQSVQVDGQAR	Yes	1102.53	546.3	12.39	143.2	48	6058	6190	7375	No
TENX	VSYQLADGGEPQSVQVDGQAR	Yes	1102.53	645.3	12.39	143.2	51	3491	ND	ND	No
TENX	VSYQLADGGEPQSVQVDGQAR	Yes	1102.53	773.4	12.39	143.2	51	6795	8202	7542	No
TENX	YEVTVVSVR	Yes	526.29	460.3	11.99	68.9	34.7	8772	65291	64723	No
TENX	YEVTVVSVR	Yes	526.29	559.4	11.99	68.9	22.7	4120	49441	42553	No
TENX	YEVTVVSVR	Yes	526.29	660.4	11.99	68.9	25.7	11271	103103	127088	No
TENX	YEVTVVSVR	Yes	526.29	759.5	11.99	68.9	22.7	16516	154180	174610	No
TERA	GILLYGPPGTGK	Yes	586.84	284.2	17.01	76.7	28.3	4498979	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
TERA	GILLYGPPGTGK	Yes	586.84	397.3	17.01	76.7	25.3	2054979	ND	ND	No
TERA	GILLYGPPGTGK	Yes	586.84	556.3	17.01	76.7	37.3	2704608	ND	ND	No
TERA	GILLYGPPGTGK	Yes	586.84	776.4	17.01	76.7	28.3	3607605	ND	ND	No
TERA	GPELLTMWFGESEANVR	Yes	968.47	510.3	25.12	125.9	42.1	32903	ND	ND	No
TERA	GPELLTMWFGESEANVR	Yes	968.47	611.3	25.12	125.9	42.1	27418	ND	ND	No
TERA	GPELLTMWFGESEANVR	Yes	968.47	675.3	25.12	125.9	42.1	16781	ND	ND	No
TERA	GPELLTMWFGESEANVR	Yes	968.47	861.4	25.12	125.9	51.1	52118	ND	ND	No
TERA	IVSQLLTLMDGLK	Yes	715.92	563.3	25.12	93.4	31	73621	ND	ND	No
TERA	IVSQLLTLMDGLK	Yes	715.92	676.4	25.12	93.4	31	66108	ND	ND	No
TERA	IVSQLLTLMDGLK	Yes	715.92	777.4	25.12	93.4	34	153418	ND	ND	No
TERA	IVSQLLTLMDGLK	Yes	715.92	890.5	25.12	93.4	34	163928	ND	ND	No
TERA	LDQLIYIPLPDEK	Yes	778.93	470.3	22.52	101.5	36.8	207753	ND	ND	No
TERA	LDQLIYIPLPDEK	Yes	778.93	698.4	22.52	101.5	36.8	254852	ND	ND	No
TERA	LDQLIYIPLPDEK	Yes	778.93	811.5	22.52	101.5	33.8	99288	ND	ND	No
TERA	LDQLIYIPLPDEK	Yes	778.93	974.5	22.52	101.5	36.8	152145	ND	ND	No
TERA	LIVDEAINEDNSVVSLSQPK	No									
TERA	MDELQLFR	Yes	526.27	563.3	20.14	68.9	25.7	1497727	ND	ND	No
TERA	MDELQLFR	Yes	526.27	676.4	20.14	68.9	28.7	764992	ND	ND	No
TERA	MDELQLFR	Yes	526.27	805.5	20.14	68.9	28.7	1144786	ND	ND	No
TERA	MDELQLFR	Yes	526.27	920.5	20.14	68.9	28.7	931093	ND	ND	No
TERA	NAPAIIFIDELDAIAPK	Yes	906	283.1	25.23	117.9	51.4	186563	ND	ND	No
TERA	NAPAIIFIDELDAIAPK	Yes	906	315.2	25.23	117.9	39.4	474413	ND	ND	No
TERA	NAPAIIFIDELDAIAPK	Yes	906	467.3	25.23	117.9	39.4	396688	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
TERA	NAPAIIFIDELDAIAPK	Yes	906	971.5	25.23	117.9	45.4	161600	ND	ND	No
TERA	VINQILTEMDGMSTK	Yes	840.42	455.3	20.73	109.4	36.5	42351	ND	ND	No
TERA	VINQILTEMDGMSTK	Yes	840.42	523.3	20.73	109.4	48.5	32057	ND	ND	No
TERA	VINQILTEMDGMSTK	Yes	840.42	568.3	20.73	109.4	36.5	43772	ND	ND	No
TERA	VINQILTEMDGMSTK	Yes	840.42	999.4	20.73	109.4	45.5	25215	ND	ND	No
TERA	WALSQSNPSALR	Yes	665.35	543.3	15.70	86.8	40.8	236156	ND	ND	No
TERA	WALSQSNPSALR	Yes	665.35	744.4	15.70	86.8	34.8	140646	ND	ND	No
TERA	WALSQSNPSALR	Yes	665.35	872.5	15.70	86.8	40.8	108706	ND	ND	No
TERA	WALSQSNPSALR	Yes	665.35	959.5	15.70	86.8	37.8	198078	ND	ND	No
TETN	GGTLSTPQTGSENDALYEYLR	Yes	758.03	451.3	18.32	98.8	45.2	26070	57488	127897	No
TETN	GGTLSTPQTGSENDALYEYLR	Yes	758.03	580.3	18.32	98.8	33.2	27615	78447	148246	No
TETN	GGTLSTPQTGSENDALYEYLR	Yes	758.03	856.5	18.32	98.8	36.2	24411	57916	121498	No
TETN	GGTLSTPQTGSENDALYEYLR	Yes	758.03	927.5	18.32	98.8	42.2	8539	26011	35394	No
TETN	LDTLAQEVALLK	Yes	657.39	330.2	20.73	85.8	31.4	288305	108076	112901	No
TETN	LDTLAQEVALLK	Yes	657.39	543.4	20.73	85.8	28.4	166789	54874	67833	No
TETN	LDTLAQEVALLK	Yes	657.39	800.5	20.73	85.8	31.4	234436	72253	82161	No
TETN	LDTLAQEVALLK	Yes	657.39	871.5	20.73	85.8	31.4	327551	117259	116678	No
TETN	NWETEITAQPDGGK	Yes	773.36	301.1	14.20	100.8	39.5	39847	16015	16039	No
TETN	NWETEITAQPDGGK	Yes	773.36	430.2	14.20	100.8	36.5	22521	ND	ND	No
TETN	NWETEITAQPDGGK	Yes	773.36	473.2	14.20	100.8	45.5	71276	16226	20415	No
TETN	NWETEITAQPDGGK	Yes	773.36	886.5	14.20	100.8	36.5	7687	ND	ND	No
TF	DLIYTLYYWK	Yes	689.36	496.3	23.40	89.9	41.8	29662	ND	ND	No
TF	DLIYTLYYWK	Yes	689.36	659.3	23.40	89.9	29.8	19663	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
TF	DLIYTLYYWK	Yes	689.36	772.4	23.40	89.9	29.8	15927	ND	ND	No
TF	DLIYTLYYWK	Yes	689.36	873.5	23.40	89.9	29.8	41176	ND	ND	No
TF	ENSPLNVS	No									
TF	TILEWEPKPVNQVYTVQISTK	No									
TF	TNTNEFLIDVDK	Yes	704.85	262.1	16.41	91.9	42.5	30695	ND	ND	No
TF	TNTNEFLIDVDK	Yes	704.85	476.2	16.41	91.9	33.5	42009	ND	ND	No
TF	TNTNEFLIDVDK	Yes	704.85	589.3	16.41	91.9	36.5	26405	ND	ND	No
TF	TNTNEFLIDVDK	Yes	704.85	978.5	16.41	91.9	33.5	6032	ND	ND	No
TF	VNVTVEDER	Yes	530.77	304.2	8.33	69.5	31.9	19286	ND	ND	No
TF	VNVTVEDER	Yes	530.77	647.3	8.33	69.5	31.9	9265	ND	ND	No
TF	VNVTVEDER	Yes	530.77	748.3	8.33	69.5	25.9	11384	ND	ND	No
TF	VNVTVEDER	Yes	530.77	847.4	8.33	69.5	25.9	8832	ND	ND	No
TFR1	GFVEPDHYVVVGAQR	Yes	558.29	431.2	13.84	73	26	49644	ND	ND	No
TFR1	GFVEPDHYVVVGAQR	Yes	558.29	629.4	13.84	73	35	41201	ND	ND	No
TFR1	GFVEPDHYVVVGAQR	Yes	558.29	728.4	13.84	73	35	44628	ND	ND	No
TFR1	GFVEPDHYVVVGAQR	Yes	558.29	891.5	13.84	73	35	19282	ND	ND	No
TFR1	LTTDFGNAEK	Yes	548.27	518.3	10.05	71.7	35.6	137300	ND	ND	No
TFR1	LTTDFGNAEK	Yes	548.27	665.3	10.05	71.7	35.6	173153	ND	ND	No
TFR1	LTTDFGNAEK	Yes	548.27	780.4	10.05	71.7	26.6	114665	ND	ND	No
TFR1	LTTDFGNAEK	Yes	548.27	881.4	10.05	71.7	26.6	191020	ND	ND	No
TFR1	LTVSNVLK	Yes	437.27	473.3	13.35	57.4	27.7	22190	ND	14654	Yes (Based on Transition Ratios)
TFR1	LTVSNVLK	Yes	437.27	560.3	13.35	57.4	21.7	106673	ND	7404	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
TFR1	LTVSNVLK	Yes	437.27	659.4	13.35	57.4	21.7	204610	ND	4608	No
TFR1	LTVSNVLK	Yes	437.27	760.5	13.35	57.4	21.7	105968	ND	1904	No
TFR1	SAFSNLFGGEPLSYTR	Yes	873.43	620.3	21.91	113.7	40.9	105074	ND	ND	No
TFR1	SAFSNLFGGEPLSYTR	Yes	873.43	736.4	21.91	113.7	40.9	179977	ND	ND	No
TFR1	SAFSNLFGGEPLSYTR	Yes	873.43	922.5	21.91	113.7	37.9	60848	ND	ND	No
TFR1	SAFSNLFGGEPLSYTR	Yes	873.43	979.5	21.91	113.7	40.9	225397	ND	ND	No
TFR1	SSGLPNIPVQTISR	Yes	734.91	345.2	15.38	95.8	34.8	173063	23359	13151	No
TFR1	SSGLPNIPVQTISR	Yes	734.91	476.3	15.38	95.8	43.8	20532	941	ND	Yes (Based on Transition Ratios)
TFR1	SSGLPNIPVQTISR	Yes	734.91	669.4	15.38	95.8	34.8	81733	10189	10855	No
TFR1	SSGLPNIPVQTISR	Yes	734.91	800.5	15.38	95.8	37.8	445547	71744	59224	No
TGFA	HEKPSALLK	Yes	341.54	267.1	7.42	45.1	24	243729	ND	22130	No
TGFA	HEKPSALLK	Yes	341.54	373.3	7.42	45.1	21	82377	ND	6261	No
TGFA	HEKPSALLK	Yes	341.54	531.4	7.42	45.1	21	34805	ND	2971	No
TGFA	HEKPSALLK	Yes	341.54	763.4	7.42	45.1	24	ND	ND	ND	No
THAS	DELNGFFNK	Yes	542.26	261.2	16.22	71	32.4	99542	ND	ND	No
THAS	DELNGFFNK	Yes	542.26	612.3	16.22	71	26.4	91029	ND	ND	No
THAS	DELNGFFNK	Yes	542.26	726.4	16.22	71	26.4	125863	ND	ND	No
THAS	DELNGFFNK	Yes	542.26	839.4	16.22	71	26.4	88895	ND	ND	No
THAS	HPKPSPFIGNLTFFR	Yes	586.65	683.4	20.13	76.7	30.5	4889	ND	ND	No
THAS	HPKPSPFIGNLTFFR	Yes	586.65	797.4	20.13	76.7	27.5	5984	ND	ND	No
THAS	HPKPSPFIGNLTFFR	Yes	586.65	854.5	20.13	76.7	30.5	20738	ND	ND	No
THAS	HPKPSPFIGNLTFFR	Yes	586.65	967.5	20.13	76.7	30.5	4201	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
THAS	QQHRPFTYLPFGAGPR	No									
THAS	QVLVENFSNFTNR	Yes	784.4	341.2	17.04	102.2	37	7047	ND	ND	No
THAS	QVLVENFSNFTNR	Yes	784.4	651.3	17.04	102.2	37	2806	ND	ND	No
THAS	QVLVENFSNFTNR	Yes	784.4	738.4	17.04	102.2	46	3661	ND	ND	No
THAS	QVLVENFSNFTNR	Yes	784.4	999.5	17.04	102.2	40	2879	ND	ND	No
THAS	SVADSVLFLR	Yes	553.81	647.4	19.09	72.4	26.9	34423	ND	ND	No
THAS	SVADSVLFLR	Yes	553.81	734.5	19.09	72.4	35.9	144594	ND	ND	No
THAS	SVADSVLFLR	Yes	553.81	849.5	19.09	72.4	26.9	93672	ND	ND	No
THAS	SVADSVLFLR	Yes	553.81	920.5	19.09	72.4	26.9	197218	ND	ND	No
THY1	HENTSSSPIQYEFSLTR	Yes	665.99	623.4	16.49	86.9	31.5	55252	ND	ND	No
THY1	HENTSSSPIQYEFSLTR	Yes	665.99	743.3	16.49	86.9	31.5	56561	ND	ND	No
THY1	HENTSSSPIQYEFSLTR	Yes	665.99	752.4	16.49	86.9	31.5	43172	ND	ND	No
THY1	HENTSSSPIQYEFSLTR	Yes	665.99	915.5	16.49	86.9	31.5	48093	ND	ND	No
THY1	VLYLSAFTSK	Yes	564.82	376.2	18.19	73.9	24.4	164628	ND	ND	No
THY1	VLYLSAFTSK	Yes	564.82	640.3	18.19	73.9	27.4	228055	ND	ND	No
THY1	VLYLSAFTSK	Yes	564.82	753.4	18.19	73.9	27.4	148061	ND	ND	No
THY1	VLYLSAFTSK	Yes	564.82	916.5	18.19	73.9	27.4	238103	ND	ND	No
TIMP1	FVGTPEVNQTTLYQR	Yes	876.95	304.2	13.68	114.1	50.1	42361	ND	ND	No
TIMP1	FVGTPEVNQTTLYQR	Yes	876.95	405.2	13.68	114.1	41.1	86343	ND	ND	No
TIMP1	FVGTPEVNQTTLYQR	Yes	876.95	466.2	13.68	114.1	41.1	33269	ND	ND	No
TIMP1	FVGTPEVNQTTLYQR	Yes	876.95	781.4	13.68	114.1	50.1	29940	ND	ND	No
TIMP1	GFQALGDAADIR	Yes	617.32	404.2	15.02	80.6	29.7	18350	20272	21745	No
TIMP1	GFQALGDAADIR	Yes	617.32	717.4	15.02	80.6	26.7	26480	20134	23247	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
TIMP1	GFQALGDAADIR	Yes	617.32	830.4	15.02	80.6	29.7	9015	9210	8472	No
TIMP1	GFQALGDAADIR	Yes	617.32	901.5	15.02	80.6	29.7	8840	6723	6657	No
TIMP1	SEEFLIAGK	Yes	497.27	275.2	13.80	65.1	33.4	1100256	ND	ND	No
TIMP1	SEEFLIAGK	Yes	497.27	388.3	13.80	65.1	30.4	333435	ND	ND	No
TIMP1	SEEFLIAGK	Yes	497.27	648.4	13.80	65.1	24.4	289175	ND	ND	No
TIMP1	SEEFLIAGK	Yes	497.27	777.5	13.80	65.1	24.4	604882	ND	ND	No
TIMP3	EGPFGTLVYTIK	Yes	662.86	524.3	20.04	86.5	31.7	135417	ND	ND	No
TIMP3	EGPFGTLVYTIK	Yes	662.86	736.5	20.04	86.5	31.7	91324	ND	ND	No
TIMP3	EGPFGTLVYTIK	Yes	662.86	837.5	20.04	86.5	31.7	85440	ND	ND	No
TIMP3	EGPFGTLVYTIK	Yes	662.86	894.5	20.04	86.5	31.7	165691	ND	ND	No
TIMP3	GWAPPDK	No									
TIMP3	SIINATDP	No									
TIMP3	YQYLLTGR	Yes	507.27	292.1	13.38	66.4	24.8	285060	ND	ND	No
TIMP3	YQYLLTGR	Yes	507.27	446.3	13.38	66.4	24.8	69028	ND	ND	No
TIMP3	YQYLLTGR	Yes	507.27	559.4	13.38	66.4	33.8	103673	ND	ND	No
TIMP3	YQYLLTGR	Yes	507.27	722.4	13.38	66.4	24.8	167700	ND	ND	No
TLL1	DGTSENSPLIGR	Yes	623.31	555.4	10.11	81.4	38.9	75382	ND	ND	No
TLL1	DGTSENSPLIGR	Yes	623.31	756.4	10.11	81.4	35.9	48203	ND	ND	No
TLL1	DGTSENSPLIGR	Yes	623.31	885.5	10.11	81.4	38.9	15918	ND	ND	No
TLL1	DGTSENSPLIGR	Yes	623.31	972.5	10.11	81.4	38.9	20285	ND	ND	No
TLL1	IPDPLVATGNK	Yes	562.82	326.2	13.51	73.6	27.3	558154	ND	ND	No
TLL1	IPDPLVATGNK	Yes	562.82	490.3	13.51	73.6	36.3	451741	ND	ND	No
TLL1	IPDPLVATGNK	Yes	562.82	799.5	13.51	73.6	30.3	775491	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
TLL1	IPDPLVATGNK	Yes	562.82	914.5	13.51	73.6	27.3	197005	ND	ND	No
TLL1	LNGTITTPGWPK	Yes	642.85	584.3	14.95	83.9	39.8	ND	ND	ND	No
TLL1	LNGTITTPGWPK	Yes	642.85	685.4	14.95	83.9	33.8	ND	ND	ND	No
TLL1	LNGTITTPGWPK	Yes	642.85	786.4	14.95	83.9	30.8	ND	ND	ND	No
TLL1	LNGTITTPGWPK	Yes	642.85	899.5	14.95	83.9	30.8	ND	ND	ND	No
TLL1	VPLQFSGQNEK	Yes	623.83	438.3	11.05	81.5	32.9	65616	ND	ND	No
TLL1	VPLQFSGQNEK	Yes	623.83	662.3	11.05	81.5	38.9	141045	ND	ND	No
TLL1	VPLQFSGQNEK	Yes	623.83	809.4	11.05	81.5	38.9	185487	ND	ND	No
TLL1	VPLQFSGQNEK	Yes	623.83	937.4	11.05	81.5	38.9	57522	ND	ND	No
TLL1	YDYVEIWSGLSSESK	No									
TNF12	AAPFLTYFGLFQVH	Yes	805.92	387.2	24.73	105	35	13854	ND	ND	No
TNF12	AAPFLTYFGLFQVH	Yes	805.92	530.3	24.73	105	41	17946	ND	ND	No
TNF12	AAPFLTYFGLFQVH	Yes	805.92	700.4	24.73	105	38	25829	ND	ND	No
TNF12	AAPFLTYFGLFQVH	Yes	805.92	847.4	24.73	105	38	26432	ND	ND	No
TNF12	INSSSPLR	Yes	437.24	385.3	7.87	57.4	21.7	48202	ND	20009	Yes (Based on Transition Ratios)
TNF12	INSSSPLR	Yes	437.24	559.3	7.87	57.4	21.7	43082	ND	ND	No
TNF12	INSSSPLR	Yes	437.24	646.4	7.87	57.4	21.7	161880	102375	128800	Yes (Based on Transition Ratios)
TNF12	INSSSPLR	Yes	437.24	760.4	7.87	57.4	21.7	78335	ND	2926	Yes (Based on Transition Ratios)
TNF12	LDLLVDGVLALR	Yes	648.9	342.2	24.43	84.7	34.1	147922	20487	38492	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
TNF12	LDLLVDGVLALR	Yes	648.9	743.4	24.43	84.7	31.1	92585	19567	15321	No
TNF12	LDLLVDGVLALR	Yes	648.9	842.5	24.43	84.7	31.1	ND	7634	8257	Yes (Based on Manual Review)
TNF12	LDLLVDGVLALR	Yes	648.9	955.6	24.43	84.7	34.1	ND	ND	ND	Yes (Based on Manual Review)
TNF12	QIGEFIVTR	Yes	531.8	276.2	14.86	69.6	25.9	53844	ND	ND	No
TNF12	QIGEFIVTR	Yes	531.8	635.4	14.86	69.6	34.9	45556	ND	ND	No
TNF12	QIGEFIVTR	Yes	531.8	787.4	14.86	69.6	25.9	8687	ND	ND	No
TNF12	QIGEFIVTR	Yes	531.8	821.5	14.86	69.6	31.9	114316	ND	ND	No
TNF12	TLPWAHLK	Yes	322.52	260.2	14.76	42.6	20	53678	ND	ND	No
TNF12	TLPWAHLK	Yes	322.52	397.3	14.76	42.6	20	2594	ND	ND	No
TNF12	TLPWAHLK	Yes	322.52	468.3	14.76	42.6	17	68474	ND	ND	No
TNF12	TLPWAHLK	Yes	322.52	654.4	14.76	42.6	14	58265	ND	ND	No
TNR6	DITSDSENSNFR	Yes	692.8	330.2	9.47	90.4	33	31381	ND	ND	No
TNR6	DITSDSENSNFR	Yes	692.8	637.3	9.47	90.4	42	21881	ND	ND	No
TNR6	DITSDSENSNFR	Yes	692.8	853.4	9.47	90.4	42	22483	ND	ND	No
TNR6	DITSDSENSNFR	Yes	692.8	968.4	9.47	90.4	36	14188	ND	ND	No
TNR6	IQTIILK	Yes	414.78	260.2	13.19	54.5	26.8	150318	ND	ND	No
TNR6	IQTIILK	Yes	414.78	373.3	13.19	54.5	29.8	152683	ND	ND	No
TNR6	IQTIILK	Yes	414.78	587.4	13.19	54.5	20.8	336294	ND	ND	No
TNR6	IQTIILK	Yes	414.78	715.5	13.19	54.5	20.8	127895	ND	ND	No
TNR6	NDNVQDTAEQK	Yes	631.29	443.2	5.78	82.4	27.3	72669	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
TNR6	NDNVQDTAEQK	Yes	631.29	691.3	5.78	82.4	30.3	47864	ND	ND	No
TNR6	NDNVQDTAEQK	Yes	631.29	819.4	5.78	82.4	27.3	109579	ND	ND	No
TNR6	NDNVQDTAEQK	Yes	631.29	918.5	5.78	82.4	27.3	25191	ND	ND	No
TNR6	NEIQSLV	No									
TNR6	SVNAQVTDINSK	Yes	638.33	677.3	8.80	83.3	30.6	26027	ND	ND	No
TNR6	SVNAQVTDINSK	Yes	638.33	776.4	8.80	83.3	30.6	25518	ND	ND	No
TNR6	SVNAQVTDINSK	Yes	638.33	904.5	8.80	83.3	30.6	13643	ND	ND	No
TNR6	SVNAQVTDINSK	Yes	638.33	975.5	8.80	83.3	30.6	6362	ND	ND	No
TPIS	ELASQPDVDGFLVGGASLKPEFVDIINAK	No									
TPIS	SNVSDAVAQSTR	Yes	617.81	562.3	8.43	80.7	26.7	53539	ND	ND	No
TPIS	SNVSDAVAQSTR	Yes	617.81	661.4	8.43	80.7	29.7	21213	ND	ND	No
TPIS	SNVSDAVAQSTR	Yes	617.81	847.4	8.43	80.7	35.7	15436	ND	ND	No
TPIS	SNVSDAVAQSTR	Yes	617.81	934.5	8.43	80.7	29.7	35543	ND	ND	No
TPIS	TATPQQAQEVHEK	Yes	489.58	413.2	5.82	64.2	31.5	59207	ND	ND	No
TPIS	TATPQQAQEVHEK	Yes	489.58	512.3	5.82	64.2	28.5	26239	ND	ND	No
TPIS	TATPQQAQEVHEK	Yes	489.58	840.4	5.82	64.2	25.5	25009	ND	ND	No
TPIS	TATPQQAQEVHEK	Yes	489.58	968.5	5.82	64.2	19.5	5103	ND	ND	No
TPIS	VVFEQTK	Yes	425.74	376.2	8.40	55.9	24.2	64946	ND	ND	No
TPIS	VVFEQTK	Yes	425.74	505.3	8.40	55.9	21.2	49112	ND	ND	No
TPIS	VVFEQTK	Yes	425.74	652.3	8.40	55.9	21.2	486456	ND	ND	No
TPIS	VVFEQTK	Yes	425.74	751.4	8.40	55.9	21.2	64050	ND	ND	No
TPIS	VVLAYEPVWAIGTGK	Yes	801.95	312.2	20.93	104.5	37.8	ND	9482	15308	Yes (Based on Manual Review)

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
TPIS	VVLAYEPVWAIGTGK	Yes	801.95	362.2	20.93	104.5	34.8	89190	3915	7956	No
TPIS	VVLAYEPVWAIGTGK	Yes	801.95	383.3	20.93	104.5	34.8	139849	7577	12094	No
TPIS	VVLAYEPVWAIGTGK	Yes	801.95	928.5	20.93	104.5	34.8	167799	13107	11863	No
TRFL	ADAVTLDGGFIYEAGLAPYK	Yes	1036.02	407.2	21.21	134.6	48.1	15413	ND	ND	No
TRFL	ADAVTLDGGFIYEAGLAPYK	Yes	1036.02	571.3	21.21	134.6	48.1	2916	ND	ND	No
TRFL	ADAVTLDGGFIYEAGLAPYK	Yes	1036.02	648.4	21.21	134.6	57.1	3344	ND	ND	No
TRFL	ADAVTLDGGFIYEAGLAPYK	Yes	1036.02	719.4	21.21	134.6	48.1	2849	ND	ND	No
TRFL	FQLFGSPSGQK	Yes	598.31	276.1	16.37	78.2	28.8	1388951	ND	ND	No
TRFL	FQLFGSPSGQK	Yes	598.31	660.3	16.37	78.2	37.8	157791	ND	ND	No
TRFL	FQLFGSPSGQK	Yes	598.31	807.4	16.37	78.2	28.8	387590	ND	ND	No
TRFL	FQLFGSPSGQK	Yes	598.31	920.5	16.37	78.2	28.8	322162	ND	ND	No
TRFL	LRPVAAEVYGTER	Yes	487.6	462.2	10.83	63.9	22.4	142957	1268	ND	No
TRFL	LRPVAAEVYGTER	Yes	487.6	608.4	10.83	63.9	22.4	27211	ND	ND	No
TRFL	LRPVAAEVYGTER	Yes	487.6	625.3	10.83	63.9	22.4	141347	3496	ND	No
TRFL	LRPVAAEVYGTER	Yes	487.6	737.4	10.83	63.9	22.4	93835	2506	ND	No
TRFL	VPSHAVVAR	Yes	312.52	345.2	6.10	41.3	16.5	38398	ND	1790149	Yes (Based on Transition Ratios)
TRFL	VPSHAVVAR	Yes	312.52	444.3	6.10	41.3	19.5	44379	ND	1540	No
TRFL	VPSHAVVAR	Yes	312.52	515.3	6.10	41.3	19.5	81835	ND	5549	No
TRFL	VPSHAVVAR	Yes	312.52	739.4	6.10	41.3	10.5	ND	ND	ND	No
TRFL	YYGYTGAFR	Yes	549.26	450.2	13.16	71.9	26.7	76835	ND	ND	No
TRFL	YYGYTGAFR	Yes	549.26	714.4	13.16	71.9	26.7	53107	ND	ND	No
TRFL	YYGYTGAFR	Yes	549.26	771.4	13.16	71.9	26.7	413048	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
TRFL	YYGYTGAFR	Yes	549.26	934.4	13.16	71.9	26.7	41023	ND	ND	No
TSP1	FQDLVDAVR	Yes	531.78	391.2	14.82	69.6	25.9	139448	ND	ND	No
TSP1	FQDLVDAVR	Yes	531.78	559.3	14.82	69.6	25.9	135339	ND	ND	No
TSP1	FQDLVDAVR	Yes	531.78	672.4	14.82	69.6	34.9	78199	ND	ND	No
TSP1	FQDLVDAVR	Yes	531.78	787.4	14.82	69.6	25.9	324827	ND	ND	No
TSP1	FTGSQPFGQGVEHATANK	Yes	625.97	261.2	11.27	81.8	38.5	ND	ND	17659	Yes (Based on Manual Review)
TSP1	FTGSQPFGQGVEHATANK	Yes	625.97	504.3	11.27	81.8	38.5	ND	ND	10888	Yes (Based on Manual Review)
TSP1	FTGSQPFGQGVEHATANK	Yes	625.97	521.2	11.27	81.8	26.5	22090	9087	11946	No
TSP1	FTGSQPFGQGVEHATANK	Yes	625.97	926.5	11.27	81.8	35.5	7556	3730	1551	No
TSP1	FVFGTTPEDILR	Yes	465.58	288.2	20.74	61.1	27.3	33398	ND	ND	No
TSP1	FVFGTTPEDILR	Yes	465.58	516.3	20.74	61.1	21.3	31507	11257	17673	No
TSP1	FVFGTTPEDILR	Yes	465.58	645.4	20.74	61.1	24.3	22856	9340	15332	No
TSP1	FVFGTTPEDILR	Yes	465.58	742.4	20.74	61.1	21.3	34227	12158	15597	No
TSP1	GFLLLASLR	Yes	495.31	318.2	23.25	64.9	21.3	ND	141668	285281	No
TSP1	GFLLLASLR	Yes	495.31	375.2	23.25	64.9	33.3	ND	29364	40659	No
TSP1	GFLLLASLR	Yes	495.31	446.3	23.25	64.9	27.3	ND	100807	204220	No
TSP1	GFLLLASLR	Yes	495.31	559.4	23.25	64.9	24.3	ND	175194	330863	No
TSP1	GTSQNDPNWVVR	Yes	686.83	373.3	11.85	89.6	29.7	11667	13952	48759	No
TSP1	GTSQNDPNWVVR	Yes	686.83	770.4	11.85	89.6	38.7	27410	34205	66462	No
TSP1	GTSQNDPNWVVR	Yes	686.83	885.5	11.85	89.6	32.7	4634	2142	5334	Yes (Based on Transition

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
											Ratios)
TSP1	GTSQNDPNWVVR	Yes	686.83	999.5	11.85	89.6	38.7	6281	6393	12291	No
TTHY	TSESGELHGLTTEEEFVEGIYK	Yes	819.06	480.3	19.88	106.7	45.3	10047	ND	ND	No
TTHY	TSESGELHGLTTEEEFVEGIYK	Yes	819.06	609.3	19.88	106.7	39.3	11879	ND	ND	No
TTHY	TSESGELHGLTTEEEFVEGIYK	Yes	819.06	708.4	19.88	106.7	39.3	8446	ND	ND	No
TTHY	TSESGELHGLTTEEEFVEGIYK	Yes	819.06	855.5	19.88	106.7	39.3	9453	ND	ND	No
TTHY	VEIDTK	Yes	352.7	457.2	6.78	46.5	15	53034	ND	ND	No
TTHY	VEIDTK	Yes	352.7	476.3	6.78	46.5	18	220871	ND	ND	No
TTHY	VEIDTK	Yes	352.7	605.3	6.78	46.5	18	146056	ND	ND	No
TYPH	ALQEALVLSDR	Yes	607.84	490.3	14.64	79.4	26.2	28234	990	ND	No
TYPH	ALQEALVLSDR	Yes	607.84	702.4	14.64	79.4	29.2	23916	ND	ND	No
TYPH	ALQEALVLSDR	Yes	607.84	773.5	14.64	79.4	32.2	25174	ND	ND	No
TYPH	ALQEALVLSDR	Yes	607.84	902.5	14.64	79.4	29.2	18976	ND	ND	No
TYPH	EQEELLAPADGTVELVR	Yes	623.66	742.4	17.56	81.5	29.4	12904	ND	ND	No
TYPH	EQEELLAPADGTVELVR	Yes	623.66	773.5	17.56	81.5	38.4	28915	ND	ND	No
TYPH	EQEELLAPADGTVELVR	Yes	623.66	888.5	17.56	81.5	32.4	21622	ND	ND	No
TYPH	EQEELLAPADGTVELVR	Yes	623.66	959.5	17.56	81.5	32.4	8910	ND	ND	No
TYPH	LSEADIR	No									
TYPH	TLVGVGASLGLR	Yes	571.85	673.4	17.25	74.8	27.7	211681	ND	ND	No
TYPH	TLVGVGASLGLR	Yes	571.85	772.5	17.25	74.8	27.7	43012	ND	ND	No
TYPH	TLVGVGASLGLR	Yes	571.85	829.5	17.25	74.8	27.7	192191	ND	ND	No
TYPH	TLVGVGASLGLR	Yes	571.85	928.6	17.25	74.8	27.7	73164	ND	ND	No
TYPH	VAAALDDGSALGR	Yes	608.32	675.3	11.15	79.5	38.3	19577	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
TYPH	VAAALDDGSALGR	Yes	608.32	790.4	11.15	79.5	29.3	26728	ND	ND	No
TYPH	VAAALDDGSALGR	Yes	608.32	903.5	11.15	79.5	29.3	11366	ND	ND	No
TYPH	VAAALDDGSALGR	Yes	608.32	974.5	11.15	79.5	38.3	6458	ND	ND	No
UGGG1	DLSQNFPTK	Yes	525.27	345.2	10.82	68.8	34.6	956000	ND	ND	No
UGGG1	DLSQNFPTK	Yes	525.27	606.3	10.82	68.8	25.6	90920	ND	ND	No
UGGG1	DLSQNFPTK	Yes	525.27	734.4	10.82	68.8	25.6	81940	ND	ND	No
UGGG1	DLSQNFPTK	Yes	525.27	821.4	10.82	68.8	25.6	383897	ND	ND	No
UGGG1	FTILDSQGK	Yes	504.77	534.3	13.22	66.1	24.7	390793	ND	ND	No
UGGG1	FTILDSQGK	Yes	504.77	647.3	13.22	66.1	24.7	335210	ND	ND	No
UGGG1	FTILDSQGK	Yes	504.77	760.4	13.22	66.1	24.7	454157	ND	ND	No
UGGG1	FTILDSQGK	Yes	504.77	861.5	13.22	66.1	24.7	69405	ND	ND	No
UGGG1	IIGPLEDSELFNQDDFHLLENIILK	No									
UGGG1	LGIEGLSLHNVLK	Yes	696.91	413.2	19.28	90.9	33.2	7789	ND	ND	No
UGGG1	LGIEGLSLHNVLK	Yes	696.91	610.4	19.28	90.9	42.2	11508	ND	ND	No
UGGG1	LGIEGLSLHNVLK	Yes	696.91	810.5	19.28	90.9	36.2	18861	ND	ND	No
UGGG1	LGIEGLSLHNVLK	Yes	696.91	980.6	19.28	90.9	36.2	12310	ND	ND	No
UGGG1	YVLEPEISFTSDNSFAK	Yes	649.65	505.3	19.66	84.8	30.7	14504	ND	ND	No
UGGG1	YVLEPEISFTSDNSFAK	Yes	649.65	681.3	19.66	84.8	30.7	8297	ND	ND	No
UGGG1	YVLEPEISFTSDNSFAK	Yes	649.65	768.4	19.66	84.8	27.7	23699	ND	ND	No
UGGG1	YVLEPEISFTSDNSFAK	Yes	649.65	869.4	19.66	84.8	27.7	20982	ND	ND	No
UGGG2	ANPGAWILR	No									
UGGG2	FLGPLDEDFYAEDFYLLEK	Yes	1162.55	389.2	24.65	151	59.7	5209	ND	ND	No
UGGG2	FLGPLDEDFYAEDFYLLEK	Yes	1162.55	502.3	24.65	151	59.7	4857	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
UGGG2	FLGPLDEDFYAEDFYLLEK	Yes	1162.55	643.3	24.65	151	50.7	2428	ND	ND	No
UGGG2	FLGPLDEDFYAEDFYLLEK	Yes	1162.55	665.4	24.65	151	56.7	3147	ND	ND	No
UGGG2	IIFVDADQIVR	No									
UGGG2	ILFLDVLFPLAVDK	Yes	801.98	374.2	24.95	104.5	37.8	184983	ND	ND	No
UGGG2	ILFLDVLFPLAVDK	Yes	801.98	642.4	24.95	104.5	46.8	202682	ND	ND	No
UGGG2	ILFLDVLFPLAVDK	Yes	801.98	701.4	24.95	104.5	34.8	87395	ND	ND	No
UGGG2	ILFLDVLFPLAVDK	Yes	801.98	902.5	24.95	104.5	37.8	125535	ND	ND	No
UGGG2	INEENTAISR	Yes	573.79	262.2	7.52	75	27.7	8281	ND	ND	No
UGGG2	INEENTAISR	Yes	573.79	661.4	7.52	75	24.7	4196	ND	ND	No
UGGG2	INEENTAISR	Yes	573.79	790.4	7.52	75	30.7	7901	ND	ND	No
UGGG2	INEENTAISR	Yes	573.79	919.4	7.52	75	24.7	7352	ND	ND	No
UGPA	GGTLTQYEGK	Yes	527.26	496.2	9.86	69	34.7	722087	ND	ND	No
UGPA	GGTLTQYEGK	Yes	527.26	624.3	9.86	69	25.7	513359	ND	ND	No
UGPA	GGTLTQYEGK	Yes	527.26	725.3	9.86	69	28.7	1838226	ND	ND	No
UGPA	GGTLTQYEGK	Yes	527.26	838.4	9.86	69	22.7	378421	ND	ND	No
UGPA	GLPDNISSVLNK	Yes	628.85	261.2	18.04	82.1	39.2	229506	25460	13892	No
UGPA	GLPDNISSVLNK	Yes	628.85	760.5	18.04	82.1	36.2	68617	9863	13837	No
UGPA	GLPDNISSVLNK	Yes	628.85	874.5	18.04	82.1	36.2	119530	3359	ND	No
UGPA	GLPDNISSVLNK	Yes	628.85	989.5	18.04	82.1	33.2	61588	ND	ND	No
UGPA	GTVIIIANHGDR	Yes	633.35	371.2	12.12	82.7	33.4	375157	ND	ND	No
UGPA	GTVIIIANHGDR	Yes	633.35	598.3	12.12	82.7	33.4	129762	ND	ND	No
UGPA	GTVIIIANHGDR	Yes	633.35	669.3	12.12	82.7	33.4	283337	ND	ND	No
UGPA	GTVIIIANHGDR	Yes	633.35	895.5	12.12	82.7	36.4	365353	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
UGPA	IDIPPGAVLENK	Yes	633.36	261.2	15.81	82.7	39.4	236639	ND	ND	No
UGPA	IDIPPGAVLENK	Yes	633.36	730.4	15.81	82.7	39.4	65711	ND	ND	No
UGPA	IDIPPGAVLENK	Yes	633.36	827.5	15.81	82.7	33.4	542953	ND	ND	No
UGPA	IDIPPGAVLENK	Yes	633.36	924.5	15.81	82.7	30.4	835198	ND	ND	No
UGPA	IFNTNNLWISLAAVK	Yes	852.48	317.2	25.01	111	37	ND	ND	ND	No
UGPA	IFNTNNLWISLAAVK	Yes	852.48	588.4	25.01	111	43	32659	ND	ND	No
UGPA	IFNTNNLWISLAAVK	Yes	852.48	701.5	25.01	111	43	19383	ND	ND	No
UGPA	IFNTNNLWISLAAVK	Yes	852.48	887.5	25.01	111	40	28332	ND	ND	No
UGPA	IQRPPEDSIQPYEK	Yes	567.29	536.3	11.66	74.2	29.5	439122	ND	ND	No
UGPA	IQRPPEDSIQPYEK	Yes	567.29	664.3	11.66	74.2	26.5	111491	ND	ND	No
UGPA	IQRPPEDSIQPYEK	Yes	567.29	721.4	11.66	74.2	32.5	45755	ND	ND	No
UGPA	IQRPPEDSIQPYEK	Yes	567.29	923.5	11.66	74.2	32.5	127914	ND	ND	No
UGPA	LVEIAQVPK	Yes	498.81	343.2	14.12	65.3	33.4	413214	ND	ND	No
UGPA	LVEIAQVPK	Yes	498.81	542.3	14.12	65.3	27.4	686080	16153	4681	No
UGPA	LVEIAQVPK	Yes	498.81	655.4	14.12	65.3	24.4	654379	7910	5058	No
UGPA	LVEIAQVPK	Yes	498.81	784.5	14.12	65.3	24.4	2727237	35953	19219	No
UGPA	NENTFLDLTVQQIEHLNK	Yes	719.37	511.3	24.46	93.8	43.2	116966	56496	37002	No
UGPA	NENTFLDLTVQQIEHLNK	Yes	719.37	753.4	24.46	93.8	43.2	49363	13403	4814	No
UGPA	NENTFLDLTVQQIEHLNK	Yes	719.37	881.5	24.46	93.8	43.2	49230	12478	5952	No
UGPA	NENTFLDLTVQQIEHLNK	Yes	719.37	947.4	24.46	93.8	31.2	1269	43706	28610	No
UGPA	SFENSLGINVPR	Yes	666.85	272.2	17.80	87	28.8	1597343	ND	ND	No
UGPA	SFENSLGINVPR	Yes	666.85	485.3	17.80	87	31.8	566189	2118	ND	No
UGPA	SFENSLGINVPR	Yes	666.85	768.5	17.80	87	40.8	379973	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
UGPA	SFENSLGINVPR	Yes	666.85	969.5	17.80	87	37.8	220762	ND	ND	No
UGPA	TLDGGLNVIQLETAVGAAIK	Yes	661.71	459.3	24.99	86.4	28.3	7822	ND	ND	No
UGPA	TLDGGLNVIQLETAVGAAIK	Yes	661.71	558.4	24.99	86.4	31.3	7512	ND	ND	No
UGPA	TLDGGLNVIQLETAVGAAIK	Yes	661.71	730.4	24.99	86.4	28.3	9465	ND	ND	No
UGPA	TLDGGLNVIQLETAVGAAIK	Yes	661.71	770.4	24.99	86.4	31.3	9670	ND	ND	No
UPAR	LWEEGEELELVEK	No									
UPAR	LWGGTLLWT	No									
UTER	LVDTLPQKPR	No									
UTER	VIETLLMDTPSSYEAAMELFSPDQDMR	No									
VA0D1	ADDYEQVK	Yes	484.22	302.1	6.89	63.5	20.8	60785	ND	ND	No
VA0D1	ADDYEQVK	Yes	484.22	666.3	6.89	63.5	20.8	32399	ND	ND	No
VA0D1	ADDYEQVK	Yes	484.22	781.4	6.89	63.5	23.8	129833	ND	ND	No
VA0D1	ADDYEQVK	Yes	484.22	896.4	6.89	63.5	23.8	29963	ND	ND	No
VA0D1	LHLQSTDYGNFLANEASPLTVSVIDDR	No									
VA0D1	LLFEGAGSNPGDK	Yes	652.83	416.2	13.34	85.2	40.2	665185	45287	57417	Yes (Based on Transition Ratios)
VA0D1	LLFEGAGSNPGDK	Yes	652.83	674.3	13.34	85.2	31.2	213096	ND	ND	No
VA0D1	LLFEGAGSNPGDK	Yes	652.83	802.4	13.34	85.2	34.2	483152	ND	ND	No
VA0D1	LLFEGAGSNPGDK	Yes	652.83	931.4	13.34	85.2	31.2	119809	ND	1695	Yes (Based on Transition Ratios)
VA0D1	LYPEGLAQLAR	Yes	615.85	558.3	16.73	80.4	38.6	27510	ND	ND	No
VA0D1	LYPEGLAQLAR	Yes	615.85	728.4	16.73	80.4	38.6	42475	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
VA0D1	LYPEGLAQLAR	Yes	615.85	857.5	16.73	80.4	38.6	16382	ND	ND	No
VA0D1	LYPEGLAQLAR	Yes	615.85	954.5	16.73	80.4	29.6	21297	ND	ND	No
VA0D1	NVADYYPEYK	Yes	631.29	285.2	12.06	82.4	27.3	105708	ND	ND	No
VA0D1	NVADYYPEYK	Yes	631.29	536.3	12.06	82.4	39.3	314919	ND	ND	No
VA0D1	NVADYYPEYK	Yes	631.29	699.3	12.06	82.4	30.3	35635	ND	ND	No
VA0D1	NVADYYPEYK	Yes	631.29	977.4	12.06	82.4	30.3	34928	ND	ND	No
VAV3	LQAETELINR	Yes	593.83	289.2	11.74	77.6	31.6	33547	ND	ND	No
VAV3	LQAETELINR	Yes	593.83	515.3	11.74	77.6	37.6	22596	ND	ND	No
VAV3	LQAETELINR	Yes	593.83	874.5	11.74	77.6	37.6	10865	ND	ND	No
VAV3	LQAETELINR	Yes	593.83	945.5	11.74	77.6	28.6	45821	ND	ND	No
VAV3	NDQNLYQVFINYK	Yes	829.91	358.1	20.55	108.1	48	6568	ND	ND	No
VAV3	NDQNLYQVFINYK	Yes	829.91	424.2	20.55	108.1	39	9021	ND	ND	No
VAV3	NDQNLYQVFINYK	Yes	829.91	472.2	20.55	108.1	45	4370	ND	ND	No
VAV3	NDQNLYQVFINYK	Yes	829.91	783.4	20.55	108.1	45	3233	ND	ND	No
VAV3	QFQLSIENLNQPVLLFGRPQGDGEIR	No									
VAV3	TPIALATGIRPFPTEESINDEDIYK	No									
VAV3	VTWDSAQVFDLAQTLR	Yes	617.32	517.3	23.26	80.6	26	35935	ND	ND	No
VAV3	VTWDSAQVFDLAQTLR	Yes	617.32	588.3	23.26	80.6	29	49353	ND	ND	No
VAV3	VTWDSAQVFDLAQTLR	Yes	617.32	816.5	23.26	80.6	29	38344	ND	ND	No
VAV3	VTWDSAQVFDLAQTLR	Yes	617.32	963.5	23.26	80.6	32	16187	ND	ND	No
VEGFA	QLELNER	Yes	451.24	418.2	9.23	59.2	22.4	25222	6361	ND	No
VEGFA	QLELNER	Yes	451.24	531.3	9.23	59.2	31.4	21985	ND	ND	No
VEGFA	QLELNER	Yes	451.24	598.3	9.23	59.2	19.4	ND	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
VEGFA	QLELNER	Yes	451.24	660.3	9.23	59.2	31.4	30155	ND	ND	No
VEGFA	SWSVYVGAR	Yes	512.76	274.1	14.21	67.1	25.1	151808	ND	ND	No
VEGFA	SWSVYVGAR	Yes	512.76	565.3	14.21	67.1	34.1	35217	ND	ND	No
VEGFA	SWSVYVGAR	Yes	512.76	664.4	14.21	67.1	34.1	14399	ND	ND	No
VEGFA	SWSVYVGAR	Yes	512.76	751.4	14.21	67.1	25.1	78236	ND	ND	No
VEGFC	DLEEQLR	Yes	451.73	288.2	11.05	59.3	31.4	37427	ND	ND	No
VEGFC	DLEEQLR	Yes	451.73	416.3	11.05	59.3	31.4	31039	ND	ND	No
VEGFC	DLEEQLR	Yes	451.73	545.3	11.05	59.3	22.4	73407	ND	ND	No
VEGFC	DLEEQLR	Yes	451.73	674.3	11.05	59.3	22.4	124074	ND	ND	No
VEGFC	EAPAAAAAFESGLDLSDAEPDAGEATAYASK	Yes	999.46	440.2	19.07	129.9	51.5	ND	ND	1736	No
VEGFC	EAPAAAAAFESGLDLSDAEPDAGEATAYASK	Yes	999.46	468.2	19.07	129.9	45.5	2740	ND	ND	No
VEGFC	EAPAAAAAFESGLDLSDAEPDAGEATAYASK	Yes	999.46	653.3	19.07	129.9	48.5	3501	ND	ND	No
VEGFC	EAPAAAAAFESGLDLSDAEPDAGEATAYASK	Yes	999.46	897.4	19.07	129.9	45.5	2725	ND	2278	No
VEGFC	EQANLNSR	Yes	466.23	262.2	5.81	61.1	23	8410	ND	ND	No
VEGFC	EQANLNSR	Yes	466.23	376.2	5.81	61.1	23	16467	ND	ND	No
VEGFC	EQANLNSR	Yes	466.23	603.3	5.81	61.1	23	10949	ND	ND	No
VEGFC	EQANLNSR	Yes	466.23	674.4	5.81	61.1	26	15774	ND	ND	No
VEGFC	FAAAHYNTEILK	Yes	689.36	260.2	12.61	89.9	38.8	53796	ND	ND	No
VEGFC	FAAAHYNTEILK	Yes	689.36	373.3	12.61	89.9	38.8	13503	ND	ND	No
VEGFC	FAAAHYNTEILK	Yes	689.36	498.2	12.61	89.9	41.8	15206	ND	ND	No
VEGFC	FAAAHYNTEILK	Yes	689.36	880.5	12.61	89.9	35.8	9134	ND	ND	No
VEGFC	NQPLNPGK	Yes	434.24	301.2	6.36	57	30.6	345650	ND	ND	No
VEGFC	NQPLNPGK	Yes	434.24	340.2	6.36	57	18.6	5015	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
VEGFC	NQPLNPGK	Yes	434.24	528.3	6.36	57	24.6	23787	ND	ND	No
VEGFC	NQPLNPGK	Yes	434.24	625.4	6.36	57	21.6	504659	ND	ND	No
VEGFD	AASSLEELLR	Yes	544.8	659.4	18.13	71.3	29.5	92110	ND	ND	No
VEGFD	AASSLEELLR	Yes	544.8	772.5	18.13	71.3	26.5	39860	ND	ND	No
VEGFD	AASSLEELLR	Yes	544.8	859.5	18.13	71.3	26.5	32188	ND	ND	No
VEGFD	AASSLEELLR	Yes	544.8	946.5	18.13	71.3	26.5	36504	ND	ND	No
VEGFD	DLIQHPK	Yes	425.74	381.2	7.61	55.9	27.2	245233	ND	ND	No
VEGFD	DLIQHPK	Yes	425.74	509.3	7.61	55.9	21.2	264184	ND	ND	No
VEGFD	DLIQHPK	Yes	425.74	607.3	7.61	55.9	21.2	66402	ND	ND	No
VEGFD	DLIQHPK	Yes	425.74	622.4	7.61	55.9	24.2	525032	ND	ND	No
VEGFD	FAATFYDIETLK	Yes	473.58	361.2	19.80	62.1	30.7	9738	ND	ND	No
VEGFD	FAATFYDIETLK	Yes	473.58	538.3	19.80	62.1	18.7	15255	ND	ND	No
VEGFD	FAATFYDIETLK	Yes	473.58	603.4	19.80	62.1	21.7	11445	ND	ND	No
VEGFD	FAATFYDIETLK	Yes	473.58	718.4	19.80	62.1	21.7	15280	ND	ND	No
VEGFD	QLFEISVPLTSVPELVPVK	Yes	1048.11	343.2	24.51	136.2	45.6	22469	ND	ND	No
VEGFD	QLFEISVPLTSVPELVPVK	Yes	1048.11	518.3	24.51	136.2	48.6	13070	ND	ND	No
VEGFD	QLFEISVPLTSVPELVPVK	Yes	1048.11	631.3	24.51	136.2	48.6	9026	ND	ND	No
VEGFD	QLFEISVPLTSVPELVPVK	Yes	1048.11	781.5	24.51	136.2	51.6	13705	ND	ND	No
VEGFD	VIDEEWQR	No									
VGFR1	AFPSPEVVWLK	Yes	636.85	260.2	20.72	83.2	39.5	44444	ND	ND	No
VGFR1	AFPSPEVVWLK	Yes	636.85	545.3	20.72	83.2	39.5	57610	ND	ND	No
VGFR1	AFPSPEVVWLK	Yes	636.85	870.5	20.72	83.2	30.5	254335	ND	ND	No
VGFR1	AFPSPEVVWLK	Yes	636.85	957.5	20.72	83.2	33.5	47315	ND	ND	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
VGFR1	AVSSFPDPALYPLGSR	Yes	838.94	529.3	18.75	109.2	39.4	155980	ND	ND	No
VGFR1	AVSSFPDPALYPLGSR	Yes	838.94	692.4	18.75	109.2	45.4	81127	ND	ND	No
VGFR1	AVSSFPDPALYPLGSR	Yes	838.94	805.5	18.75	109.2	48.4	34675	ND	ND	No
VGFR1	AVSSFPDPALYPLGSR	Yes	838.94	973.5	18.75	109.2	45.4	204507	ND	ND	No
VGFR1	GSVESSAYLTVQGTSDK	Yes	864.92	507.2	12.30	112.6	37.6	4938	ND	ND	No
VGFR1	GSVESSAYLTVQGTSDK	Yes	864.92	635.3	12.30	112.6	40.6	3667	ND	ND	No
VGFR1	GSVESSAYLTVQGTSDK	Yes	864.92	835.4	12.30	112.6	40.6	3465	ND	ND	No
VGFR1	GSVESSAYLTVQGTSDK	Yes	864.92	948.5	12.30	112.6	40.6	2286	ND	ND	No
VGFR1	LGDLLQANVQQDGK	Yes	749.9	286.1	13.67	97.7	44.5	54523	26406	20504	No
VGFR1	LGDLLQANVQQDGK	Yes	749.9	788.4	13.67	97.7	35.5	4668	ND	ND	No
VGFR1	LGDLLQANVQQDGK	Yes	749.9	859.4	13.67	97.7	35.5	6757	ND	ND	No
VGFR1	LGDLLQANVQQDGK	Yes	749.9	987.5	13.67	97.7	35.5	6732	ND	ND	No
VGFR1	NILLSENNVVK	No									
VTNC	ATWLSLFSSEESNLGANNYDDYR	No									
VTNC	AVRPGYPK	Yes	296.51	327.2	6.32	39.2	15.7	6367	92689	72802	No
VTNC	AVRPGYPK	Yes	296.51	481.3	6.32	39.2	15.7	27437	255258	227635	No
VTNC	AVRPGYPK	Yes	296.51	561.3	6.32	39.2	15.7	18980	200622	161279	No
VTNC	AVRPGYPK	Yes	296.51	644.4	6.32	39.2	21.7	ND	ND	ND	No
VTNC	DSWEDIFELLFWGR	Yes	906.93	418.2	25.02	118	42.4	ND	ND	ND	No
VTNC	DSWEDIFELLFWGR	Yes	906.93	565.3	25.02	118	39.4	ND	ND	ND	No
VTNC	DSWEDIFELLFWGR	Yes	906.93	633.2	25.02	118	39.4	ND	ND	ND	No
VTNC	DSWEDIFELLFWGR	Yes	906.93	746.3	25.02	118	42.4	ND	ND	ND	No
VTNC	DVWGIEGPIDAAFTR	Yes	823.91	458.2	22.99	107.3	41.8	135315	1427037	1390869	No

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
VTNC	DVWGIEGPIDAAFTR	Yes	823.91	565.3	22.99	107.3	47.8	65041	822465	782320	No
VTNC	DVWGIEGPIDAAFTR	Yes	823.91	890.5	22.99	107.3	38.8	42981	466249	466003	No
VTNC	DVWGIEGPIDAAFTR	Yes	823.91	947.5	22.99	107.3	41.8	79699	841124	863797	No
VTNC	FEDGVLDPDYPR	Yes	711.83	277.1	14.87	92.8	36.8	54677	46289	42226	No
VTNC	FEDGVLDPDYPR	Yes	711.83	647.3	14.87	92.8	39.8	101207	113099	93204	No
VTNC	FEDGVLDPDYPR	Yes	711.83	762.3	14.87	92.8	33.8	29624	26645	22977	No
VTNC	FEDGVLDPDYPR	Yes	711.83	875.4	14.87	92.8	33.8	40350	44668	45099	No
VWC2	AGDLQVRPR	No									
VWC2	QAWVSQGGGAK	Yes	544.78	389.2	8.18	71.3	35.5	25619	ND	ND	No
VWC2	QAWVSQGGGAK	Yes	544.78	604.3	8.18	71.3	26.5	73085	ND	ND	No
VWC2	QAWVSQGGGAK	Yes	544.78	703.4	8.18	71.3	29.5	26025	ND	ND	No
VWC2	QAWVSQGGGAK	Yes	544.78	889.5	8.18	71.3	23.5	14476	ND	ND	No
VWC2	VNELGRPAR	Yes	506.29	456.2	6.51	66.3	33.8	3964	2266	ND	No
VWC2	VNELGRPAR	Yes	506.29	766.4	6.51	66.3	27.8	3295	1937	ND	No
VWC2	VNELGRPAR	Yes	506.29	837.5	6.51	66.3	27.8	3459	2174	ND	No
WNT3A	ENRPDAR	No									
WNT3A	ESAFVHAIASAGVAFAVTR	No									
WNT3A	GWVETLRPR	No									
WNT3A	HQGSPGK	Yes	355.68	410.2	4.70	46.9	21.2	2625	ND	ND	No
WNT3A	HQGSPGK	Yes	355.68	445.2	4.70	46.9	21.2	2465	ND	ND	No
WNT3A	HQGSPGK	Yes	355.68	564.3	4.70	46.9	15.2	761	ND	ND	No
WNT3A	HQGSPGK	Yes	355.68	573.3	4.70	46.9	18.2	2147	ND	ND	No
WNT3A	YTYFK	No									

Table S5. MRM assay of individual proteins.

Protein (_HUMAN)	Peptide	MS/MS spectrum	Precursor ion (m/z)	Fragment ion (m/z)	Retention time (minutes)	Declustering potential	Collision energy	Area of synthetic peptide	Area in control sample	Area in disease sample	Interference
WT1	GVAAGSSSSVK	Yes	475.25	594.3	5.61	62.3	23.4	25524	ND	ND	No
WT1	GVAAGSSSSVK	Yes	475.25	651.3	5.61	62.3	23.4	150008	ND	ND	No
WT1	GVAAGSSSSVK	Yes	475.25	722.4	5.61	62.3	23.4	82831	ND	ND	No
WT1	GVAAGSSSSVK	Yes	475.25	793.4	5.61	62.3	23.4	146726	ND	ND	No
WT1	IHTHGVFR	Yes	483.77	251.2	7.42	63.4	26.8	29716	ND	ND	No
WT1	IHTHGVFR	Yes	483.77	352.2	7.42	63.4	29.8	3380	ND	ND	No
WT1	IHTHGVFR	Yes	483.77	615.3	7.42	63.4	29.8	10203	ND	ND	No
WT1	IHTHGVFR	Yes	483.77	716.4	7.42	63.4	26.8	16313	ND	ND	No
WT1	NQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFK	No									
WT1	SDELVR	Yes	359.69	274.2	7.34	47.4	27.3	24409	16999	26861	No
WT1	SDELVR	Yes	359.69	387.3	7.34	47.4	18.3	25914	36660	47230	No
WT1	SDELVR	Yes	359.69	516.3	7.34	47.4	15.3	48541	11164	11414	Yes (Based on Transition Ratios)
WT1	SDELVR	Yes	359.69	631.3	7.34	47.4	15.3	6572	ND	ND	No
WT1	YGPFGPPPPSQASSGQAR	Yes	600.96	518.3	12.52	78.5	28.2	32210	ND	ND	No
WT1	YGPFGPPPPSQASSGQAR	Yes	600.96	522.2	12.52	78.5	25.2	38072	ND	ND	No
WT1	YGPFGPPPPSQASSGQAR	Yes	600.96	676.3	12.52	78.5	28.2	34811	ND	ND	No
WT1	YGPFGPPPPSQASSGQAR	Yes	600.96	716.3	12.52	78.5	37.2	12647	ND	ND	No
ZA2G	DIVEYYNDSNGSHVLQGR	No									
ZA2G	DYIEFNK	No									
ZA2G	EIPAWVPFDPAAQITK	Yes	891.98	560.3	22.39	116.1	50.7	16541	32548	38460	No
ZA2G	EIPAWVPFDPAAQITK	Yes	891.98	597.3	22.39	116.1	38.7	65109	109189	123785	No
ZA2G	EIPAWVPFDPAAQITK	Yes	891.98	696.4	22.39	116.1	38.7	135200	213709	229458	No

Table S5. MRM assay of individual proteins.											
Protein (_HUMAN)	**Peptide**	**MS/MS spectrum**	**Precursor ion (m/z)**	**Fragment ion (m/z)**	**Retention time (minutes)**	**Declustering potential**	**Collision energy**	**Area of synthetic peptide**	**Area in control sample**	**Area in disease sample**	**Interference**
ZA2G	EIPAWVPFDPAAQITK	Yes	891.98	728.4	22.39	116.1	50.7	121509	231479	281981	No
ZA2G	WEAEPVYVQR	Yes	638.82	316.1	12.78	83.4	27.6	16515	209041	192944	No
ZA2G	WEAEPVYVQR	Yes	638.82	761.4	12.78	83.4	30.6	10249	179191	141908	No
ZA2G	WEAEPVYVQR	Yes	638.82	890.5	12.78	83.4	30.6	3846	12584	9269	Yes (Based on Transition Ratios)
ZA2G	WEAEPVYVQR	Yes	638.82	961.5	12.78	83.4	39.6	5243	55122	45265	No
ZA2G	YSLTYIYTGLSK	No									
ZG16B	LDGQISSAYPSQEGQVLVGIYGQYQLLGIK	No									
ZG16B	LGALGGNTQEVTLQPGEYITK	Yes	1095.08	524.3	16.75	142.3	50.7	3979	ND	ND	No
ZG16B	LGALGGNTQEVTLQPGEYITK	Yes	1095.08	807.4	16.75	142.3	56.7	29400	ND	ND	No
ZG16B	LGALGGNTQEVTLQPGEYITK	Yes	1095.08	935.5	16.75	142.3	50.7	3297	ND	ND	No
ZG16B	LGALGGNTQEVTLQPGEYITK	Yes	1095.08	941.5	16.75	142.3	56.7	3176	ND	ND	No
ZG16B	VSVGLLLVK	No									
ZG16B	YFSTTEDYDHEITGLR	Yes	649.63	311.1	15.07	84.8	27.7	122109	ND	ND	No
ZG16B	YFSTTEDYDHEITGLR	Yes	649.63	559.4	15.07	84.8	39.7	36330	ND	ND	No
ZG16B	YFSTTEDYDHEITGLR	Yes	649.63	825.5	15.07	84.8	36.7	37697	ND	ND	No
ZG16B	YFSTTEDYDHEITGLR	Yes	649.63	940.5	15.07	84.8	39.7	13783	ND	ND	No
ZG16B	YFYFGK	No									

Note: See (17) for definition of terminologies.

- Protein: UniProt protein name
- Peptide: Peptide sequence. If no peptide was sequenced for the protein, it is labeled as "No peptide".
- MS/MS spectrum: Whether MS/MS spectrum was successfully acquired using MRM-triggered MS/MS spectrum: Yes or No. If No, MRM assay was not developed for the peptide.

- Precursor ion (m/z): The mass-to-charge ratio of the precursor ion.
- Fragment ion (m/z): The mass-to-charge ratio of the fragment (product) ion.
- Retention time (minutes): Peptide retention time in minutes.
- Declustering potential: Deculstering potential for the precursor ion.
- Collision Energy: Optimized collision energy of the fragment ion.
- Area of synthetic peptide: Peak area obtained from a mix of synthetic peptides.
- Area in control sample: Peak area obtained from a pooled control sample.
- Area in disease sample: Peak area obtained from a pooled lung cancer sample.
- Interference: Whether interference was observed on the transition in the two biological samples.