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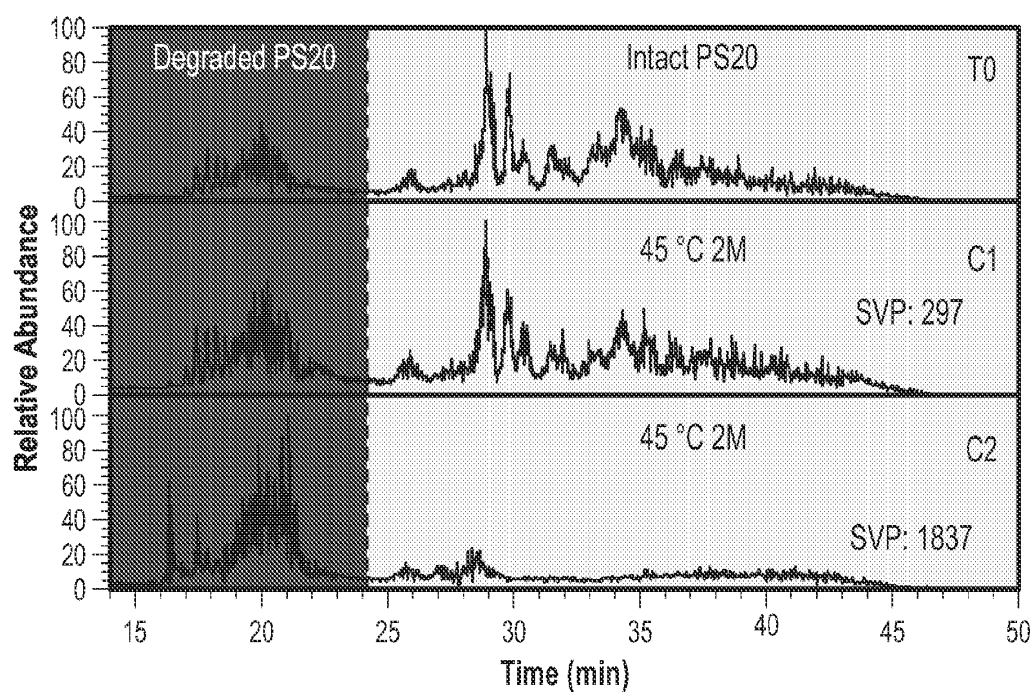


FIG. 1

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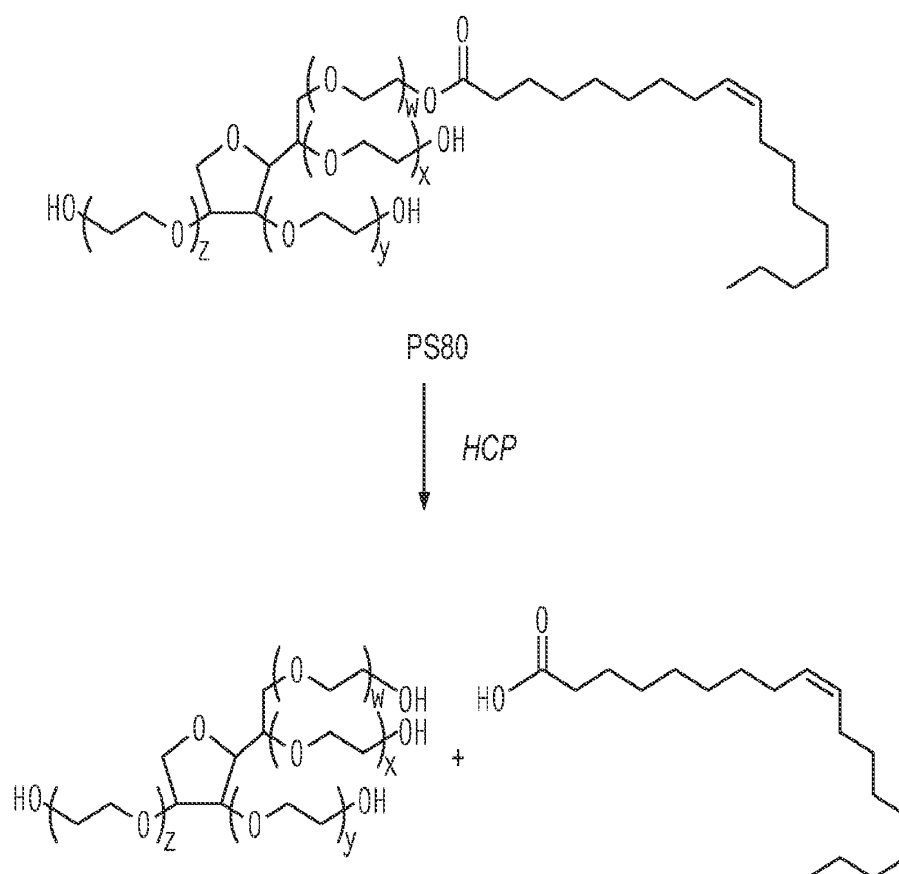


FIG. 2

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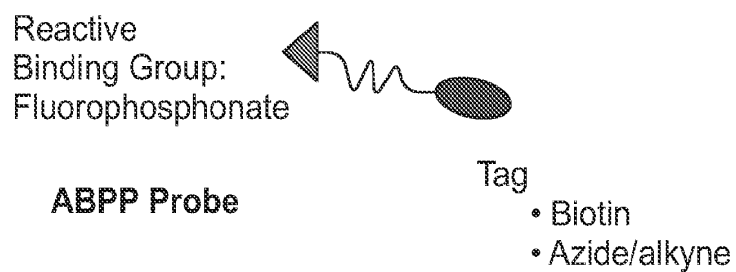


FIG. 3A

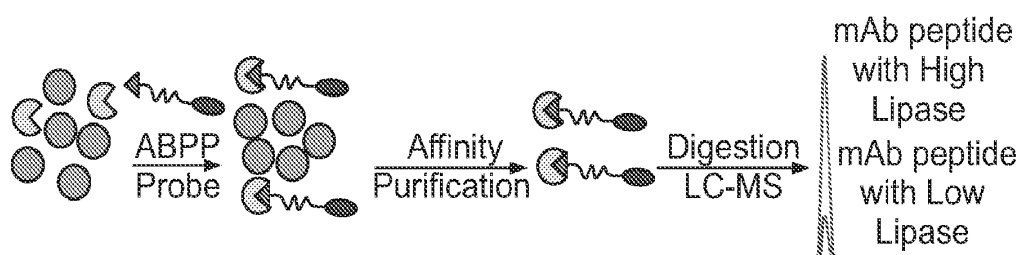


FIG. 3B

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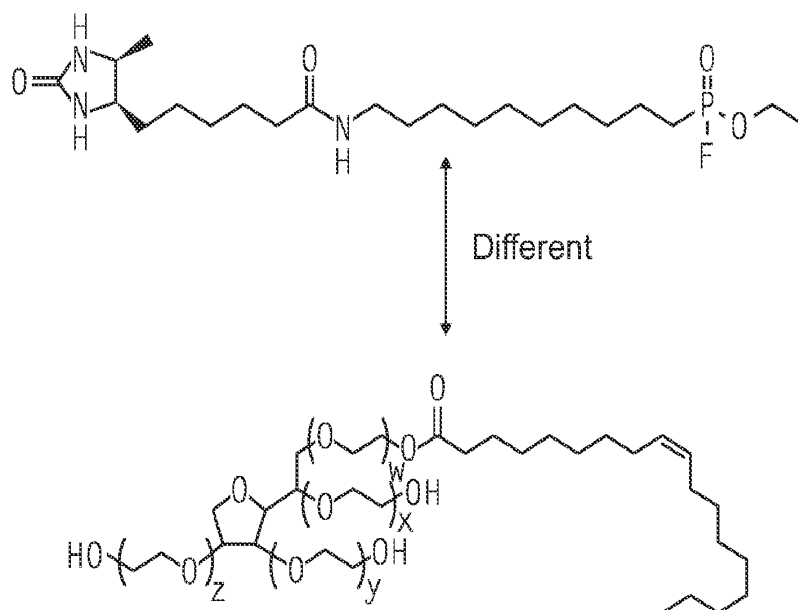


FIG. 4A

**Biotin Tag for
Affinity Purification**

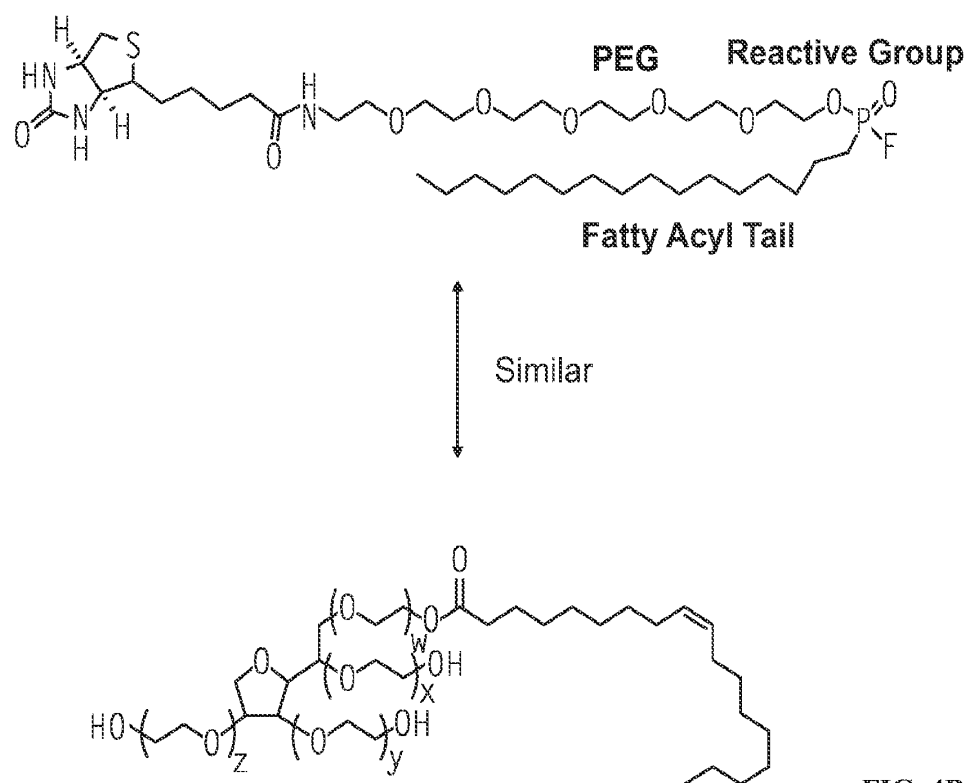


FIG. 4B

Serial Number	Accession	Description	Fold change to tryptic digestion			
			DMSO	FP-desthiobiotin	FP-biotin	Novel Probe
Lipases						
1	A0A061IHN3	Platelet-activating factor acetylhydrolase 2, cytoplasmic-like protein (PLA2G7)	0.0	4.6	8.8	12.3
2	G3IK30	Glycerol-3-phosphate acyltransferase 3	2.0	1.7	2.3	35.4
3	G3HGO9	1-acyl-sn-glycerol-3-phosphate acyltransferase delta	0.2	0.5	0.5	70.7
4	A0A061IL50	Monoacylglycerol lipase ABHD6-like protein	0.1	27.0	61.6	61.4
5	G3GRE5	Lysophospholipase-like protein 1	ND	0.5	2.4	58.7
6	G3I6H4	Phospholipase DDHD1 (F fragment)	0.1	0.1	0.2	121.1
7	A0A061IKA1	Lipoprotein lipase	0.0	50.0	94.4	112.7
8	G3HKV9	Group XV phospholipase A2	0.1	83.5	183.7	301.9
9	G3H1I9	Phospholipase DDHD2	0.0	0.0	0.2	182.2
10	G3HQY6	Lipase (Lysosomal acid lipase)	0.0	0.1	0.1	32.8
11	G3GWW5	Phospholipase A2 (cytosolic phospholipase A2 alpha)	ND	ND	0.3	950.8
12	A0A061HWK1	Hormone-sensitive lipase-like protein	ND	D	D	D
13	G3H8X2	1-acyl-sn-glycerol-3-phosphate acyltransferase gamma	D	D	ND	D
14	G3H6Z2	Monoacylglycerol lipase ABHD12	ND	D	ND	D
15	G3H0Y7	Cytosolic phospholipase A2 delta	ND	ND	ND	D

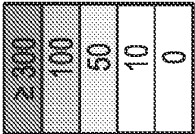
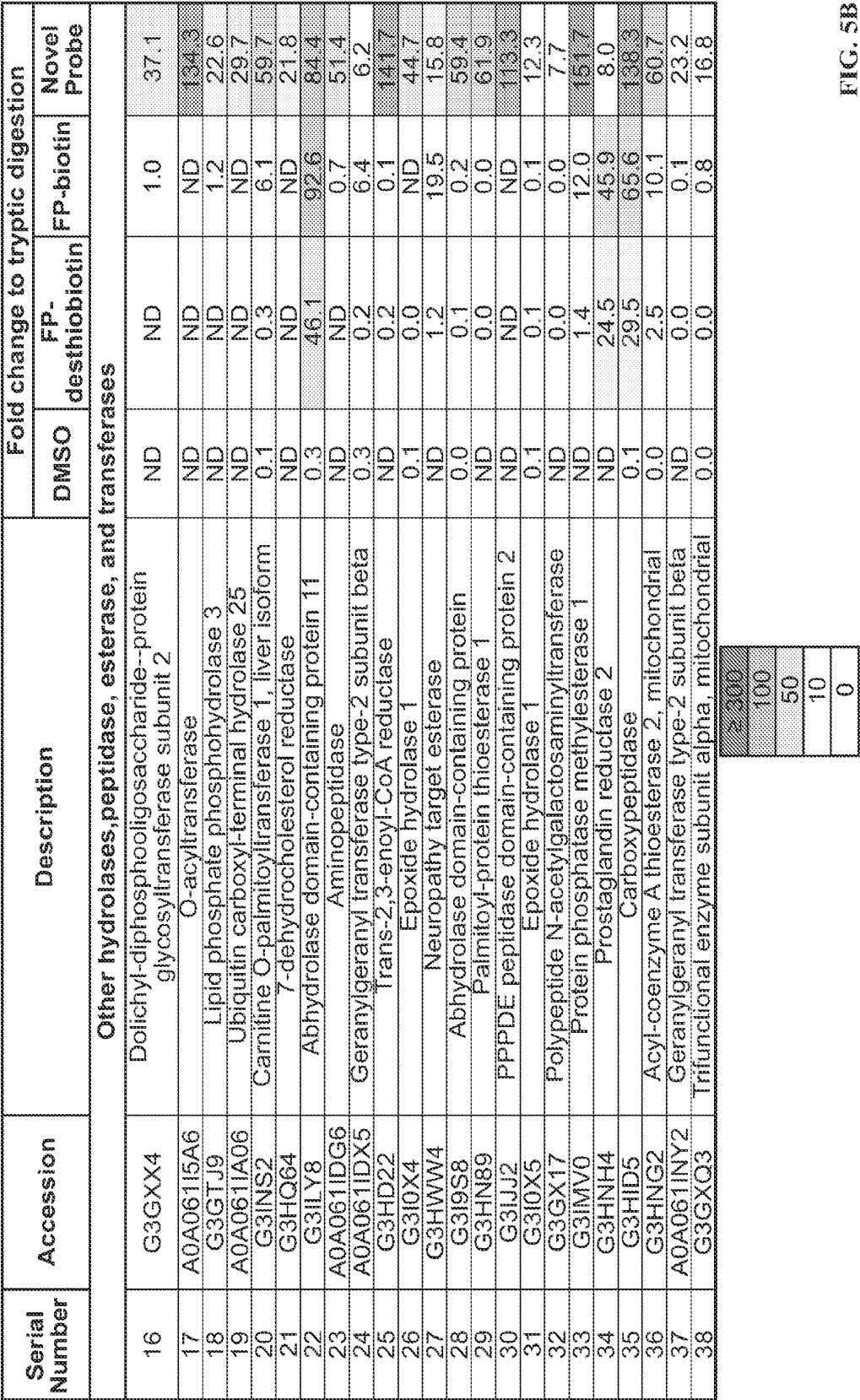


FIG. 5A



Serial Number	Accession	Description	Fold change to tryptic digestion			
			DMSO	FP-desthiobiotin	FP-biotin	Novel Probe
39	G3I4A7	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	0.0	0.1	0.1	2.4
40	G3H8V5	Carboxypeptidase	0.0	11.3	19.9	24.0
41	G3IP80	Acyl-protein thioesterase 2	0.1	31.0	45.3	28.6
42	G3I366	Prolyl endopeptidase	0.0	20.8	75.1	91.9
43	G3I3W4	S-formylglutathione hydrolase	0.0	0.8	3.7	77.0
44	A0A061I7Y2	Endonuclease domain-containing 1 protein	D	D	D	D
45	A0A098KX93	Lysosomal thioesterase PPT2-like protein	ND	D	D	D
46	G3GYL6	Cytosolic carboxypeptidase 2	ND	ND	ND	D
47	G3H3L4	NADH-cytochrome b5 reductase	ND	ND	ND	D
48	G3HF97	Abhydrolase domain-containing protein	ND	ND	ND	D
49	G3HUW5	tRNA (guanine(26)-N(2))-dimethyltransferase	ND	ND	ND	D
50	G3IEF0	UbiA prenyltransferase domain-containing protein 1	ND	ND	ND	D
51	G3H7Y9	GPI mannosyltransferase 1	ND	ND	ND	D
52	G3GTP1	Abhydrolase domain-containing protein 13	ND	ND	ND	D
Trypsin Abundance						
Sample Group			DMSO	FP-desthiobiotin	FP-biotin	REGN Probe
Trypsin (porcine)			3.9E+09	3.4E+09	3.4E+09	3.4E+09

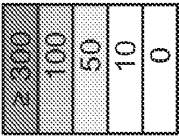


FIG. 5C

Accession	Description	DMSO			FF-α-statin			FF-β-oxid			Novel probe			Tyrosinase	p-value of FF-β-oxid vs Novel probe	
		Replicate 1	Replicate 2	Replicate 3	Replicate 1	Replicate 2	Replicate 3	Replicate 1	Replicate 2	Replicate 3	Replicate 1	Replicate 2	Replicate 3			
Lipase																
A0A061HNS	Platelet-activating factor acetylhydrolase 2, cytoplasmic-like protein (PLA2G7)	3.2E+05	3.6E+05	3.9E+05	6.3E+08	5.8E+08	6.1E+08	1.1E+09	1.2E+09	1.7E+09	1.5E+09	1.5E+09	1.4E+09	1.3E+08	1.2E+08	**
G3K3D	Glycerol-3-phosphate acyltransferase 3			9.0E+05	6.8E+05		8.0E+05	1.0E+06		1.7E+07	1.6E+07	1.5E+07		4.4E+05		**
G3HQC9	1-acyl-sn-glycerol-3-phosphate acyltransferase delta	1.3E+05	1.2E+05	1.1E+05	1.3E+05	1.4E+05	5.4E+05	2.2E+05	4.8E+05	4.1E+07	3.6E+07	3.8E+07	5.5E+05	5.4E+05		**
A0A061L50	Monoglycerol lipase ABHD6-like protein	3.9E+05	4.3E+05	3.0E+04	8.1E+07	8.1E+07	8.7E+07	1.8E+08	1.9E+08	2.0E+08	1.8E+08	1.8E+08	1.8E+08	5.3E+06	2.1E+06	
G3GRE5	Lysophospholipase-like protein 1				8.9E+05	1.0E+06	3.3E+06	9.2E+06	4.7E+06	1.1E+07	2.0E+08	1.9E+08	2.7E+06	4.0E+06	3.7E+06	**
G3B6H4	Phospholipase DDHD1 (Fragment)	1.0E+05	2.1E+05		4.1E+05	3.5E+05	3.9E+05	8.3E+05	9.6E+05	8.0E+05	4.3E+08	4.4E+08	3.9E+06	3.9E+06	3.3E+06	**
A0A061KA1	Lipoprotein lipase		1.7E+05		2.3E+08	2.4E+08	2.5E+08	4.4E+08	4.5E+08	4.7E+08	6.0E+08	5.3E+08	3.3E+06	5.5E+06	5.8E+06	*
G3HKV9	Group XV phospholipase A2			3.2E+05	4.1E+08	4.1E+08	4.2E+08	9.1E+08	9.2E+08	9.2E+08	1.6E+09	1.4E+09	4.8E+06	5.0E+06	5.3E+06	**
G3H19	Phospholipase DDHD2	1.3E+05	2.0E+05	1.2E+05		1.5E+05	2.0E+05	2.9E+06	1.5E+06	5.0E+05	1.5E+09	1.4E+09	9.2E+06	7.2E+06	6.9E+06	**
G3HQY6	Lipase (lysosomal acid lipase)	3.5E+05			8.8E+05	1.0E+06	1.2E+06	1.7E+06	1.7E+06	2.2E+06	4.0E+08	4.8E+08	1.3E+07	1.3E+07	1.4E+07	**
G3GNW5	Phospholipase A2 (cytosolic phospholipase A2 alpha)							4.8E+05	3.7E+05	1.6E+09	1.4E+09	1.4E+09	2.4E+06	1.8E+06	6.5E+05	**
A0A061HWK1	Hormone-sensitive lipase-like protein				8.3E+06	7.4E+06		1.4E+07	1.4E+07	4.8E+07	4.5E+07	4.4E+07				**
G3H8X2	1-acyl-sn-glycerol-3-phosphate acyltransferase gamma			1.8E+05			1.9E+05			3.5E+07	3.1E+07	2.9E+07				**
G3H6Z2	Monoglycerol lipase ABHD12				1.9E+05					2.2E+07	1.8E+07	3.1E+07				**
G3H0Y7	Cytosolic phospholipase A2 delta									1.6E+07	1.6E+07	1.5E+07				**

FIG. 6A

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Accession	Description	DMSO			PP-omega			Novel probe			Typical Digestion	p-value of PP-omega vs Novel probe			
		Replicate 1	Replicate 2	Replicate 3	Replicate 1	Replicate 2	Replicate 3	Replicate 1	Replicate 2	Replicate 3					
		Other hydrolases, peptidase, esterase, and transferases													
G3GX4	Dolichyl-diphosphoglycosyltransferase subunit 2					2.7E+05		7.9E+06	8.6E+06	1.4E+07		2.8E+05	**		
A0A0615A6	O-acetyltransferase							6.4E+07	7.9E+07	7.5E+07		5.9E+05	**		
G3GTJ9	Lipid phosphate phosphohydrolase 3					1.0E+06	5.5E+05	1.5E+07	1.4E+07	1.5E+07		4.4E+05	6.2E+05	**	
A0A0614A6	Ubiquitin carboxy-terminal hydrolase 25							2.8E+07	2.8E+07	2.8E+07		9.2E+05		**	
G3INS2	Camitline O-palmitoyltransferase 1, liver isoform	1.2E+05	3.1E+05	4.3E+05	2.4E+05	6.2E+06	5.7E+06	6.5E+06	6.4E+07	5.9E+07	5.8E+07	1.1E+06	9.9E+05	**	
G3H064	7-dehydrocholesterol reductase							3.1E+07	2.6E+07	2.4E+07		1.3E+06	8.9E+05	**	
G3ILY8	Abhydrolase domain-containing protein 11	3.6E+05	6.0E+07	6.1E+07	6.3E+07	1.3E+08	1.2E+08	1.2E+08	1.1E+08	1.0E+08			1.3E+06		
A0A061DC6	Aminopeptidase					1.0E+06	8.3E+05	2.3E+06	1.0E+08	9.1E+07	1.0E+08	1.7E+06	1.9E+06	2.2E+06	**
A0A061DX5	Geranylgeranyl transferase type-2 subunit beta	4.6E+05	6.3E+05	4.8E+05	4.5E+05	1.3E+07	1.2E+07	1.4E+07	9.3E+06	9.4E+06	1.8E+07	2.0E+06	2.8E+06	1.7E+06	**
G3HD22	Trans-2,3-enoyl-CoA reductase			5.0E+05	4.8E+05	4.0E+05		2.4E+05	3.1E+08	2.9E+08	3.2E+08	2.1E+06	2.8E+06	3.0E+06	**
G3DX4	Epoxide hydrolase 1	7.9E+04	1.0E+05	4.3E+05	9.5E+04	1.5E+05			1.7E+08	1.2E+08	1.1E+08	2.7E+06	3.4E+06	3.6E+06	**
G3HW4	Neuropathy target esterase			3.9E+06	3.9E+06	6.0E+07	6.5E+07	6.4E+07	5.5E+07	5.3E+07	4.6E+07		6.1E+06	3.6E+05	**
G3NS8	Abhydrolase domain-containing protein	1.3E+05	3.6E+05	3.0E+05	3.7E+05	8.3E+05	4.8E+05	7.7E+05	2.1E+08	2.0E+08	2.2E+08	3.9E+06	3.6E+06	3.1E+06	**
G3HN89	Palmitoyl-protein thioesterase 1				1.1E+05	1.9E+05		2.9E+05	4.0E+08	4.4E+08	3.9E+08	7.5E+06	6.8E+06	6.0E+06	**
G3LU2	PPPDE peptidase domain-containing protein 2								8.2E+08	7.8E+08	7.6E+08	7.2E+06	6.9E+06	6.5E+06	**
G3DX5	Epoxide hydrolase 1	7.1E+05	4.6E+05	5.3E+05	9.8E+05	8.4E+05	1.4E+06	1.3E+06	1.2E+08	1.1E+08	1.1E+08	1.1E+07	1.1E+07	5.7E+06	**
G3GX17	Polypeptide N-acetylgalactosaminyltransferase			1.7E+05	1.5E+05		8.1E+05	2.8E+05	6.5E+05	1.2E+08	1.0E+08	1.4E+07	1.3E+07	1.5E+07	**
G3MW0	Protein phosphatase methyltransferase 1			2.2E+07	2.1E+07	2.3E+07	2.0E+05	1.9E+08	2.6E+09	2.4E+09	2.4E+09	1.9E+07	1.4E+07	1.6E+07	**
G3NH4	Prostaglandin reductase 2			4.4E+06	4.3E+08	4.2E+08	8.0E+08	7.7E+08	8.4E+08	1.5E+08	1.3E+08	1.8E+07	1.7E+07	1.7E+07	**
G3HD5	Carboxypeptidase	1.5E+06	2.2E+06	5.6E+05	7.6E+08	6.8E+08	1.6E+09	1.4E+09	3.5E+09	3.3E+09	3.2E+09	2.6E+07	2.2E+07	2.4E+07	**
G3HNG2	Acyl-coenzyme A thioesterase 2, mitochondrial	1.2E+05		6.9E+07	5.0E+07	6.7E+07	2.3E+08	2.3E+08	1.6E+09	1.5E+09	1.5E+09	2.9E+07	2.1E+07	2.4E+07	**

FIG. 6B

[illegible]

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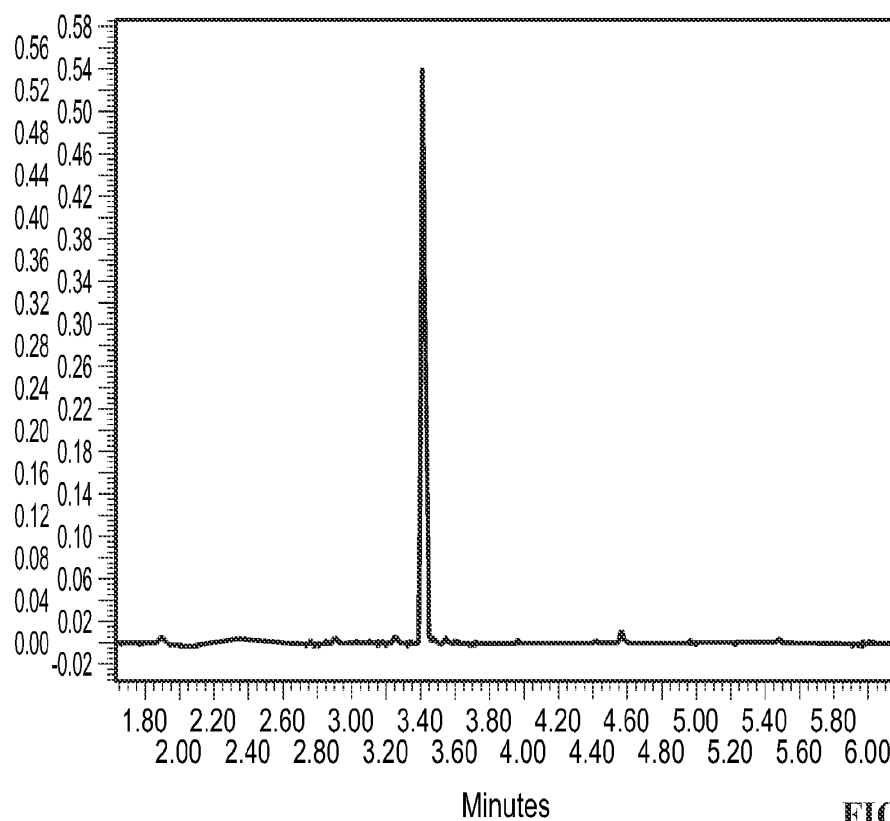


FIG. 7A

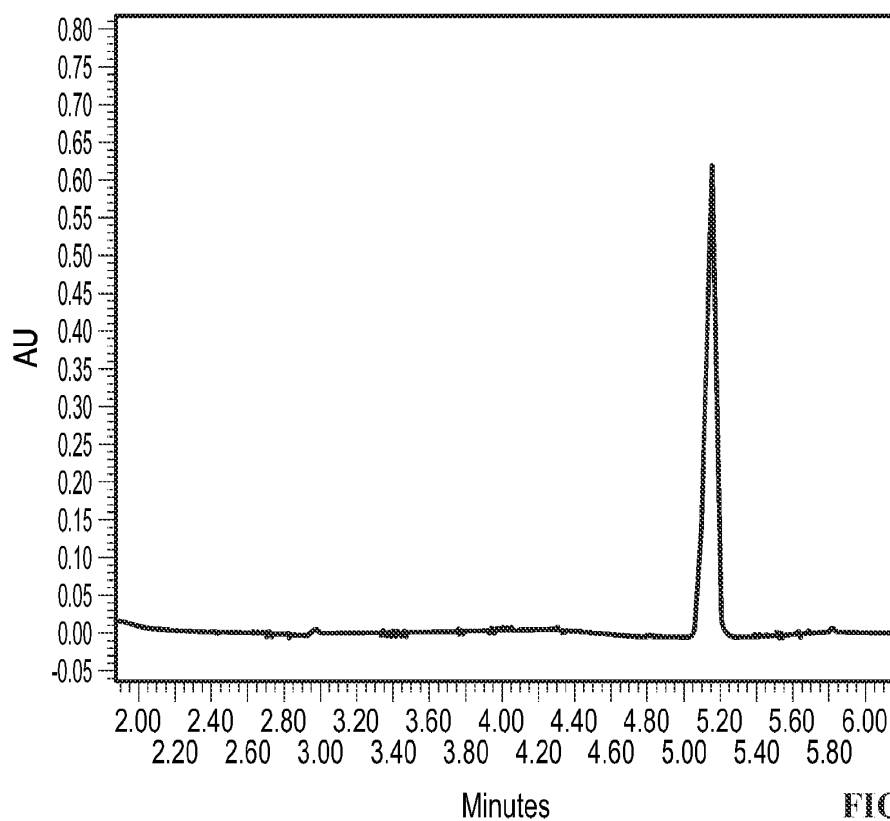


FIG. 7B

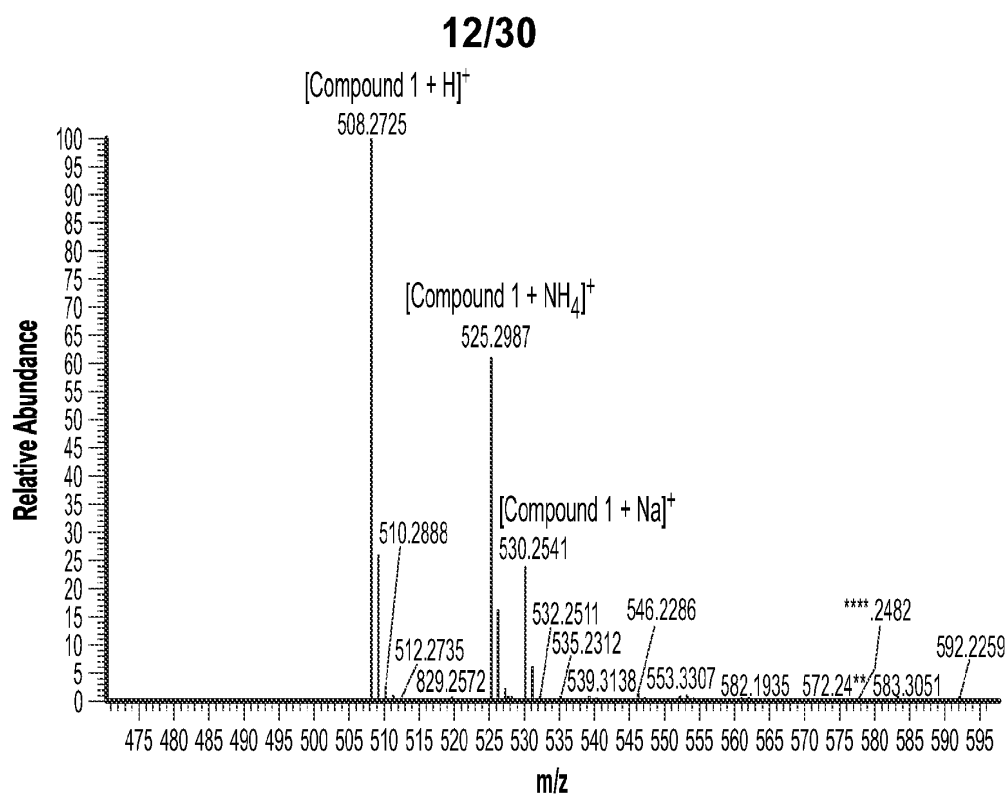


FIG. 7C

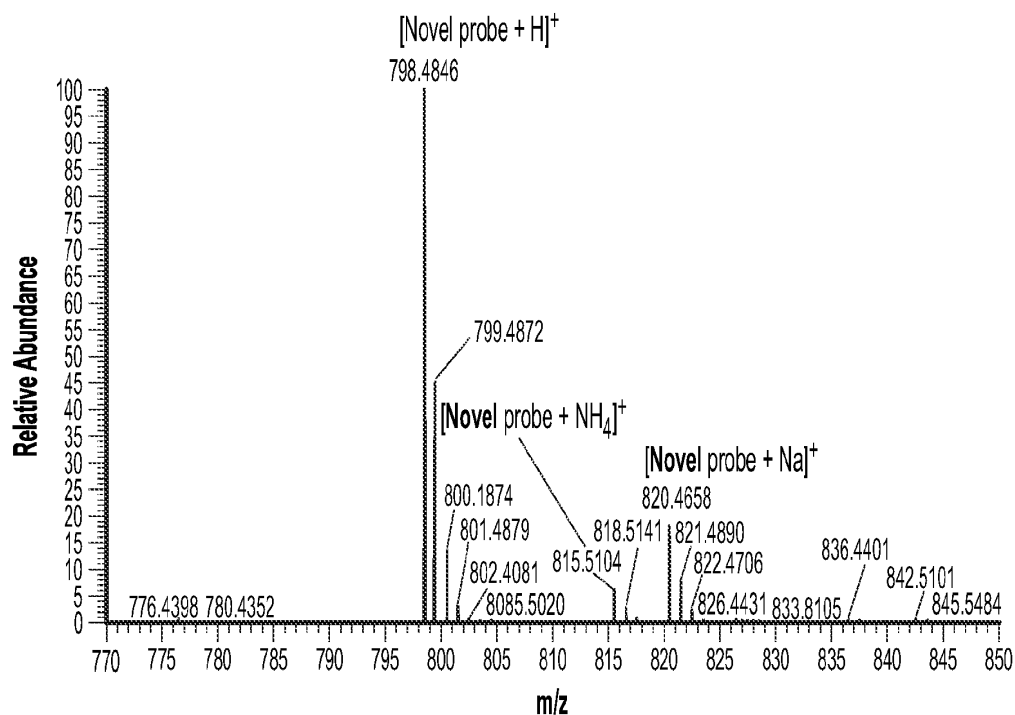


FIG. 7D

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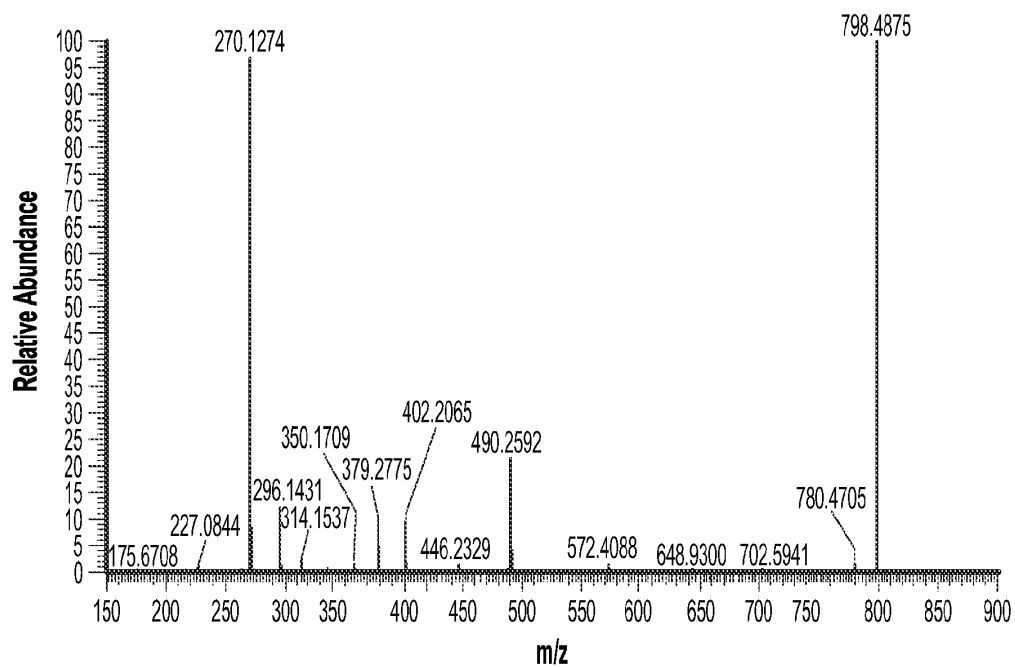


FIG. 7E

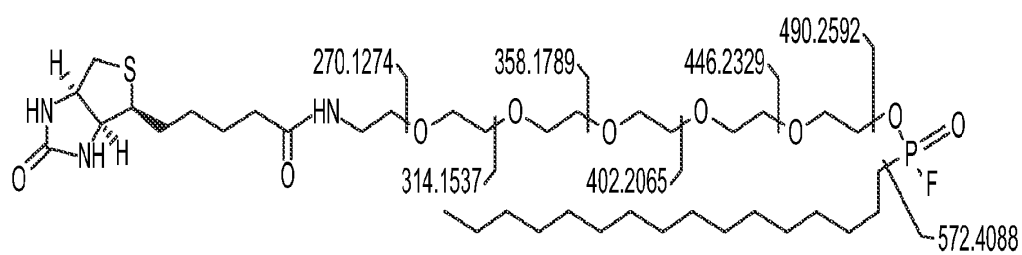


FIG. 7F

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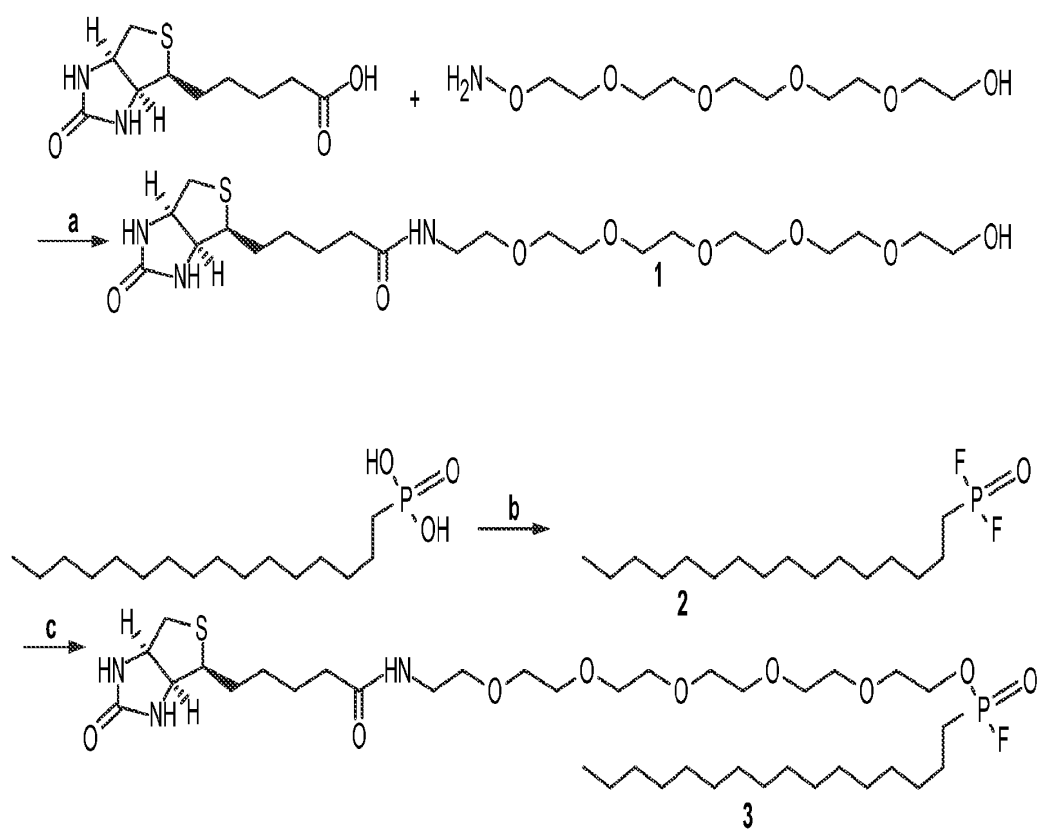


FIG. 8A

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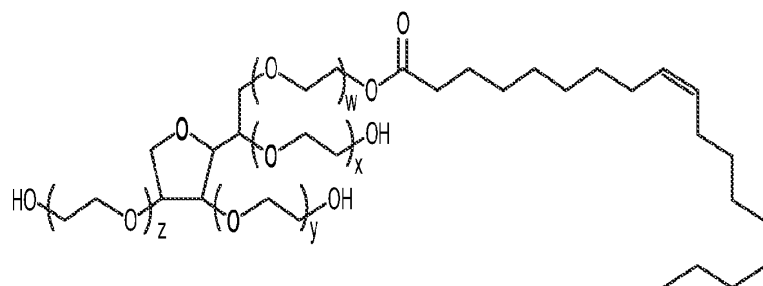


FIG. 8B

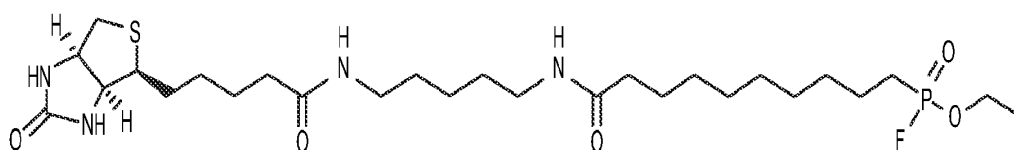


FIG. 8C

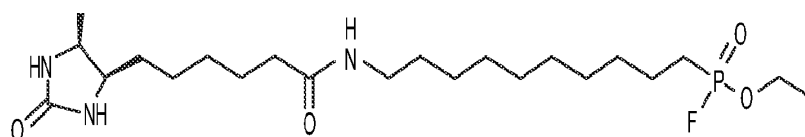


FIG. 8D

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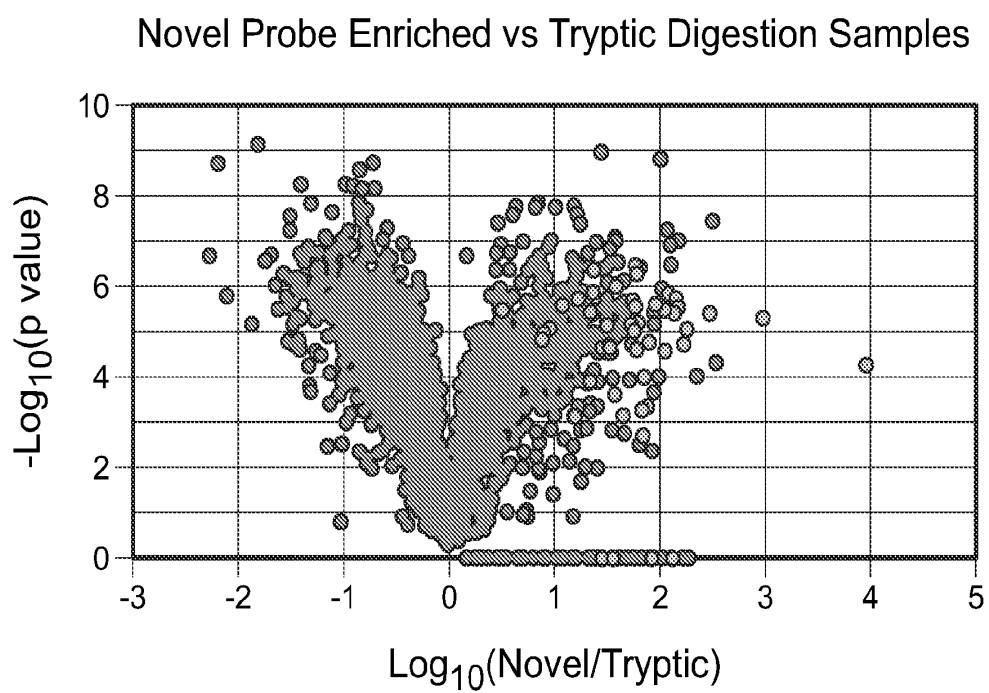


FIG. 9

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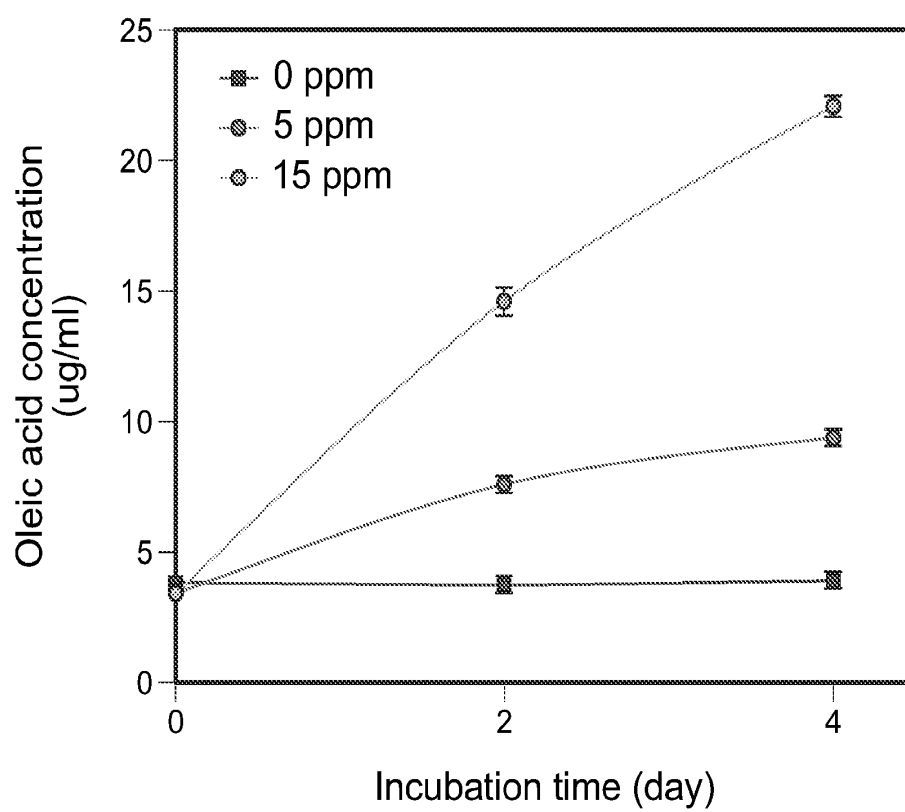


FIG. 10

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Num- ber	Accession	Description	Novel Probe Enriched			Tryptic Digestion			Average of Novel	Average of Tryptic	Novel/Tryptic	p value
			Replicate 1	Replicate 2	Replicate 3	Replicate 1	Replicate 2	Replicate 3				
1	G3GV53	Prolyl endopeptidase-like OS=Cricetulus griseus GN=179_001584.F	282001029	262137900	257298679		18338.6504	40635.7773	2.67E+08	29407.21387	9059.719	5.34833E-05
2	G3GW55	Phospholipase A2 OS=Cricetulus griseus GN=179_002240 PE=4 SV=1	1579951574	1421E+09	1419013028	2391483.5	1611753.25	645954.438	1.47E+09	1549730.396	950.7713	5.09962E-06
3	G3J7H8	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial C	419776435	388367016	38884280	1195123.5	1104189.5		3.98E+08	1148616.5	346.4386	4.70504E-05
4	AOA061HC0	Transmembrane 9 superfamily member OS=Cricetulus griseus GN	599757900	596357196	616897731	26853914.25	1913025.5	1110188.25	6.04E+08	1903042.667	317.5288	3.60263E-08
5	G3HKV9	Group XV phospholipase A2 OS=Cricetulus griseus GN=179_011341	1587117446	1413E+09	1510353043	4569738.88	5038954	5328866.56	1.50E+09	4979186.479	301.9374	3.82899E-06
6	G3IMZ0	Very low-density lipoprotein receptor OS=Cricetulus griseus GN=	184977608	173919978	164271808	467254.738	1080684.97		1.74E+08	773859.7031	225.3215	9.64831E-05
7	Q8U293	Gap junction protein OS=Cricetulus griseus GN=H671_2g5891 PE=2	74376124.9	795393980	779576716		417327.906		7.73E+07	417327.9063	185.2051	NA
8	G3H1I9	Phospholipase DDHD2 OS=Cricetulus griseus GN=179_004018 PE=4	1531695043	1354E+09	1358726442	9198809.56	7213307.31	6879866.63	1.41E+09	7763934.5	182.1504	9.03166E-06
9	G3H6H1	Arylacetamide deacetylase-like 1 OS=Cricetulus griseus GN=179_0	5041922727	447919635	42785495	2424694	3082155.5	2802361	4.60E+08	2896380.167	170.6	1.83885E-05
10	G3IMF9	Solute carrier family 12 member 7 OS=Cricetulus griseus GN=179_0	139384754	110719116	121782880	730395.5			1.24E+08	730395.5	169.5801	NA
11	G3HEK6	Glucocorticoid receptor OS=Cricetulus griseus GN=179_008992 PE=	805512089	820115489	843038828	4548349.88	18512.88	5790963.5	8.23E+08	5385942.083	152.7846	9.57285E-08
12	G3IMV0	Protein phosphatase methyltransferase 1 OS=Cricetulus griseus GN=	2806316742	2361E+09	2396802647	186833589.9	14258040.8	15610194.3	2.45E+09	16103941.65	151.6708	2.89435E-06
13	G3HD22	Trans-2,3-enoyl-CoA reductase OS=Cricetulus griseus GN=179_008	312010693	290765847	318082276	2066000.38	2776548.38	1661125.63	3.07E+08	2167891.458	141.7458	1.81209E-06
14	G3H1D5	Carboxypeptidase OS=Cricetulus griseus GN=179_003960 PE=3 SV=3	3537326155	3296E+09	3152770980	2595901.4	122203097.2	24044037.6	3.33E+09	24068716.28	139.2931	3.97722E-06
15	AOA061ISA	O-acyltransferase OS=Cricetulus griseus GN=H671_5g14889 PE=3 S	84265245.2	78567181	74888977		589770.688		7.92E+07	589770.6875	134.3457	NA
16	G3J7N3	Uncharacterized protein OS=Cricetulus griseus GN=179_019521 PE=	321674302	308088305	302426189	1945668.88	2351848.81	2887447.94	3.11E+08	2394988.542	129.8822	3.35895E-07
17	G3HWX8	Estradiol 17-beta-dehydrogenase 12 OS=Cricetulus griseus GN=179	213435599	216627900	206541632	1367972.13	2222804.189	1428392.25	2.12E+08	1674802.021	126.7026	1.21763E-07
18	G3HQT1	Antigen peptide transporter 2 OS=Cricetulus griseus GN=179_0131	45577790.4	44003010	51721829			377613.906	4.71E+07	377613.9063	124.7327	NA
19	G3J6H4	Phospholipase DD-HD1 (Fragment) OS=Cricetulus griseus GN=179	465180533	425962850	436520863	3920051	3793835	3254686.5	4.43E+08	3655457.5	121.0742	1.50905E-06
20	AOA061IB2	Protein copy-2 isoform 1 (Fragment) OS=Cricetulus griseus GN=179	30622626.6	30633494	30633049.8	254138.87	5261888.094		3.05E+07	258013.4844	118.3648	5.90629E-08
21	G3JJJ2	PPPDE peptidase domain-containing protein 2 OS=Cricetulus griseus	824730576	747373480	755371192	7247013.56	6817570.5	6479942.25	7.76E+08	6948175.438	113.2849	3.10954E-06
22	AOA061IKA	Lipoprotein lipase OS=Cricetulus griseus GN=H671_1g2493 PE=3 S	598449650	527452679	510897289	3347565.22	462772.91	5624535.31	5.42E+08	4811624.479	112.6933	2.53827E-05
23	G3IGD1	Transmembrane protein 33 OS=Cricetulus griseus GN=179_022816	117936309	109838109	109517452	1004829.75	1037287.19	1112601.38	1.12E+08	1051572.771	106.9166	1.11779E-06
24	G3JY8	Dedicator of cytokinesis protein 8 OS=Cricetulus griseus GN=179_0	34347196.6	34224625	34146875		321794.594		3.42E+07	321794.5938	106.4019	NA
25	AOA061IP5	Protein VIPF3-like protein OS=Cricetulus griseus GN=H671_1g1528	139887642	140165494	13882636	1417575.88	1219950	1483369.63	1.39E+08	1373631.833	101.4696	1.51658E-09

FIG. 11A

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26	P49130	Lysosome-associated membrane glycoprotein 2 OS=Cricetulus griseus	115239464	89486228	97466472	890923.5	987614.875	1187235.88	1.01E+08	1021924.75	98.58494	9.89479E-05
27	G3H5Y9	Tetraspanin OS=Cricetulus griseus GN=H671_xg19997 PE=3 SV=1	132145080	118651914	124742118	1087127.38	1620884.13	1176578.88	1.25E+08	1294893.458	96.67406	2.94144E-06
28	G3I366	Prolyl endopeptidase OS=Cricetulus griseus GN=I79_017667 PE=4	21069E+10	1.935E+10	1.867E+10	218078876	20861803	212130906	1.96E+10	212940528.1	91.91888	2.60339E-06
29	G3I416	Pyruvate carboxylase OS=Cricetulus griseus GN=PC PE=2 SV=1	1730543123	1.602E+09	151327233	21854274.1	16529109.4	16047602.7	1.62E+09	18143662.06	89.03388	7.22465E-06
30	G3HEA9	Minor histocompatibility antigen H13 OS=Cricetulus griseus GN=I79	295068207	229189517	22391989	3145618.75	2652787.25	2409800	2.49E+08	2802735.333	88.8	0.00022273
31	AOA061IEZ	Exocyst complex component 8-like protein OS=Cricetulus griseus	176286069	157620869	17170751	1966192.88	1532844.63	2234878.69	1.69E+08	1911305.396	88.17842	3.85175E-06
32	AOA061HV	FUN14 domain-containing protein 1 OS=Cricetulus griseus GN=H6	34487712	30532223	2876402		355717.594		3.13E+07	355717.5938	87.89401	NA
33	G3I1Y8	Abhydrolase domain-containing protein 11 OS=Cricetulus griseus GN=	121822015	110014907	10463386			1328292.13	1.12E+08	1328292.125	84.44184	NA
34	AOA061IQ	Lysophosphatidic acid phosphatase type 6 OS=Cricetulus griseus GN=	72654248	56430626	4768579.5		596884.563	806181.313	5.89E+07	701432.9375	84.00452	0.004294574
35	G3HCM4	CAAX prenyl protease 1-like OS=Cricetulus griseus GN=I79_00823	95367454.6	83823829	81917154.9	1920888.69	756112	639533.875	8.70E+07	1105511.521	78.7293	1.72002E-05
36	G3I3W4	S-formylglutathione hydrolase OS=Cricetulus griseus GN=I79_018	2.4162E+10	1.743E+10	1.778E+10	277757380	251039940	241950070	1.98E+10	256915796.6	77.03328	0.000434934
37	G3HCQ9	1-acyl-sn-glycerol-3-phosphate acyltransferase delta OS=Cricetulus	40985031.8	36481553	38132087.3	550070.125	539789.625		3.85E+07	544929.875	70.71165	9.77991E-05
38	G3GLUX6	Receptor expression-enhancing protein OS=Cricetulus griseus GN=	97644775	86858247	9798430.5	1339354.63			9.42E+07	1339351.625	70.30453	NA
39	G3GV66	Sn1-specific diacylglycerol lipase beta OS=Cricetulus griseus GN=I7	136407369	102650876	105541775		1579582.63	1716954	1.15E+08	1648273.313	69.68909	0.001953683
40	G3I3H3	Palmitin-like phospholipase domain-containing protein 2 OS=Cricetuli	595010244	533294678	396125967	7129539.69	7718089.56	7910088.16	5.08E+08	7383899.135	66.98529	0.001521389
41	P21448	Multidrug resistance protein 1 OS=Cricetulus griseus GN=ABCB1 P	154509146	147161928	145501320	2702184.19	2235614.28	1792209.13	1.49E+08	2243335.865	66.44456	3.84824E-07

FIG. 11A (Cont.)

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Num- ber	Accession	Description	Novel Probe Enriched			Tryptic Digestion			Average of Novel	Novel/Tryptic	p value
			Replicate 1	Replicate 2	Replicate 3	Replicate 1	Replicate 2	Replicate 3			
42	G3HOL7	Squalene synthetase OS=Cricetulus griseus GN=179_003679 PE=4	31561749.3	21671129	29402368.7	320629.031	542954.75		2.75E-07	63.79249	0.003001182
43	G3HN89	Palmitoyl-protein thioesterase 1 OS=Cricetulus griseus GN=179_0	404182895	444781701	393576329	7493622.81	6802911.91	5955385.5	4.14E+08	61.94765	6.39825E-06
44	AOAO611L5	Monoglycerol lipase ABHD6-like protein OS=Cricetulus griseus GN=179_0	207828661	178162447	178570138	1848959	56281693.13	2071182.06	1.88E+08	61.35324	2.39228E-05
45	G3HNG2	Asp-coenzyme A thioesterase 2, mitochondrial OS=Cricetulus griseus GN=179_0	1558310402	1455E+09	1491929796	20840998	28866328.2	24495102.8	1.50E+09	60.70463	5.23114E-07
46	G3I2V6	Plexin-B2 OS=Cricetulus griseus GN=179_017750 PE=4 SV=1	28734742.1	28543428	25313305.3			453731.063	2.75E+07	60.67947	NA
47	G3INS2	Carnitine O-palmitoyltransferase 1, liver isoform OS=Cricetulus griseus GN=179_0	64050667.9	58858063	59063189	1117745.75	918623.25	993885.625	6.03E+07	59.72169	2.99632E-06
48	G3I958	Alcohol dehydrogenase domain-containing protein OS=Cricetulus griseus GN=179_0	210187364	202463355	215734970	3398946.75	3577138.5	3096433	2.09E+08	59.43576	3.67647E-07
49	G3GRE5	Lysophospholipase-like protein 1 OS=Cricetulus griseus GN=179_0	218641928	196415909	191494552	2702064.44	3959963.19	3668720.38	2.02E+08	58.71336	9.27897E-06
50	G3HLM0	Dehydrogenase domain-containing protein OS=Cricetulus griseus GN=179_0	50498080.1	46421894	48026251.4	886210.625	706291.125	901448.25	4.76E+07	57.31719	2.5394E-06
51	G3HO83	Alcohol dehydrogenase domain-containing protein 10, mitochondrial (fragment) OS=Cricetulus griseus GN=179_0	160587316	138680357	150173922	2094037.63	2982308.75	2779964.75	1.50E+08	57.22044	1.03222E-05
52	G3HJ14	Lysosomal Pro-X carboxypeptidase OS=Cricetulus griseus GN=179_0	103700469	103679418	9511370.3	1345189.63	2326289.75	1729900.75	1.01E+08	56.00279	2.11548E-06
53	G3GX36	Fanconi anemia group D2 protein-like OS=Cricetulus griseus GN=179_0	521589858	461451781	44372035	7593031.13	10119234.9	8621713.59	4.76E+08	54.17577	1.91987E-05
54	AOAO611B*	Tetraspanin OS=Cricetulus griseus GN=H671_3g9876 PE=3 SV=1	47262641	43166472	41588171	956891.57	63436.375	828304.438	4.40E+07	51.79142	7.03863E-06
55	G3GWC7	High affinity cationic amino acid transporter 1 OS=Cricetulus griseus GN=179_0	44070616	38252293	35870762.5		762092.813		3.94E+07	51.69697	NA
56	AOAO611D*	Aminopeptidase OS=Cricetulus griseus GN=H671_2g6297 PE=3 SV=1	102373075	90557614	101030910	1671866.75	1886236.19	2157753	9.80E+07	51.42915	6.80067E-06
57	AOAO611E*	DNA mismatch repair protein Mlh1-like protein OS=Cricetulus griseus GN=179_0	71535509.1	68461541	63214418	1507174.69	1141888.56		6.77E+07	51.14046	0.00011551
58	G3I516	Major facilitator superfamily domain-containing protein 1 OS=Cricetulus griseus GN=179_0	30962476.5	24330462	2674894			570780.438	2.74E+07	47.92726	NA
59	G3H177	Vesicular integral-membrane protein VIP36 OS=Cricetulus griseus GN=179_0	34517616.8	28675165	2851683.3	706860.938		552949	2.92E+07	46.41148	0.00177827
60	G3HNY7	Rho GTPase-activating protein 28 OS=Cricetulus griseus GN=179_0	21524194.1	19142333	16723751	415341.594			1.91E+07	46.0587	NA
61	AOAO611H*	Putative cleft lip and palate transmembrane protein 1 like protein OS=Cricetulus griseus GN=179_0	47626488.8	46510462	42452315.1	1118345.75	893454.063	940528.938	4.52E+07	45.92621	3.9807E-06
62	G3IDS7	Monocarboxylate transporter 1 OS=Cricetulus griseus GN=179_0	190735276	185726154	179387896	4372806.5	429285	3385678	1.84E+08	45.92262	7.43094E-07
63	AOAO611B*	Retinol OS=Cricetulus griseus GN=H671_3g10174 PE=4 SV=1	981379640	996032536	85236258	21414324.6	18693301	20080124.1	9.10E+08	45.35432	9.74759E-06

FIG. 11B

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64	G3GSS3	Midasin OS=Cricetulus griseus GN=179_000691 PE=4 SV=1	64306321	61333911	56796590	768569438	803723430	245921225	6.08E+07	1343835.042	45.25278	6.12849E-06
65	G3HKW4	Solute carrier family 12 member 4 OS=Cricetulus griseus GN=179_0	42371340.8	42441536	41322894	1247123.88		621722.313	4.20E+07	934423.0938	44.99595	2.25531E-06
66	G3IOX4	Epoxide hydrolase 1 OS=Cricetulus griseus GN=179_017016 PE=4	167856033	121879649	113258985	2655329.44	3402287.44	2952068.13	1.34E+08	3006581.667	44.67946	0.000747131
67	AOAO61HY	Phosphorylase b kinase regulatory subunit alpha, skeletal muscle	18903439.3	15494670	14123840.6	395654.656			1.62E+07	385654.6563	41.93903	NA
68	G3IE7	Extended synaptotagmin-2 OS=Cricetulus griseus GN=179_019435	410880522	387307794	369392403	10151124.1	7774195.19	9952632.06	3.89E+08	9292650.438	41.88035	3.06067E-06
69	AOAO61HT	Myeloid-associated differentiation marker-like protein OS=Cricetulus	284958748	271020035	26402873	7219608	6680710.5	5840187.5	2.73E+08	6580168.667	41.53894	8.53929E-07
70	G3IX5	Protein RER1 OS=Cricetulus griseus GN=179_017404 PE=4 SV=1	392725283	371689163	341851333	10847117.5	4412838	11632087.4	3.69E+08	8864013.625	41.13729	8.80634E-06
71	G3IMY2	Solute carrier family 12 member 7 OS=Cricetulus griseus GN=179_0	33120342	33706274	35051469	613094.063	1033994.06	838890.875	3.40E+07	828659.6667	40.98188	2.89604E-07
72	G3H4F5	Myosin-IXb OS=Cricetulus griseus GN=179_005156 PE=4 SV=1	272814967	265254266	236134655	5003540.75	9967611.81	4589332.81	2.58E+08	6488828.458	39.78339	1.20874E-05
73	G3GX5	Fanconi anemia group D2 protein-like OS=Cricetulus griseus GN=17	66929918.5	64116687	64938830.5	1861280.75	1354607.75	1839080.25	6.53E+07	1694656.25	38.75832	9.99794E-08
74	AOAO61IM	Abhydrolase domain-containing protein 16A OS=Cricetulus griseus	184868450	172667791	177316322	1968806.38	2566911.25	9341567.31	1.78E+08	4625761.646	38.54159	1.09168E-06

FIG. 11B (Cont.)

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Num- ber	Accession	Description	Novel Probe Enriched			Tryptic Digestion			Average of Novel	Average of Tryptic	Novel/Tryptic	p value
			Replicate 1	Replicate 2	Replicate 3	Replicate 1	Replicate 2	Replicate 3				
75	G3GS61	PRA1 family protein OS=Cricetulus griseus GN=I79_000373 PE=3 SV=1	55423808	56359214	43650201			1355371.25	5.18E+07	1345371.25	38.51062	NA
76	G3HT78	Gamma-tubulin complex component OS=Cricetulus griseus GN=I79_000373 PE=3 SV=1	25333324	22267518	2253680.6			609607.813	2.34E+07	609607.813	38.35057	NA
77	A0A0611G	Multidrug resistance-associated protein 1 OS=Cricetulus griseus GN=I79_000373 PE=3 SV=1	323828700	333754697	337517327	10053484	7826672.5	8775381	3.32E+08	8885179.167	37.33186	8.05616E-08
78	G3GT82	Prolyl 3-hydroxylase 2 OS=Cricetulus griseus GN=I79_000857 PE=4	41040488.5	36346673	35591301.8	850671.125	1174854.13		3.77E+07	1012762.625	37.18491	0.000236722
79	G3GXX4	Dolichyl-diphosphoglycerate-protein glycosyltransferase	7936480.5	8681037.5	14141100.5		275651.969		1.02E+07	275651.9688	37.07407	NA
80	G3H317	Neuron navigator 1 OS=Cricetulus griseus GN=I79_004834 PE=4 SV=1	34468610.8	30610592	25688745.9	899568.563	789461.625		3.03E+07	844015.0838	35.84764	0.001463832
81	G3HK30	Glycerol-3-phosphate acyltransferase 3 OS=Cricetulus griseus GN=I79_0009	16541166.3	15684646	14946246.3		444209.875		1.57E+07	444209.875	35.39773	NA
82	G3H25	Exocyst complex component 4 OS=Cricetulus griseus GN=I79_0009	20927558.5	16633646	16931416.5	341647.563	491196.906	715629.75	1.82E+07	516158.0729	35.19117	0.000110391
83	G3DL3	Interferon-inducible protein OS=Cricetulus griseus GN=I79_02179	196324103	204594930	193364176	5829411.31	5814874.5	5336637.25	1.98E+08	5680307.688	34.99711	2.79802E-07
84	G3HWF3	Autophagy-related protein 9 OS=Cricetulus griseus GN=I79_01531	25886056	25679232	23635288.5	721600.75	798523.125	642538.25	2.51E+07	720887.75	34.77223	2.27744E-06
85	G3HC98	DNA polymerase sigma OS=Cricetulus griseus GN=I79_008102 PE=1	16272520.3	18163825	14340107.5		470397.469		1.63E+07	470397.4688	34.564	NA
86	G3GYM8	Fatty acid amide hydrolase 1 OS=Cricetulus griseus GN=I79_00293	261841621	232044471	220809075	6938242.67	7441882.5	6381536.38	2.38E+08	8620487.182	34.42894	2.29452E-05
87	A0A0611EY	Exocyst complex component OS=Cricetulus griseus GN=H671_398	54182436.1	45105544	51844537	910223.5	1636307.38	1875028.88	5.04E+07	1473853.25	34.18082	2.88053E-05
88	G3H14	Golgin subfamily A member 5 OS=Cricetulus griseus GN=I79_0172	92045686.5	91124268	88041939.3	2785141.63	3524831	1829232.44	9.04E+07	2713068.354	33.32167	1.47515E-07
89	G3HQY6	Lipase OS=Cricetulus griseus GN=I79_013245 PE=3 SV=1	404324825	479720559	435586932	1316427.1	1327386.8	13759443.9	4.40E+08	13399059.25	32.82848	2.03948E-05
90	A0A0611N	ADP/ATP translocase 2-like protein OS=Cricetulus griseus GN=H671_398	96480928.3	96898750	88854803	1644265.88	5383956.75	1543808.19	9.31E+07	2857343.804	32.57507	9.60957E-06
91	A0A061U*	WD repeat-containing protein 7 isoform 1 OS=Cricetulus griseus GN=I79_0006	29821949.8	3167736	27154476.3	1019402.94	946448.813	764410.375	2.95E+07	910087.375	32.44896	1.2549E-05
92	A0A061IK*	Phosphate carrier protein OS=Cricetulus griseus GN=H671_163498	96435209.5	96328735	90187136	2732855	2389757.5	3069288.25	9.43E+07	2914000.25	32.36697	7.82914E-07
93	G3GSM5	Transferrin receptor protein 1 OS=Cricetulus griseus GN=I79_0006	89464512.6	58580558	80394933.2	3576785.72	1115877.06	3305395.41	8.52E+07	2667019.398	31.96078	3.65953E-06
94	G3S680	Carnitine O-palmitoyltransferase 1, liver isoform OS=Cricetulus griseus GN=I79_0006	160673609	159123421	14224711	4772657	4986020.88	4734493	1.54E+08	4831056.968	31.87858	7.30767E-06
95	G3DR5	Telomere-associated protein RIF1 OS=Cricetulus griseus GN=I79_0	306663542	310411255	293249193	10314468.6	8496798.84	9878776.31	3.03E+08	9663347.917	31.69761	3.79332E-07
96	G3GS82	Multidrug resistance-associated protein 4 (Fragment) OS=Cricetulus g	224742302	199820773	207774100	7824638	5733382.5	6602247.75	2.11E+08	6719889.417	31.36645	5.07266E-05

FIG. 11C

97	A0A06111*	Vitamin K-dependent protein 5 OS=Cricetulus griseus GN=H671_4	145068905	128055755	121350073	504269563	415827238	338277556	1.31E+08	4194897854	313466	2.80541E-05
98	G3HSZ8	Atlastin-2 (Fragment) OS=Cricetulus griseus GN=I79_013998 PE=4	814813574	76366347	753232615	363343675	306558263	7570845	7.77E+07	2485704625	3126826	1.7987E-06
99	M5AJ86	Acetyl-CoA carboxylase 1 OS=Cricetulus griseus GN=Acaca PE=151	19085E+10	1.77E+10	17337E+10	644491059	580247950	587021387	1.80E+10	603920132.1	2987169	2.6053E-06
100	A0A0611A*	Ubiquitin carboxyl-terminal hydrolase 25 OS=Cricetulus griseus GN=I79	27794472	26013474	28223336	9216015			2.73E+07	9216015	2966983	NA

FIG. 11C (Cont.)

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Num- ber	Accession	Description	FP-biotin Enriched			Tryptic Digestion			Average of FP-biotin	Average of Tryptic	FP- biotin/Tryptic	p value
			Replicate 1	Replicate 2	Replicate 3	Replicate 1	Replicate 2	Replicate 3				
1	G3GV63	Prolyl endopeptidase-like OS=Cricetulus griseus GN=179_001	147837503	145118041	148703497		18338.65	40635.7773	1.47E-08	29487.2139	4993.33886	9.73437E-07
2	G3I7H8	Methylenetetrahydrofolate synthetase subunit alpha, mitochondrial	401628886	384495747	409431792	1195123.5	1104109.5		3.99E-08	1149816.5	346.6536959	1.50719E-05
3	G3HKV9	Group XV phospholipase A2 OS=Cricetulus griseus GN=179_0	906097367	917469224	920448684	4569738.88	5030954	5328866.56	9.15E-08	4979186.48	183.690364	1.60339E-09
4	G3H8F2	Acylamino acid-releasing enzyme OS=Cricetulus griseus GN=179_0	9300336065	8.63E+09	9.59E+09	71121899.5	65581130	72649834.9	9.17E-09	69787554.8	131.4464724	2.83806E-06
5	G3H8H1	Arylamidase deacylase-like 1 OS=Cricetulus griseus GN=179_0	344253219	32979715	357390960	2424664	3062055.5	2802361	3.45E-08	2696360.17	127.9037704	5.40997E-07
6	G3IY8	Dedicator of cytokinesis protein 8 OS=Cricetulus griseus GN=179_0	34038688	37238236	32312330	321794.59			3.45E-07	321794.594	107.3037024	NA
7	G3J4L6	Pyruvate carboxylase OS=Cricetulus griseus GN=PC PE=2 SV=1	1804498536	1.817E+09	1.891E+09	21854274.1	16529109	16047602.7	1.84E-09	18143662.1	101.2888302	1.48405E-07
8	A0A061IKA1	Lipoprotein lipase OS=Cricetulus griseus GN=H671_102493	443088009	447854928	471086427	3347565.22	5462772.9	5824535.31	4.54E-08	4811624.48	94.35547661	4.17967E-07
9	G3IY8	Abhydrolase domain-containing protein 11 OS=Cricetulus griseus	126294098	120025867	127615664			1328292.13	1.23E-08	1328292.13	92.5814489	NA
10	G3I368	Prolyl endopeptidase OS=Cricetulus griseus GN=179_017687	1558861+10	1.575E+10	1.661E+10	218078876	208611803	212130806	1.60E-01	212940528	75.05640135	4.92323E-07
11	G3IEN9	Keratin, type II cytoskeletal 71 OS=Cricetulus griseus GN=179_0	115152359	110453376	1558653.4			1029188.63	7.57E-07	1029188.63	73.57394059	NA
12	A0A061IAW7	Dipeptidyl-peptidase 9 OS=Cricetulus griseus GN=H671_5g1	5182145701	5.803E+09	6.145E+09	85057164.2	67785514	81784013.1	5.71E-09	78208897.2	73.10193.38	1.8511E-05
13	G3H1D5	Carboxypeptidase OS=Cricetulus griseus GN=179_003360 PE=1	1594970760	1.407E+09	1.746E+09	25959014.1	22203087	24044037.6	1.58E-09	24069716.3	65.61378752	4.57633E-05
14	A0A061IL50	Monooxygenase-like protein ABHD6-like protein OS=Cricetulus griseus	181553144	186055559	199052812	1848989.5	5281683.1	2071162.06	1.89E-08	3067271.56	61.58153868	2.06891E-06
15	G3HSV5	Transcription elongation factor a protein 1 OS=Cricetulus griseus	1470180736	1.509E+09	1.509E+09	30781506	29611069	29499585.5	1.51E-09	29964053	50.36661457	1.65202E-07
16	G3I4H4	Prostaglandin reductase 2 OS=Cricetulus griseus GN=179_017	801469418	767017446	839401599	18433026.3	16972020	17039416.9	8.03E-08	17481467.6	45.91309242	1.50175E-06
17	G3I80	Acyl-protein thioesterase 2 OS=Cricetulus griseus GN=179_0	4607323059	4.679E+09	4.551E+09	108668424	10082165	967994.76	4.61E-09	101848022	45.29002428	1.38571E-08
18	G3H83	Abhydrolase domain-containing protein 10, mitochondrial	102545985	99635468	110973296	2094037.63	2982308.8	2779964.75	1.04E-08	2618770.38	39.86027845	3.75502E-06
19	M6A186	Acetyl-CoA carboxylase 1 OS=Cricetulus griseus GN=Acaca PE=1	2.1753e+10	2.146e+10	2.278E+10	644491059	580247950	587071387	2.20E-10	603920132	36.42306721	3.6577E-07
20	G3GYM8	Fatty acid amide hydrolase 1 OS=Cricetulus griseus GN=179_0	188623179	188703320	209358026	6938242.67	7441682.5	6381536.38	1.96E-08	6920487.18	28.25824783	5.33609E-06
21	G3IFN9	Tripeptidyl-peptidase 2 OS=Cricetulus griseus GN=179_0225	2051083431	206978534	203854775	4435121.06	10420631	10196670.4	2.05E-08	8337540.69	24.62423725	4.28502E-08
22	G3H52	R3H domain-containing protein C19orf22 OS=Cricetulus griseus	807765303	101635113	96621118	5392252	3710548.3	3486830	9.30E-07	4188910.08	22.19878875	7.41487E-05
23	G3IX5	Protein RER1 OS=Cricetulus griseus GN=179_017404 PE=4 SV=1	177113649	190673874	203868272	10847117.5	4412836	11632087.4	1.91E-08	8964013.63	21.33619373	1.4967E-05
24	G3H8V5	Carboxypeptidase OS=Cricetulus griseus GN=179_008816 PE=1	1699449880	2.253E+09	1.678E+09	115280256	90715650	77650979.8	1.88E-09	94549662.5	19.85149381	0.00350255
25	A0A061ICV3	Pantetheinase OS=Cricetulus griseus GN=H671_2q6527 PE=4	150054318	147378820	159603885	8227840.88	7734309.8	7441384	1.52E-08	7801178.21	19.52853831	1.30666E-06
26	G3HWW4	Neuropathy target esterase OS=Cricetulus griseus GN=179_0	60324667.1	65342155	63651798		6120618.2	383102.666	6.31E-07	3241860.42	19.48604679	0.000120236
27	G3GWL0	Syntaxin-18 OS=Cricetulus griseus GN=179_002223 PE=3 SV=1	122431232	123624688	106877728	6172349	5721747	6342675	1.18E-08	6078923.67	19.35285846	1.61829E-05
28	A0A061HZ94	Peptidyl-prolyl cis-trans isomerase OS=Cricetulus griseus GN=179_0	479199925	222496806	471590874	24774277	24204410	18476032	3.91E-08	22484906.2	17.39370843	0.00589463
29	A0A061HU22	Platelet-activating factor acetylhydrolase 1B subunit gamma	1807690340	2.186E+09	1.878E+09	116721461	112531465	113716837	1.95E-09	113716837	17.12764843	3.38571E-05
30	G3H8V0	Nuclear transcription factor y subunit gamma OS=Cricetulus griseus	10955560	10293037	11748650	754129.75	744848.63	690160.813	1.10E-07	729719.729	15.07576388	8.53374E-06
31	A0A061BM4	Glycogen synthase kinase-3 beta-like isoform 3 OS=Cricetulus griseus	33983207.3	33419579	30641818	4545308	1376407.9	1474381.38	3.27E-07	2465359.08	13.25629798	1.63615E-05
32	G3HGS2	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Ord	1783911698	1.833E+09	1.87E+09	135944113	137922652	142236784	1.83E-09	139807850	13.1960654	1.44922E-07

FIG. 12A

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33	A0A061ER6	Tripeptidyl-peptidase 2 isoform 1 OS=Cricetulus griseus GN=7	9374517732	9.606E+09	9.898E+09	779679686	713278975	697363682	9.63E-09	730107448	13.18469914	2.65148E-07
34	G3HMO	Protein phosphatase methyltransferase 1 OS=Cricetulus griseus	195672027	191358530	193630080	18683559.9	14258041	15610194.3	1.94E-08	16183941.6	11.95960477	3.2318E-08
35	G3-NG2	Acyl-coenzyme A thioesterase 2, mitochondrial OS=Cricetulus	249183402	234383511	266891506	20840998	28886528	24495102.8	2.50E-08	24740876.3	10.109594	1.00928E-05
36	A0A061577	Biotin-protein ligase OS=Cricetulus griseus GN=H671_4g120	3105639.31	3522684.2	3739429.7		414188.03	346621.313	3.46E-06	380404.672	9.084845624	0.00052179
37	A0A061IH-N3	Platelet-activating factor acetylhydrolase 2, cytoplasmic-like	1130298270	1.094E+09	1.185E+09	137312550	130801724	121375231	1.14E-09	128829835	8.754202624	1.48435E-06
38	A0A061IPK9	tRNA (guanine-N(7))-methyltransferase OS=Cricetulus griseus	15165867	17684134	16479759	2154178	1919257.4	2351706.75	1.64E-07	2141714.04	7.677613824	2.08836E-05
39	G3GXD7	Fatty-acid synthase OS=Cricetulus griseus GN=79_002427 Pf	2.711E+10	2.685E+10	2.736E+10	368773205	3.514E+09	3428616867	2.71E-10	3543575087	7.648876474	7.26465E-09
40	A0A061I2M3	Neuropathy target esterase (fragment) OS=Cricetulus griseus	107570347	111536044	113304673	15952948.3	16285786	12886819	1.11E-08	14975084.4	7.39920292	6.23488E-07
41	G3JIG1	Carboxylic ester hydrolase OS=Cricetulus griseus GN=79_12	5592730	4804109.5	5633936.2		764125.06		5.34E-06	764125.063	6.993065501	NA
42	A0A061IDX5	Geranylgeranyl transferase type-2 subunit beta OS=Cricetulus	12589231.6	11928722	13582439		1978541.3		1.27E-07	1978541.25	6.422306049	NA

FIG. 12A (Cont.)

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Num- ber	Accession	Description	FP-biotin Enriched			Tryptic Digestion			Average of FP-biotin	Average of tryptic	FP- biotin/tryptic	p value
			Replicate 1	Replicate 2	Replicate 3	Replicate 1	Replicate 2	Replicate 3				
43	A0A061H850	Golgi membrane protein 1 (Fragment) OS=Cricetulus griseus	3115825.75	2888776.8	3346902.3		497421.53		3.11E+06	497421.531	6.246616578	NA
44	G3N82	Carbamate O-palmitoyltransferase 1, liver isoform OS=Cricetulus griseus	6166615.92	5720520.5	6486894.6	111745.75	918623.25	993885.625	6.12E+06	1010084.88	6.063461082	1.2028E-05
45	G3H19	Isomaltase-hydrolyzing esterase 1-like OS=Cricetulus griseus	129970020	127301346	140003738	23071290.6	22026680	21219081.6	1.32E+08	22103677.4	5.986578058	4.72139E-06
46	G3H1F5	Phosphatidylinositol transfer protein alpha isoform OS=Cricetulus griseus	394989436	431626142	416083977	90997062.9	88826285	88259980.3	4.14E+08	89691442.8	4.618424816	3.44923E-06
47	G3HCT9	Testis-expressed sequence 2 protein OS=Cricetulus griseus	70102304	71958456	71782808	19075203	16409155	17207575	7.13E+07	17563977.7	4.058373945	3.41104E-07
48	G3HRJ7	Catenin delta-1 OS=Cricetulus griseus GN=H671_2g589	200703599	246598786	230090721	54780757.3	57781180	63849292.4	2.26E+08	58803739.1	3.839851864	0.000129416
49	G3H3F6	Kynurenine formamidase OS=Cricetulus griseus GN=AF-MID	274530244	264679293	274372163	76751486	71944050	68753518	2.71E+08	72483018	3.741481902	4.92192E-07
50	G3GVW2	Putative hydrolase RBBP9 OS=Cricetulus griseus GN=I79_001	47613620.9	44155830	51820401	12684029.8	12915833	12947624	4.79E+07	12849162.3	3.725014599	4.70076E-05
51	G33W4	S-formylglutathione hydrolase OS=Cricetulus griseus GN=I79	954472754	919430945	976720941	277757380	251039940	241350070	9.50E+08	256915797	3.698520006	2.00014E-06
52	G3HFN9	RNA polymerase I-specific transcription initiation factor RRN	2476729	2589845.5	2498890.5	720389.875			2.52E+06	720389.875	3.491477208	NA
53	Q8U293	Gap junction protein OS=Cricetulus griseus GN=H671_2g589	1421328.25	1566784.5	1274485.5		417327.91		1.42E+06	417327.906	3.404675465	NA
54	G3N86	Dipeptidyl-peptidase 2 OS=Cricetulus griseus GN=I79_02559	69847961	69772604	79263781	22632169.3	22278160	22061771.9	7.30E+07	22324033.7	3.268291486	4.40976E-05
55	G3DW2	Unclassified protein C13orf27-like OS=Cricetulus griseus	34630183.9	33779853	35816728	1140412.9	10447429	13220802.5	3.47E+07	11602881.5	2.994272457	1.12456E-05
56	G3H6X4	Splicing factor 3B subunit 5 OS=Cricetulus griseus GN=I79_00	191979843	200296459	210808021	77104415	72016007	69540367.3	2.01E+08	72888929.7	2.758072562	1.31555E-05
57	G3905	E3 ubiquitin-protein ligase UBR4 OS=Cricetulus griseus GN=	277835027	288639634	348081195	117087516	117407664	117136063	2.98E+08	117208748	2.544063163	0.000979201
58	A0A061JUA4	ATP-dependent RNA helicase DHX29 OS=Cricetulus griseus	66766116.1	62022268	64324304	23300903.7	27157601	26339261.6	6.44E+07	25629255.5	2.511617869	1.33139E-05
59	G3GRE5	Lysophospholipase-like protein 1 OS=Cricetulus griseus GN=	9221533.25	4673589.3	10635066	2702064.44	3959953.2	3668720.38	8.18E+06	3443579.33	2.374485567	0.0303030536
60	A0A061HQ5	Lysophosphatidic acid phosphatase type 8 OS=Cricetulus griseus	2022479.31	1903331.6	831960.63		596884.56	808181.313	1.60E+06	701432.938	2.283312366	0.085917312
61	A0A061H514	DNA mismatch repair protein Mlh1-like protein OS=Cricetulus griseus	2860109.75	2541466.5	3391314.3	1507174.69	1141888.6		2.93E+06	1324531.63	2.212830139	0.0055471
62	G3G772	Coatomer subunit gamma OS=Cricetulus griseus GN=I79_003	102637773	103504594	98244698	49725018.7	46941015	47374903.5	1.01E+08	48013645.6	2.113196317	4.21303E-06
63	A0A061IFK2	Anoctamin OS=Cricetulus griseus GN=H671_2g5570 PE=3 SV=	9529213.94	9360241.9	8420667.9	3913351.25	5155688.5	3968191	9.10E+06	4342410.58	2.086387338	0.000435303
64	G3SD6	UPF0368 protein C11orf67-like OS=Cricetulus griseus GN=I79	4556008.06	4287474.1	3288072		1954381.9		4.04E+06	1954381.98	2.065708256	NA
65	G3MZ0	Very low-density lipoprotein receptor OS=Cricetulus griseus	1378503.5	1832372.6	1513610.1	467254.438	1080665		1.57E+06	773969.703	2.034766404	0.03422615
66	G3H50	Carbamate O-palmitoyltransferase 1, liver isoform OS=Cricetulus g	8534028.97	8997283.8	11429834	4772657	4986020.9	4734493	9.62E+06	4831056.96	1.991361813	0.003171936
67	G3D45	Integrin-linked kinase-associated serine/threonine phospho	8391544.78	8643541.5	10088025	5487355.19	4398674.6	4247579.75	9.04E+06	4711203.17	1.919758118	0.001390751
68	G3DS7	Monocarboxylate transporter 1 OS=Cricetulus griseus GN=I7	7671867.5	6928372.5	7702379.2	4372806.5	4283296	3385678	7.44E+06	4017259.83	1.851064336	0.00154398
69	G3IS74	Palatin-like phospholipase domain-containing protein 7 OS	27061582.3	24876032	27960399	15913157.3	15077483	12433069	2.66E+07	14472909.7	1.940634579	0.00047357
70	A0A061HW32	Hormone-sensitive lipase-like protein (Fragment) OS=Cricetulus	67342559.5	71105717	71963482	47091980	41610616	41614192	7.21E+07	43438869.3	1.68066138	0.00051542
71	G3HM2	Unclassified protein C20orf135-like OS=Cricetulus griseus	203303543	189983116	192059873	120539873	120113440	11411189	1.95E+08	116254867	1.049994373	3.85279E-05
72	G3H5Y9	Tetraspanin OS=Cricetulus griseus-like GN=H671_2g15897 PE=	2048085.19	2384745.9	1908515.2	1067127.38	1628884.1	1175578.88	2.1E+06	1294863.46	1.632686295	0.009792958
73	G3HQ10	Proteasome subunit beta type OS=Cricetulus griseus GN=H6	120502028	129256617	108723825	77261470.5	73080838	72730821	1.19E+08	74357709.9	1.602534424	0.000787108
74	G3H1F9	Chromosome-associated kinesin KIF-4 OS=Cricetulus griseus	16524810	17008904	18236948	10624059.8	12477315	10299637.8	1.73E+07	11133737.5	1.551759889	0.001016176

FIG. 12B

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Num- ber	Accession	Description	FP-biotin Enriched			FP-biotin Enriched			Average of FP-biotin	Average of Tryptic	FP- biotin/Tryptic	p value
			Replicate 1	Replicate 2	Replicate 3	Replicate 1	Replicate 2	Replicate 3				
75	G3IDL3	Interferon-inducible protein OS=Cricetulus griseus GN=I79	8573473.41	8538602	9001667.4	5829411.31	5814874.5	5338637.25	8.70E+06	5680307.68	1.537828227	7.89638E-05
76	G3H6LB	Centrosomal protein of 170 kDa OS=Cricetulus griseus GN=I79	1883661.38	1883682	1980315.9	1378638.5	1171862.3		1.92E+06	1275200.38	1.507647834	0.002651896
77	G3H0W0	Cyclin-D1-binding protein 1 OS=Cricetulus griseus GN=I79_0	253217.5	2582117.3	2335094.3	1452510.75	1964665.1		2.48E+06	1708587.94	1.453321548	0.018188606
78	A0A061I210	ATR-interacting protein OS=Cricetulus griseus GN=H671_4q2	22881277.3	24884995	28057757	6577050.5	23539933	22929419.5	2.45E+07	17682134.4	1.38791745	0.145492782
79	Q6MRU0	Bone marrow stromal antigen 2 OS=Cricetulus griseus GN=B	11768869.3	11488738	12026222	8754698	8913751.5	8038790.5	1.18E+07	8568079.33	1.372528864	0.000252845
80	G3H5E5	Ras-related protein Ral-B OS=Cricetulus griseus GN=I79_005	6267067.88	5333126.4	6215387.4	4874607.13	3941640.6	4304711.13	5.94E+06	4373652.98	1.357795706	0.009184381
81	A0A061UC4	Glutathione S-transferase Mu 1-like protein OS=Cricetulus griseus	2981737336	2.99E+09	3.06E+09	2356742884	2.22E+09	2197071977	3.00E+09	2258422847	1.330180141	0.000103107
82	G3IGD1	Transmembrane protein 33 OS=Cricetulus griseus GN=I79_0	975226797	1265544.7	1769089	1004829.75	1037287.2	1112601.38	1.34E+06	1051572.77	1.271067704	0.145134742
83	G3GZM6	Rho guanine nucleotide exchange factor 10 OS=Cricetulus griseus	1108108	1143105.9	1244804.1		945542		1.16E+06	945542	1.231680877	NA
84	G3ID64	Vacuolar protein sorting-associated protein 13A (Fragment)	4590164.5	4386446.5	4244804	8913052.44	3477332.8	4257910.63	4.41E+06	3882765.27	1.135051446	0.050543542
85	A0A061BK7	Tetraspanin OS=Cricetulus griseus GN=H671_3g9876 PE=3 SV=1	1097523.25	913466.56	815190	956891.5	763436.38	828304.438	9.42E+06	849544.104	1.108900565	0.204458956
86	G3H10	Cleavage and polyadenylation specificity factor subunit 3 OS	44292917.8	33040334	32065165	35522928.1	36192733	31154778.1	3.65E+07	34290146.5	1.063168612	0.317416544
87	G3GS70	Importin-5 OS=Cricetulus griseus GN=I79_000383 PE=4 SV=1	681899461	68762963	750128001	67338180.5	885794249	680042262	7.07E+08	673086108	1.049751812	0.110224898
88	G3H177	Vascular integral-membrane protein VIP36 OS=Cricetulus griseus	917851.5	471322.03	465884.59	706860.938		552949	6.18E+05	628804.968	0.981660312	0.478980372
89	G3HRD9	Proteasome subunit beta type OS=Cricetulus griseus GN=I79	155960880	164549919	178408744	163685808	161044890	163708339	1.66E+08	169479879	0.981275863	0.379806168
90	G3IIN9	Retinoblastoma-binding protein 6 OS=Cricetulus griseus GN=I79	5270705.13	4883401	5230876.7	6719919.13	4778387.3	4248704.25	5.13E+06	5249003.54	0.977009745	0.440858183
91	G3HXN7	Beta-hexosaminidase OS=Cricetulus griseus GN=I79_015800	4348598.44	4985250.8	5452836.4	5257201	5009891.1	5142474.75	4.93E+06	5136522.28	0.959578273	0.280492324
92	G3IBQ9	Phenylalanine-tyrosine synthetase beta chain OS=Cricetulus griseus	85371423.5	89217087	94082894	95985613.8	93489227	93948140.5	8.96E+07	94474327	0.947952081	0.067702736
93	G3HLK6	G patch domain-containing protein 8 OS=Cricetulus griseus GN=I79_003679	1443134.84	1388580.1	1438625.6	2247583.88	712142.25	1550785.19	1.42E+06	1503503.77	0.942319012	0.427415335
94	G3H0L7	Squalene synthetase OS=Cricetulus griseus GN=I79_003679	367026.031	435203.68	376393.66	320629.031	542954.75		3.93E+05	431791.891	0.903866908	0.343003235
95	G3HMY0	Hydroxymethylglutaryl-CoA synthetase OS=Cricetulus griseus GN=I79_0	616256157	613468806	623230144	700809417	679764496	668995456	6.18E+08	683323128	0.903932786	0.001199108
96	G3IFJ6	Glutathione S-transferase A6 OS=Cricetulus griseus GN=I79_0	13992867.1	13252444	12502564	17082442.5	14965842	13717039	1.32E+07	15258474.3	0.868323505	0.057512025
97	A0A061IP05	Signal recognition particle protein OS=Cricetulus griseus GN=I79	28755307.3	27323221	32409563	35656109.8	33012258	34603575.8	2.95E+07	34423980.8	0.958942163	0.022031039
98	A0A061KW4	valyl-RNA synthetase-like protein OS=Cricetulus griseus GN=I79	774637.563	533634.13	687703.38	760815.125	837561.56	791637.25	6.65E+05	798671.313	0.835131139	0.075083147
99	Q8MHC2	MHC class I antigen Hm1-C4 OS=Cricetulus griseus PE=2 SV=	4443649.31	4369410.1	4125527.1	6235299.75	3766038.6	5557306.25	4.31E+06	5186214.88	0.831601133	0.152448376
100	A0A061I6D9	MAP kinase-activated protein kinase 2-like protein OS=Cricetulus g	3079090	2755929	2219907.5	4336157.25	2708236.5	2708848	2.68E+06	3250353.92	0.828056352	0.198956255

FIG. 12C

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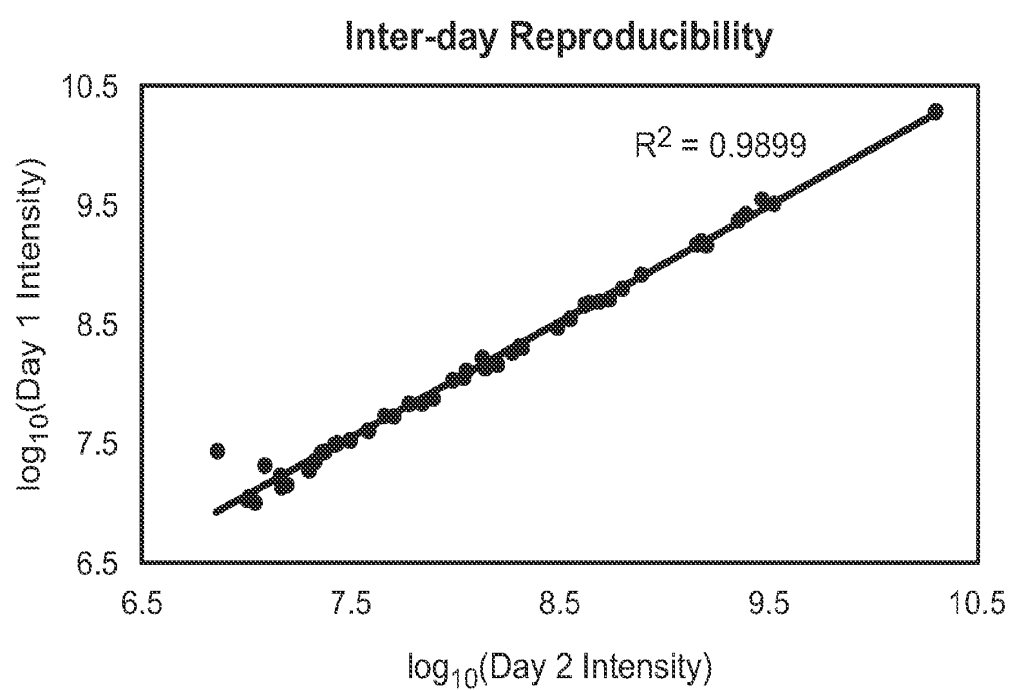


FIG. 13

Spiked Amount/ppm	Lipase Name	Novel Probe						FP-Biotin					
		Replicate 1		Replicate 2		Replicate 3		Replicate 1		Replicate 2		Replicate 3	
		PSM	Unique peptides	PSM	Unique peptides	PSM	Unique peptides	PSM	Unique peptides	PSM	Unique peptides	PSM	Unique peptides
2	LAL	14**	5**	16	6	17	7	ND	ND	ND	ND	ND	ND
	LPL	15**	7**	16	7	14	7	2	2	4	3	5	2
	PLA2G7	39**	14**	37	17	29	12	2	2	5	2	3	1
0.4	LAL	6*	4**	13	4	9	4	ND	ND	ND	ND	ND	ND
	LPL	9**	4**	8	4	10	5	3	2	ND	ND	3	2
	PLA2G7	8*	5**	18	11	12	6	2	2	3	2	3	2
0.08	LAL	6**	3**	5	2	5	2	ND	ND	ND	ND	ND	ND
	LPL	5**	2**	5	2	5	2	ND	ND	ND	ND	ND	ND
	PLA2G7	9**	6**	6	4	7	5	ND	ND	ND	ND	ND	ND
0.016	LAL	3	2	3	2	ND	ND	ND	ND	ND	ND	ND	ND
	LPL	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
	PLA2G7	2	2	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
0	LAL	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
	LPL	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
	PLA2G7	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND



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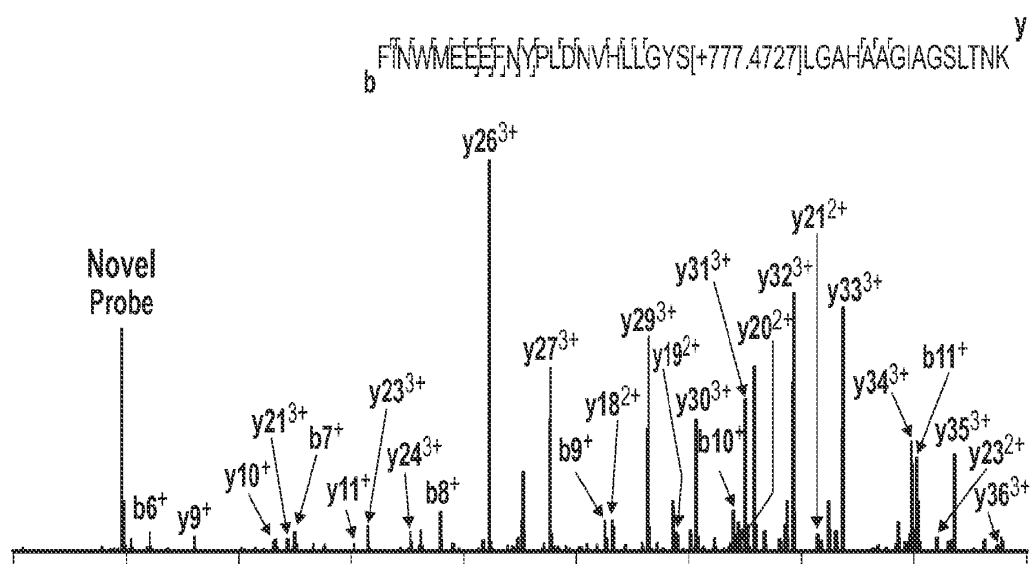


FIG. 15